

Lars G Fritsche

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

113
papers

16,035
citations

40
h-index

126
g-index

142
ext. papers

22,798
ext. citations

12.1
avg, IF

5.28
L-index

#	Paper	IF	Citations
113	A global reference for human genetic variation. <i>Nature</i> , 2015 , 526, 68-74	50.4	8599
112	A large genome-wide association study of age-related macular degeneration highlights contributions of rare and common variants. <i>Nature Genetics</i> , 2016 , 48, 134-43	36.3	769
111	Hypothetical LOC387715 is a second major susceptibility gene for age-related macular degeneration, contributing independently of complement factor H to disease risk. <i>Human Molecular Genetics</i> , 2005 , 14, 3227-36	5.6	656
110	Seven new loci associated with age-related macular degeneration. <i>Nature Genetics</i> , 2013 , 45, 433-9, 439e1-3	36.3	577
109	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. <i>Nature Genetics</i> , 2019 , 51, 237-244	36.3	516
108	Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies. <i>Nature Genetics</i> , 2018 , 50, 1335-1341	36.3	375
107	Age-related macular degeneration is associated with an unstable ARMS2 (LOC387715) mRNA. <i>Nature Genetics</i> , 2008 , 40, 892-6	36.3	320
106	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017 , 49, 1758-1766	36.3	310
105	Age-related macular degeneration: genetics and biology coming together. <i>Annual Review of Genomics and Human Genetics</i> , 2014 , 15, 151-71	9.7	293
104	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. <i>Nature Genetics</i> , 2017 , 49, 1752-1757	36.3	256
103	Systemic complement activation in age-related macular degeneration. <i>PLoS ONE</i> , 2008 , 3, e2593	3.7	255
102	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. <i>Nature Genetics</i> , 2018 , 50, 1234-1239	36.3	254
101	Defective complement control of factor H (Y402H) and FHL-1 in age-related macular degeneration. <i>Molecular Immunology</i> , 2007 , 44, 3398-406	4.3	154
100	An imbalance of human complement regulatory proteins CFHR1, CFHR3 and factor H influences risk for age-related macular degeneration (AMD). <i>Human Molecular Genetics</i> , 2010 , 19, 4694-704	5.6	153
99	CRX ChIP-seq reveals the cis-regulatory architecture of mouse photoreceptors. <i>Genome Research</i> , 2010 , 20, 1512-25	9.7	145
98	Evidence of association of APOE with age-related macular degeneration: a pooled analysis of 15 studies. <i>Human Mutation</i> , 2011 , 32, 1407-16	4.7	99
97	Characteristics Associated With Racial/Ethnic Disparities in COVID-19 Outcomes in an Academic Health Care System. <i>JAMA Network Open</i> , 2020 , 3, e2025197	10.4	97

