Ingileif Jonsdottir

List of Publications by Year
in descending order

96 papers	12,052 citations	50170 46 h-index	39575 94 g-index
104 all docs	104 docs citations	104 times ranked	25298 citing authors

#	Article	IF	Citations
1	Variant ofTREM2Associated with the Risk of Alzheimer's Disease. New England Journal of Medicine, 2013, 368, 107-116.	13.9	2,085
2	Spread of SARS-CoV-2 in the Icelandic Population. New England Journal of Medicine, 2020, 382, 2302-2315.	13.9	1,093
3	Humoral Immune Response to SARS-CoV-2 in Iceland. New England Journal of Medicine, 2020, 383, 1724-1734.	13.9	845
4	Sequence variants affecting eosinophil numbers associate with asthma and myocardial infarction. Nature Genetics, 2009, 41, 342-347.	9.4	709
5	Clonal hematopoiesis, with and without candidate driver mutations, is common in the elderly. Blood, 2017, 130, 742-752.	0.6	582
6	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	9.4	426
7	Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. Lancet, The, 2012, 380, 815-823.	6.3	373
8	Large-scale integration of the plasma proteome with genetics and disease. Nature Genetics, 2021, 53, 1712-1721.	9.4	340
9	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.	9.4	257
10	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	9.4	251
11	Genome-wide association analysis of insomnia complaints identifies risk genes and genetic overlap with psychiatric and metabolic traits. Nature Genetics, 2017, 49, 1584-1592.	9.4	248
12	Meta-analysis of genome-wide association studies identifies ten loci influencing allergic sensitization. Nature Genetics, 2013, 45, 902-906.	9.4	221
13	Variants with large effects on blood lipids and the role of cholesterol and triglycerides in coronary disease. Nature Genetics, 2016, 48, 634-639.	9.4	214
14	Graphtyper enables population-scale genotyping using pangenome graphs. Nature Genetics, 2017, 49, 1654-1660.	9.4	189
15	A genomeâ€wide association study identifies an osteoarthritis susceptibility locus on chromosome 7q22. Arthritis and Rheumatism, 2010, 62, 499-510.	6.7	178
16	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
17	VariantASGR1Associated with a Reduced Risk of Coronary Artery Disease. New England Journal of Medicine, 2016, 374, 2131-2141.	13.9	137
18	Severe osteoarthritis of the hand associates with common variants within the ALDH1A2 gene and with rare variants at 1p31. Nature Genetics, 2014, 46, 498-502.	9.4	136

