David Ellinghaus

List of Publications by Year
in descending order

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99
papers

24,055
citations

50566
48
h-index

35168
102
g-index

116
all docs

116
docs citations

116
times ranked

46318
citing authors

#	Article	IF	Citations
1	Elucidation of the genetic causes of bicuspid aortic valve disease. Cardiovascular Research, 2023, 119, 857-866.	1.8	11
2	Cross-tissue transcriptome-wide association studies identify susceptibility genes shared between schizophrenia and inflammatory bowel disease. Communications Biology, 2022, 5, 80.	2.0	12
3	Local genetic variation of inflammatory bowel disease in Basque population and its effect in risk prediction. Scientific Reports, 2022, 12, 3386.	1.6	6
4	How genetic risk contributes to autoimmune liver disease. Seminars in Immunopathology, 2022, 44, 397-410.	2.8	11
5	Novel genes and sex differences in COVID-19 severity. Human Molecular Genetics, 2022, 31, 3789-3806.	1.4	38
6	Detailed stratified GWAS analysis for severe COVID-19 in four European populations. Human Molecular Genetics, 2022, 31, 3945-3966.	1.4	46
7	Shared Genetics of Multiple System Atrophy and Inflammatory Bowel Disease. Movement Disorders, 2021, 36, 449-459.	2.2	16
8	Genome-wide study of a Neolithic Wartberg grave community reveals distinct HLA variation and hunter-gatherer ancestry. Communications Biology, 2021, 4, 113.	2.0	20
9	Exome-Wide Association Study Identifies <i>FN3KRP</i> and <i>PGP</i> as New Candidate Longevity Genes. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2021, 76, 786-795.	1.7	14
10	Transethnic analysis of the human leukocyte antigen region for ulcerative colitis reveals not only shared but also ethnicity-specific disease associations. Human Molecular Genetics, 2021, 30, 356-369.	1.4	19
11	Genome-wide analysis of 944 133 individuals provides insights into the etiology of haemorrhoidal disease. Gut, 2021, 70, 1538-1549.	6.1	21
12	BIGwas: Single-command quality control and association testing for multi-cohort and biobank-scale GWAS/PheWAS data. GigaScience, 2021, 10, .	3.3	13
13	Age-dependent impact of the major common genetic risk factor for COVID-19 on severity and mortality. Journal of Clinical Investigation, 2021, 131, .	3.9	72
14	SNPInt-GPU: Tool for Epistasis Testing with Multiple Methods and GPU Acceleration. Methods in Molecular Biology, 2021, 2212, 17-35.	0.4	2
15	Genetic background of high blood pressure is associated with reduced mortality in premature neonates. Archives of Disease in Childhood: Fetal and Neonatal Edition, 2020, 105, 184-189.	1.4	7
16	Protein-coding variants contribute to the risk of atopic dermatitis and skin-specific gene expression. Journal of Allergy and Clinical Immunology, 2020, 145, 1208-1218.	1.5	29
17	Genetic risk factors predict disease progression in Crohnâ€™s disease patients of the Swiss inflammatory bowel disease cohort. Therapeutic Advances in Gastroenterology, 2020, 13, 175628482095925.	1.4	7
18	Whole-genome sequencing of a sporadic primary immunodeficiency cohort. Nature, 2020, 583, 90-95.	13.7	148