96	Retinal transcriptome and eQTL analyses identify genes associated with age-related macular degeneration. <i>Nature Genetics</i> , 2019 , 51, 606-610	36.3	93
95	Exome chip meta-analysis identifies novel loci and East Asian-specific coding variants that contribute to lipid levels and coronary artery disease. <i>Nature Genetics</i> , 2017 , 49, 1722-1730	36.3	83
94	Association of Polygenic Risk Scores for Multiple Cancers in a Phenome-wide Study: Results from The Michigan Genomics Initiative. <i>American Journal of Human Genetics</i> , 2018 , 102, 1048-1061	11	83
93	In Silico Functional Meta-Analysis of 5,962 ABCA4 Variants in 3,928 Retinal Dystrophy Cases. <i>Human Mutation</i> , 2017 , 38, 400-408	4.7	82
92	Evidence of a causal relationship between body mass index and psoriasis: A mendelian randomization study. <i>PLoS Medicine</i> , 2019 , 16, e1002739	11.6	77
91	No clinically significant association between CFH and ARMS2 genotypes and response to nutritional supplements: AREDS report number 38. <i>Ophthalmology</i> , 2014 , 121, 2173-80	7.3	76
90	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. <i>Nature Communications</i> , 2018 , 9, 2252	17.4	71
89	Complement factor H genetic variant and age-related macular degeneration: effect size, modifiers and relationship to disease subtype. <i>International Journal of Epidemiology</i> , 2012 , 41, 250-62	7.8	70
88	CFH, C3 and ARMS2 are significant risk loci for susceptibility but not for disease progression of geographic atrophy due to AMD. <i>PLoS ONE</i> , 2009 , 4, e7418	3.7	70
87	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. <i>Journal of the National Cancer Institute</i> , 2019 , 111, 146-157	9.7	67
86	A subgroup of age-related macular degeneration is associated with mono-allelic sequence variants in the ABCA4 gene 2012 , 53, 2112-8		67
85	Variations in apolipoprotein E frequency with age in a pooled analysis of a large group of older people. <i>American Journal of Epidemiology</i> , 2011 , 173, 1357-64	3.8	67
84	Modelling the genetic risk in age-related macular degeneration. <i>PLoS ONE</i> , 2012 , 7, e37979	3.7	65
83	Risk- and non-risk-associated variants at the 10q26 AMD locus influence ARMS2 mRNA expression but exclude pathogenic effects due to protein deficiency. <i>Human Molecular Genetics</i> , 2011 , 20, 1387-99	5.6	57
82	First Genome-Wide Association Study of Latent Autoimmune Diabetes in Adults Reveals Novel Insights Linking Immune and Metabolic Diabetes. <i>Diabetes Care</i> , 2018 , 41, 2396-2403	14.6	57
81	Genome-wide analysis yields new loci associating with aortic valve stenosis. <i>Nature Communications</i> , 2018 , 9, 987	17.4	56
80	Genome-wide Study of Atrial Fibrillation Identifies Seven Risk Loci and Highlights Biological Pathways and Regulatory Elements Involved in Cardiac Development. <i>American Journal of Human Genetics</i> , 2018 , 102, 103-115	11	53
79	Protein-altering and regulatory genetic variants near GATA4 implicated in bicuspid aortic valve. <i>Nature Communications</i> , 2017 , 8, 15481	17.4	52

78	HDL-cholesterol levels and risk of age-related macular degeneration: a multiethnic genetic study using Mendelian randomization. <i>International Journal of Epidemiology</i> , 2017 , 46, 1891-1902	7.8	45
77	Scalable generalized linear mixed model for region-based association tests in large biobanks and cohorts. <i>Nature Genetics</i> , 2020 , 52, 634-639	36.3	41
76	Exploring and visualizing large-scale genetic associations by using PheWeb. <i>Nature Genetics</i> , 2020 , 52, 550-552	36.3	41
75	A Scalable Bayesian Method for Integrating Functional Information in Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2017 , 101, 404-416	11	41
74	A genome-wide association study with 1,126,563 individuals identifies new risk loci for Alzheimer's disease. <i>Nature Genetics</i> , 2021 , 53, 1276-1282	36.3	40
73	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. <i>Nature Genetics</i> , 2020 , 52, 494-504	36.3	39
72	Genome-wide analysis of disease progression in age-related macular degeneration. <i>Human Molecular Genetics</i> , 2018 , 27, 929-940	5.6	37
71	Age-related macular degeneration and functional promoter and coding variants of the apolipoprotein E gene. <i>Human Mutation</i> , 2009 , 30, 1048-53	4.7	34
70	Expanding the spectrum of PTH1R mutations in patients with primary failure of tooth eruption. <i>Clinical Oral Investigations</i> , 2014 , 18, 377-84	4.2	32
69	Bivariate Analysis of Age-Related Macular Degeneration Progression Using Genetic Risk Scores. <i>Genetics</i> , 2017 , 206, 119-133	4	31
68	Global Prevalence of Post COVID-19 Condition or Long COVID: A Meta-Analysis and Systematic Review.. <i>Journal of Infectious Diseases</i> , 2022 ,	7	30
67	Genotype imputation in genome-wide association studies. <i>Current Protocols in Human Genetics</i> , 2013 , Chapter 1, Unit 1.25	3.2	29
66	Assessment of the contribution of CFH and chromosome 10q26 AMD susceptibility loci in a Russian population isolate. <i>British Journal of Ophthalmology</i> , 2007 , 91, 576-8	5.5	27
65	Case-control genetic association study of fibulin-6 (FBLN6 or HMCN1) variants in age-related macular degeneration (AMD). <i>Human Mutation</i> , 2007 , 28, 406-13	4.7	26
64	Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program. <i>Circulation</i> , 2020 , 142, 1633-1646	16.7	24
63	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. <i>Cell</i> , 2021 , 184, 4784-4818.e17	36.1	17
62	Sex-specific and pleiotropic effects underlying kidney function identified from GWAS meta-analysis. <i>Nature Communications</i> , 2019 , 10, 1847	17.4	22
61	UK Biobank Whole-Exome Sequence Binary Phenome Analysis with Robust Region-Based Rare-Variant Test. <i>American Journal of Human Genetics</i> , 2020 , 106, 3-12	11	21

