Eva Ellinghaus

List of Publications by Year
in descending order

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Version: 2024-02-01

56 papers	7,679 citations	81900 39 h-index	138484 58 g-index
63 all docs	63 docs citations	63 times ranked	13211 citing authors

#	Article	IF	Citations
1	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. Nature Genetics, 2012, 44, 1341-1348.	21.4	848
2	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. Nature Genetics, 2016, 48, 510-518.	21.4	617
3	Dense genotyping of immune-related disease regions identifies nine new risk loci for primary sclerosing cholangitis. Nature Genetics, 2013, 45, 670-675.	21.4	339
4	Genome-wide association study identifies a psoriasis susceptibility locus at TRAF3IP2. Nature Genetics, 2010, 42, 991-995.	21.4	331
5	Genome-wide association analysis identifies three psoriasis susceptibility loci. Nature Genetics, 2010, 42, 1000-1004.	21.4	313
6	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.	6.2	290
7	Association analyses identify six new psoriasis susceptibility loci in the Chinese population. Nature Genetics, 2010, 42, 1005-1009.	21.4	287
8	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.	21.4	280
9	Large scale meta-analysis characterizes genetic architecture for common psoriasis associated variants. Nature Communications, 2017, 8, 15382.	12.8	251
10	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.	6.2	245
11	Genome-wide association analysis in primary sclerosing cholangitis identifies two non-HLA susceptibility loci. Nature Genetics, 2011, 43, 17-19.	21.4	221
12	Extended analysis of a genome-wide association study in primary sclerosing cholangitis detects multiple novel risk loci. Journal of Hepatology, 2012, 57, 366-375.	3.7	196
13	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.	21.4	190
14	Fine Mapping Major Histocompatibility Complex Associations in Psoriasis and Its Clinical Subtypes. American Journal of Human Genetics, 2014, 95, 162-172.	6.2	182
15	Genome-wide association study for ulcerative colitis identifies risk loci at 7q22 and 22q13 (IL17REL). Nature Genetics, 2010, 42, 292-294.	21.4	177
16	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.	6.2	169
17	Genome-wide Comparative Analysis of Atopic Dermatitis and Psoriasis Gives Insight into Opposing Genetic Mechanisms. American Journal of Human Genetics, 2015, 96, 104-120.	6.2	163
18	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.	1.7	158

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19	Enhanced meta-analysis and replication studies identify five new psoriasis susceptibility loci. Nature Communications, 2015, 6, 7001.	12.8	156
20	Genome-wide meta-analysis identifies multiple novel associations and ethnic heterogeneity of psoriasis susceptibility. Nature Communications, 2015, 6, 6916.	12.8	154
21	Genome-wide association analysis in Primary sclerosing cholangitis and ulcerative colitis identifies risk loci atGPR35andTCF4. Hepatology, 2013, 58, 1074-1083.	7.3	150
22	Association Between Variants of PRDM1 and NDP52 and Crohn's Disease, Based on Exome Sequencing and Functional Studies. Gastroenterology, 2013, 145, 339-347.	1.3	149
23	Whole-genome sequencing of a sporadic primary immunodeficiency cohort. Nature, 2020, 583, 90-95.	27.8	148
24	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.	2.9	131
25	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.	7.3	110
26	Mutational Characterization of the Bile Acid Receptor TGR5 in Primary Sclerosing Cholangitis. PLoS ONE, 2010, 5, e12403.	2.5	106
27	Identification of germline susceptibility loci in ETV6-RUNX1-rearranged childhood acute lymphoblastic leukemia. Leukemia, 2012, 26, 902-909.	7.2	106
28	Genome-Wide Meta-Analysis of Psoriatic Arthritis Identifies Susceptibility Locus at REL. Journal of Investigative Dermatology, 2012, 132, 1133-1140.	0.7	99
29	Genetic signature to provide robust risk assessment of psoriatic arthritis development in psoriasis patients. Nature Communications, 2018, 9, 4178.	12.8	95
30	Identification of Immune-Relevant Factors Conferring Sarcoidosis Genetic Risk. American Journal of Respiratory and Critical Care Medicine, 2015, 192, 727-736.	5.6	94
31	Reduced FOXP3+ regulatory T cells in patients with primary sclerosing cholangitis are associated with IL2RA gene polymorphisms. Journal of Hepatology, 2014, 60, 1010-1016.	3.7	90
32	Development of a high-resolution NGS-based HLA-typing and analysis pipeline. Nucleic Acids Research, 2015, 43, e70-e70.	14.5	77
33	Imputation of KIR Types from SNP Variation Data. American Journal of Human Genetics, 2015, 97, 593-607.	6.2	73
34	Association of CLEC16A with human common variable immunodeficiency disorder and role in murine B cells. Nature Communications, 2015, 6, 6804.	12.8	63
35	Conditional analysis identifies three novel major histocompatibility complex loci associated with psoriasis. Human Molecular Genetics, 2012, 21, 5185-5192.	2.9	58
36	Genome-wide association analysis for chronic venous disease identifies EFEMP1 and KCNH8 as susceptibility loci. Scientific Reports, 2017, 7, 45652.	3.3	48