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19	Identification of low-frequency variants associated with gout and serum uric acid levels. Nature Genetics, 2011, 43, 1127-1130.	9.4	134
20	Meta-analysis of Icelandic and UK data sets identifies missense variants in SMO, IL11, COL11A1 and 13 more new loci associated with osteoarthritis. Nature Genetics, 2018, 50, 1681-1687.	9.4	131
21	Lipoprotein(a) Concentration and Risks of Cardiovascular Disease and Diabetes. Journal of the American College of Cardiology, 2019, 74, 2982-2994.	1.2	127
22	Meta-analysis of genome-wide association studies confirms a susceptibility locus for knee osteoarthritis on chromosome 7q22. Annals of the Rheumatic Diseases, 2011, 70, 349-355.	0.5	126
23	A rare IL33 loss-of-function mutation reduces blood eosinophil counts and protects from asthma. PLoS Genetics, 2017, 13, e1006659.	1.5	126
24	HLA class II sequence variants influence tuberculosis risk in populations of European ancestry. Nature Genetics, 2016, 48, 318-322.	9.4	123
25	A Variant in MCF2L Is Associated with Osteoarthritis. American Journal of Human Genetics, 2011, 89, 446-450.	2.6	115
26	Assessment of Osteoarthritis Candidate Genes in a Metaâ€Analysis of Nine Genomeâ€Wide Association Studies. Arthritis and Rheumatology, 2014, 66, 940-949.	2.9	108
27	A meta-analysis of genome-wide association studies identifies novel variants associated with osteoarthritis of the hip. Annals of the Rheumatic Diseases, 2014, 73, 2130-2136.	0.5	108
28	Genome-wide association and HLA fine-mapping studies identify risk loci and genetic pathways underlying allergic rhinitis. Nature Genetics, 2018, 50, 1072-1080.	9.4	106
29	Genetic predisposition to hypertension is associated with preeclampsia in European and Central Asian women. Nature Communications, 2020, 11, 5976.	5.8	102
30	A homozygous loss-of-function mutation leading to CYBC1 deficiency causes chronic granulomatous disease. Nature Communications, 2018, 9, 4447.	5.8	95
31	Insights into imprinting from parent-of-origin phased methylomes and transcriptomes. Nature Genetics, 2018, 50, 1542-1552.	9.4	94
32	Genome-wide analysis yields new loci associating with aortic valve stenosis. Nature Communications, 2018, 9, 987.	5.8	91
33	Identification of sequence variants influencing immunoglobulin levels. Nature Genetics, 2017, 49, 1182-1191.	9.4	90
34	Multiple transmissions of de novo mutations in families. Nature Genetics, 2018, 50, 1674-1680.	9.4	89
35	A loss-of-function variant in ALOX15 protects against nasal polyps and chronic rhinosinusitis. Nature Genetics, 2019, 51, 267-276.	9.4	83
36	Differences between germline genomes of monozygotic twins. Nature Genetics, 2021, 53, 27-34.	9.4	83

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37	Recommendations for standardization and phenotype definitions in genetic studies of osteoarthritis: the TREAT-OA consortium. Osteoarthritis and Cartilage, 2011, 19, 254-264.	0.6	82
38	FLT3 stop mutation increases FLT3 ligand level and risk of autoimmune thyroid disease. Nature, 2020, 584, 619-623.	13.7	81
39	Whole-genome sequencing identifies rare genotypes in COMP and CHADL associated with high risk of hip osteoarthritis. Nature Genetics, 2017, 49, 801-805.	9.4	75
40	GWAS of bone size yields twelve loci that also affect height, BMD, osteoarthritis or fractures. Nature Communications, 2019, 10, 2054.	5.8	74
41	An Analytical Model Applied to a Multicenter Pneumococcal Enzyme-Linked Immunosorbent Assay Study. Journal of Clinical Microbiology, 2000, 38, 2043-2050.	1.8	74
42	A Missense Variant in PLEC Increases RiskÂof Atrial Fibrillation. Journal of the American College of Cardiology, 2017, 70, 2157-2168.	1.2	73
43	Genome-wide association meta-analysis yields 20 loci associated with gallstone disease. Nature Communications, 2018, 9, 5101.	5.8	73
44	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. Communications Biology, 2021, 4, 156.	2.0	72
45	Sequence variants in ARHGAP15, COLQ and FAM155A associate with diverticular disease and diverticulitis. Nature Communications, 2017, 8, 15789.	5.8	67
46	Genetic variability in the absorption of dietary sterols affects the risk of coronary artery disease. European Heart Journal, 2020, 41, 2618-2628.	1.0	61
47	Eighty-eight variants highlight the role of T cell regulation and airway remodeling in asthma pathogenesis. Nature Communications, 2020, 11, 393.	5.8	59
48	A rare missense mutation in MYH6 associates with non-syndromic coarctation of the aorta. European Heart Journal, 2018, 39, 3243-3249.	1.0	57
49	A protein-truncating R179X variant in RNF186 confers protection against ulcerative colitis. Nature Communications, 2016, 7, 12342.	5.8	50
50	Sequence variant at 8q24.21 associates with sciatica caused by lumbar disc herniation. Nature Communications, 2017, 8, 14265.	5.8	48
51	COPA syndrome in an Icelandic family caused by a recurrent missense mutation in COPA. BMC Medical Genetics, 2017, 18, 129.	2.1	47
52	Coding variants in RPL3L and MYZAP increase risk of atrial fibrillation. Communications Biology, 2018, 1, 68.	2.0	42
53	Distinction between the effects of parental and fetal genomes on fetal growth. Nature Genetics, 2021, 53, 1135-1142.	9.4	41
54	Are the Opsonophagocytic Activities of Antibodies in Infant Sera Measured by Different Pneumococcal Phagocytosis Assays Comparable?. Vaccine Journal, 2001, 8, 363-369.	2.6	31