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19	Genomewide Association Study of Severe Covid-19 with Respiratory Failure. New England Journal of Medicine, 2020, 383, 1522-1534.	13.9	1,548
20	A benchmark of hemoglobin blocking during library preparation for mRNA-Sequencing of human blood samples. Scientific Reports, 2020, 10, 5630.	1.6	12
21	Reference-Based Haplotype Phasing with FPGAs. Lecture Notes in Computer Science, 2020, , 481-495.	1.0	3
22	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
23	Missense variants in NOX1 and p22phox in a case of very-early-onset inflammatory bowel disease are functionally linked to NOD2. Journal of Physical Education and Sports Management, 2019, 5, a002428.	0.5	13
24	VarWatchâ€"A stand-alone software tool for variant matching. PLoS ONE, 2019, 14, e0215618.	1.1	0
25	ZNF133 is associated with infliximab responsiveness in patients with inflammatory bowel diseases. Journal of Gastroenterology and Hepatology (Australia), 2019, 34, 1727-1735.	1.4	9
26	Construction and benchmarking of a multi-ethnic reference panel for the imputation of HLA class I and II alleles. Human Molecular Genetics, 2019, 28, 2078-2092.	1.4	48
27	1000Ã— faster than PLINK: Combined FPGA and GPU accelerators for logistic regression-based detection of epistasis. Journal of Computational Science, 2019, 30, 183-193.	1.5	19
28	Genetic association analysis identifies variants associated with disease progression in primary sclerosing cholangitis. Gut, 2018, 67, 1517-1524.	6.1	42
29	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. BMJ Open, 2018, 8, e018166.	0.8	15
30	RNA based individualized drug selection in breast cancer patients without patient-matched normal tissue. Oncotarget, 2018, 9, 32362-32372.	0.8	1
31	1,000x Faster Than PLINK: Genome-Wide Epistasis Detection with Logistic Regression Using Combined FPGA and GPU Accelerators. Lecture Notes in Computer Science, 2018, , 368-381.	1.0	1
32	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
33	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	3.4	376
34	Opportunities and challenges of whole-genome and -exome sequencing. BMC Genetics, 2017, 18, 14.	2.7	160
35	Genome-wide association analysis for chronic venous disease identifies EFEMP1 and KCNH8 as susceptibility loci. Scientific Reports, 2017, 7, 45652.	1.6	48
36	Genetic Factors Interact With Tobacco Smoke to Modify Risk for Inflammatory Bowel Disease in Humans and Mice. Gastroenterology, 2017, 153, 550-565.	0.6	68

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37	Genome-wide Pleiotropy Between Parkinson Disease and Autoimmune Diseases. JAMA Neurology, 2017, 74, 780.	4.5	245
38	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
39	Microbiomarkers in inflammatory bowel diseases: caveats come with caviar. Gut, 2017, 66, 1734-1738.	6.1	47
40	Fast Genome-Wide Third-order SNP Interaction Tests with Information Gain on a Low-cost Heterogeneous Parallel FPGA-GPU Computing Architecture. Procedia Computer Science, 2017, 108, 596-605.	1.2	13
41	LitDB - Keeping Track of Research Papers From Your Institute Made Simple. Source Code for Biology and Medicine, 2017, 12, 5.	1.7	0
42	Exome-wide association study reveals novel psoriasis susceptibility locus at TNFSF15 and rare protective alleles in genes contributing to type I IFN signalling. Human Molecular Genetics, 2017, 26, 4301-4313.	1.4	41
43	Genetic association with B-cell acute lymphoblastic leukemia in allogeneic transplant patients differs by age and sex. Blood Advances, 2017, 1, 1717-1728.	2.5	15
44	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. Nutrients, 2017, 9, 499.	1.7	24
45	Male-specific association between MT-ND4 11719 A/G polymorphism and ulcerative colitis: a mitochondria-wide genetic association study. BMC Gastroenterology, 2016, 16, 118.	0.8	17
46	Four Susceptibility Loci for Gallstone Disease Identified in a Meta-analysis of Genome-Wide Association Studies. Gastroenterology, 2016, 151, 351-363.e28.	0.6	74
47	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
48	Immunochip analysis identifies association of the <i> <scp>RAD</scp> 50/ <scp>IL</scp> 13 </i> region with human longevity. Aging Cell, 2016, 15, 585-588.	3.0	20
49	A Promoter Variant Within the Aryl Hydrocarbon Receptor Gene Is Associated with an Epithelial Barrier Defect in Smokers with CrohnÊ¼s Disease. Inflammatory Bowel Diseases, 2016, 22, 2356-2368.	0.9	12
50	Haplotype synthesis analysis reveals functional variants underlying known genome-wide associated susceptibility loci. Bioinformatics, 2016, 32, 2136-2142.	1.8	2
51	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	5.8	412
52	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
53	Pooled Resequencing of 122 Ulcerative Colitis Genes in a Large Dutch Cohort Suggests Population-Specific Associations of Rare Variants in MUC2. PLoS ONE, 2016, 11, e0159609.	1.1	21
54	Identification of Immune-Relevant Factors Conferring Sarcoidosis Genetic Risk. American Journal of Respiratory and Critical Care Medicine, 2015, 192, 727-736.	2.5	94