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37	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.	2.9	48
38	Fine mapping and replication of genetic risk loci in primary sclerosing cholangitis. Scandinavian Journal of Gastroenterology, 2012, 47, 820-826.	1.5	47
39	Microbiomarkers in inflammatory bowel diseases: caveats come with caviar. Gut, 2017, 66, 1734-1738.	12.1	47
40	Predicting Humoral Alloimmunity from Differences in Donor and Recipient HLA Surface Electrostatic Potential. Journal of Immunology, 2018, 201, 3780-3792.	0.8	47
41	A variant at 9p21.3 functionally implicates CDKN2B in paediatric B-cell precursor acute lymphoblastic leukaemia aetiology. Nature Communications, 2016, 7, 10635.	12.8	44
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.	2.9	41
43	Abundant Genetic Overlap between Blood Lipids and Immune-Mediated Diseases Indicates Shared Molecular Genetic Mechanisms. PLoS ONE, 2015, 10, e0123057.	2.5	40
44	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.	2.9	29
45	Association to the Glypican-5 gene in multiple sclerosis. Journal of Neuroimmunology, 2010, 226, 194-197.	2.3	20
46	Nonsyndromic cleft lip with or without cleft palate and cancer: Evaluation of a possible common genetic background through the analysis of GWAS data. Genomics Data, 2016, 10, 22-29.	1.3	19
47	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.	2.9	19
48	CD4+ T cells from patients with primary sclerosing cholangitis exhibit reduced apoptosis and down-regulation of proapoptotic Bim in peripheral blood. Journal of Leukocyte Biology, 2017, 101, 589-597.	3.3	15
49	Genetic association with B-cell acute lymphoblastic leukemia in allogeneic transplant patients differs by age and sex. Blood Advances, 2017, 1, 1717-1728.	5.2	15
50	Genomeâ€wide association study of psoriasis in an Egyptian population. Experimental Dermatology, 2019, 28, 623-627.	2.9	15
51	Frequent and sex-biased deletion of SLX4IP by illegitimate V(D)J-mediated recombination in childhood acute lymphoblastic leukemia. Human Molecular Genetics, 2014, 23, 590-601.	2.9	13
52	Replication Study of Ulcerative Colitis Risk Loci in a Lithuanianâ€“Latvian Caseâ€“Control Sample. Inflammatory Bowel Diseases, 2013, 19, 2349-2355.	1.9	10
53	Childhood acute lymphoblastic leukemia-associated risk-lociIKZF1, ARID5BandCEBPEand risk of pediatric non-Hodgkin lymphoma: a report from the Berlinâ€“Frankfurtâ€“MÃ¼nster Study Group. Leukemia and Lymphoma, 2015, 56, 814-816.	1.3	9
54	Genetic and transcriptional analysis of inflammatory bowel disease-associated pathways in patients with GUCY2C-linked familial diarrhea. Scandinavian Journal of Gastroenterology, 2018, 53, 1264-1273.	1.5	9

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55	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. Frontiers in Immunology, 2021, 12, 684326.	4.8	7
56	Genetic Variation in ABCC4 and CFTR and Acute Pancreatitis during Treatment of Pediatric Acute Lymphoblastic Leukemia. Journal of Clinical Medicine, 2021, 10, 4815.	2.4	2