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55	The genetic architecture of age-related hearing impairment revealed by genome-wide association analysis. Communications Biology, 2021, 4, 706.	2.0	30
56	Genetic insight into sick sinus syndrome. European Heart Journal, 2021, 42, 1959-1971.	1.0	27
57	The CRTAC1 Protein in Plasma Is Associated With Osteoarthritis and Predicts Progression to Joint Replacement: A Largeâ€Scale Proteomics Scan in Iceland. Arthritis and Rheumatology, 2021, 73, 2025-2034.	2.9	27
58	A rare missense mutation in CHRNA4 associates with smoking behavior and its consequences. Molecular Psychiatry, 2016, 21, 594-600.	4.1	26
59	Multiomics analysis of rheumatoid arthritis yields sequence variants that have large effects on risk of the seropositive subset. Annals of the Rheumatic Diseases, 2022, 81, 1085-1095.	0.5	26
60	Sequence variation at ANAPC1 accounts for 24% of the variability in corneal endothelial cell density. Nature Communications, 2019, 10, 1284.	5.8	24
61	Short Vi-polysaccharide abrogates T-independent immune response and hyporesponsiveness elicited by long Vi-CRM₁₉₇conjugate vaccine. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 24443-24449.	3.3	24
62	Decreased immune response to pneumococcal conjugate vaccine after 23-valent pneumococcal polysaccharide vaccine in children. Vaccine, 2014, 32, 417-424.	1.7	23
63	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology. Nature Communications, 2022, 13, 634.	5.8	21
64	Characterization of potential biomarkers of reactogenicity of licensed antiviral vaccines: randomized controlled clinical trials conducted by the BIOVACSAFE consortium. Scientific Reports, 2019, 9, 20362.	1.6	20
65	Genome-wide association identifies seven loci for pelvic organ prolapse in Iceland and the UK Biobank. Communications Biology, 2020, 3, 129.	2.0	20
66	Age and Influenza-Specific Pre-Vaccination Antibodies Strongly Affect Influenza Vaccine Responses in the Icelandic Population whereas Disease and Medication Have Small Effects. Frontiers in Immunology, 2017, 8, 1872.	2.2	19
67	Sequence Variants in TAAR5 and Other Loci Affect Human Odor Perception and Naming. Current Biology, 2020, 30, 4643-4653.e3.	1.8	19
68	Adjuvants Enhance the Induction of Germinal Center and Antibody Secreting Cells in Spleen and Their Persistence in Bone Marrow of Neonatal Mice. Frontiers in Immunology, 2019, 10, 2214.	2.2	17
69	Fourteen sequence variants that associate with multiple sclerosis discovered by meta-analysis informed by genetic correlations. Npj Genomic Medicine, 2017, 2, 24.	1.7	16
70	Large-Scale Screening for Monogenic and Clinically Defined Familial Hypercholesterolemia in Iceland. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 2616-2628.	1.1	16
71	Maturation of Mucosal Immune Responses and Influence of Maternal Antibodies. Journal of Comparative Pathology, 2007, 137, S20-S26.	0.1	15
72	Genetic Associations and Architecture of Asthma-COPD Overlap. Chest, 2022, 161, 1155-1166.	0.4	15