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55	The genetics of Crohnâ€™s disease and ulcerative colitis â€“<i>status quo</i>and beyond. Scandinavian Journal of Gastroenterology, 2015, 50, 13-23.	0.6	71
56	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
57	Parallelizing Epistasis Detection in GWAS on FPGA and GPU-Accelerated Computing Systems. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 982-994.	1.9	20
58	Vy-PER: eliminating false positive detection of virus integration events in next generation sequencing data. Scientific Reports, 2015, 5, 11534.	1.6	42
59	Genetic Evidence for <i>PLASMINOGEN</i> as a Shared Genetic Risk Factor of Coronary Artery Disease and Periodontitis. Circulation: Cardiovascular Genetics, 2015, 8, 159-167.	5.1	74
60	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
61	A genome-wide association study reveals 2 new susceptibility loci for atopic dermatitis. Journal of Allergy and Clinical Immunology, 2015, 136, 802-806.	1.5	51
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	FPGA-based Acceleration of Detecting Statistical Epistasis in GWAS. Procedia Computer Science, 2014, 29, 220-230.	1.2	24
64	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
65	Common Variants in Mendelian Kidney Disease Genes and Their Association with Renal Function. Journal of the American Society of Nephrology: JASN, 2013, 24, 2105-2117.	3.0	33
66	Genome-wide association analysis in Primary sclerosing cholangitis and ulcerative colitis identifies risk loci at<i>GPR35</i>and<i>TCF4</i>. Hepatology, 2013, 58, 1074-1083.	3.6	150
67	High-density genotyping study identifies four new susceptibility loci for atopic dermatitis. Nature Genetics, 2013, 45, 808-812.	9.4	167
68	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
69	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
70	Autophagy receptor CALCOCO2/NDP52 takes center stage in Crohn disease. Autophagy, 2013, 9, 1256-1257.	4.3	29
71	Replication Study of Ulcerative Colitis Risk Loci in a Lithuanianâ€“Latvian Caseâ€“Control Sample. Inflammatory Bowel Diseases, 2013, 19, 2349-2355.	0.9	10
72	From next-generation sequencing alignments to accurate comparison and validation of single-nucleotide variants: the pibase software. Nucleic Acids Research, 2013, 41, e16-e16.	6.5	21

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73	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	1.5	166
74	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. Human Molecular Genetics, 2012, 21, 5329-5343.	1.4	64
75	Identification of germline susceptibility loci in ETV6-RUNX1-rearranged childhood acute lymphoblastic leukemia. Leukemia, 2012, 26, 902-909.	3.3	106
76	A Novel Sarcoidosis Risk Locus for Europeans on Chromosome 11q13.1. American Journal of Respiratory and Critical Care Medicine, 2012, 186, 877-885.	2.5	51
77	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
78	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
79	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
80	Hostâ€"microbe interactions have shaped the genetic architecture of inflammatory bowel disease. Nature, 2012, 491, 119-124.	13.7	4,038
81	Meta-analysis of genome-wide association studies identifies three new risk loci for atopic dermatitis. Nature Genetics, 2012, 44, 187-192.	9.4	311
82	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
83	Genome-Wide Meta-Analysis of Psoriatic Arthritis Identifies Susceptibility Locus at REL. Journal of Investigative Dermatology, 2012, 132, 1133-1140.	0.3	99
84	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	13.7	2,400
85	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	13.7	401
86	Deep resequencing of GWAS loci identifies independent rare variants associated with inflammatory bowel disease. Nature Genetics, 2011, 43, 1066-1073.	9.4	698
87	Genetic polymorphisms of matrix metalloproteinase 3 in primary sclerosing cholangitis. Liver International, 2011, 31, 785-791.	1.9	21
88	Genome-wide association analysis in primary sclerosing cholangitis identifies two non-HLA susceptibility loci. Nature Genetics, 2011, 43, 17-19.	9.4	221
89	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
90	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

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91	A meta-analysis of genome-wide data from five European isolates reveals an association of COL22A1, SYT1, and GABRR2with serum creatinine level. BMC Medical Genetics, 2010, 11, 41.	2.1	48
92	Genome-wide association study for ulcerative colitis identifies risk loci at 7q22 and 22q13 (IL17REL). Nature Genetics, 2010, 42, 292-294.	9.4	177
93	New loci associated with kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 376-384.	9.4	710
94	Genome-wide association study identifies a psoriasis susceptibility locus at TRAF3IP2. Nature Genetics, 2010, 42, 991-995.	9.4	331
95	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
96	A comprehensive evaluation of SNP genotype imputation. Human Genetics, 2009, 125, 163-171.	1.8	139
97	Current software for genotype imputation. Human Genomics, 2009, 3, 371-80.	1.4	19
98	Sequence variants in IL10, ARPC2 and multiple other loci contribute to ulcerative colitis susceptibility. Nature Genetics, 2008, 40, 1319-1323.	9.4	534
99	LTRharvest, an efficient and flexible software for de novo detection of LTR retrotransposons. BMC Bioinformatics, 2008, 9, 18.	1.2	1,110