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73	Integrity monitoring and estimation of systematic errors in radar data systems. , 0, , .		13
74	An Analytical Model Applied to a Multicenter Pneumococcal Enzyme-Linked Immunosorbent Assay Study. Journal of Clinical Microbiology, 2000, 38, 2043-2050.	1.8	13
75	Lifelong Reduction in LDL (Low-Density Lipoprotein) Cholesterol due to a Gain-of-Function Mutation in LDLR. Circulation Genomic and Precision Medicine, 2021, 14, e003029.	1.6	12
76	A genome-wide meta-analysis uncovers six sequence variants conferring risk of vertigo. Communications Biology, 2021, 4, 1148.	2.0	12
77	Influenza infection directly alters innate IL-23 and IL-12p70 and subsequent IL-17A and IFN-Î³ responses to pneumococcus in vitro in human monocytes. PLoS ONE, 2018, 13, e0203521.	1.1	11
78	Reconstruction of a large-scale outbreak of SARS-CoV-2 infection in Iceland informs vaccination strategies. Clinical Microbiology and Infection, 2022, 28, 852-858.	2.8	11
79	Predicting the probability of death using proteomics. Communications Biology, 2021, 4, 758.	2.0	10
80	Functional dissection of inherited non-coding variation influencing multiple myeloma risk. Nature Communications, 2022, 13, 151.	5.8	10
81	Challenges in early clinical development of adjuvanted vaccines. Vaccine, 2015, 33, B47-B51.	1.7	9
82	Common and rare sequence variants influencing tumor biomarkers in blood. Cancer Epidemiology Biomarkers and Prevention, 2019, 29, cebp.1060.2018.	1.1	9
83	A meta-analysis uncovers the first sequence variant conferring risk of Bellâ€™s palsy. Scientific Reports, 2021, 11, 4188.	1.6	8
84	A genome-wide meta-analysis identifies 50 genetic loci associated with carpal tunnel syndrome. Nature Communications, 2022, 13, 1598.	5.8	8
85	A PRPH splice-donor variant associates with reduced sural nerve amplitude and risk of peripheral neuropathy. Nature Communications, 2019, 10, 1777.	5.8	7
86	LT-K63 Enhances B Cell Activation and Survival Factors in Neonatal Mice That Translates Into Long-Lived Humoral Immunity. Frontiers in Immunology, 2020, 11, 527310.	2.2	7
87	Genetic variants associated with platelet count are predictive of human disease and physiological markers. Communications Biology, 2021, 4, 1132.	2.0	7
88	Population-level deficit of homozygosity unveils CPSF3 as an intellectual disability syndrome gene. Nature Communications, 2022, 13, 705.	5.8	7
89	Animal Models of Invasive Pneumococcal Disease. , 0, , 47-58.		5
90	Polygenic risk score for ACE-inhibitor-associated cough based on the discovery of new genetic loci. European Heart Journal, 2022, 43, 4707-4718.	1.0	5

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91	Molecular benchmarks of a SARS-CoV-2 epidemic. Nature Communications, 2021, 12, 3633.	5.8	3
92	Genetic propensities for verbal and spatial ability have opposite effects on body mass index and risk of schizophrenia. Intelligence, 2021, 88, 101565.	1.6	2
93	Established risk loci for systemic lupus erythematosus at NCF2, STAT4, TNPO3, IRF5 and ITGAM associate with distinct clinical manifestations: A Danish genome-wide association study. Joint Bone Spine, 2022, 89, 105357.	0.8	1
94	Genetic architecture of band neutrophil fraction in Iceland. Communications Biology, 2022, 5, .	2.0	1
95	1227Familiality of fatal measles infections in Iceland, 1882. Analysis of a reconstructed patient cohort from a major epidemic. Open Forum Infectious Diseases, 2014, 1, S43-S43.	0.4	0
96	Welcome to the 42nd Annual Meeting of the Scandinavian Society for Immunology in Reykjavik, Iceland. Scandinavian Journal of Immunology, 2014, 79, 347-347.	1.3	0