60	GWAS of thyroid stimulating hormone highlights pleiotropic effects and inverse association with thyroid cancer. <i>Nature Communications</i> , 2020 , 11, 3981	17.4	21
59	COVID-19 outcomes, risk factors and associations by race: a comprehensive analysis using electronic health records data in Michigan Medicine 2020 ,		20
58	Cancer PRSweb: An Online Repository with Polygenic Risk Scores for Major Cancer Traits and Their Evaluation in Two Independent Biobanks. <i>American Journal of Human Genetics</i> , 2020 , 107, 815-836	11	20
57	Association of Genetic Variants With Response to Anti-Vascular Endothelial Growth Factor Therapy in Age-Related Macular Degeneration. <i>JAMA Ophthalmology</i> , 2018 , 136, 875-884	3.9	20
56	Exploring various polygenic risk scores for skin cancer in the phenomes of the Michigan genomics initiative and the UK Biobank with a visual catalog: PRSWeb. <i>PLoS Genetics</i> , 2019 , 15, e1008202	6	18
55	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. <i>Nature Communications</i> , 2020 , 11, 6417	17.4	17
54	The emerging landscape of health research based on biobanks linked to electronic health records: Existing resources, statistical challenges, and potential opportunities. <i>Statistics in Medicine</i> , 2020 , 39, 773-800	2.3	15
53	Age-related macular degeneration and coronary heart disease: evaluation of genetic and environmental associations. <i>European Journal of Medical Genetics</i> , 2013 , 56, 72-9	2.6	14
52	Improving power of association tests using multiple sets of imputed genotypes from distributed reference panels. <i>Genetic Epidemiology</i> , 2017 , 41, 744-755	2.6	13
51	A Fast and Accurate Method for Genome-Wide Time-to-Event Data Analysis and Its Application to UK Biobank. <i>American Journal of Human Genetics</i> , 2020 , 107, 222-233	11	12
50	Age-of-onset information helps identify 76 genetic variants associated with allergic disease. <i>PLoS Genetics</i> , 2020 , 16, e1008725	6	10
49	A Fast and Accurate Method for Genome-wide Scale Phenome-wide GIE Analysis and Its Application to UK Biobank. <i>American Journal of Human Genetics</i> , 2019 , 105, 1182-1192	11	10
48	Prediction of Ankylosing Spondylitis in the HUNT Study by a Genetic Risk Score Combining 110 Single-nucleotide Polymorphisms of Genome-wide Significance. <i>Journal of Rheumatology</i> , 2020 , 47, 204-210	4.1	9
47	Genes for Good: Engaging the Public in Genetics Research via Social Media. <i>American Journal of Human Genetics</i> , 2019 , 105, 65-77	11	8
46	Meta-MultiSKAT: Multiple phenotype meta-analysis for region-based association test. <i>Genetic Epidemiology</i> , 2019 , 43, 800-814	2.6	7
45	Scalable generalized linear mixed model for region-based association tests in large biobanks and cohorts		7
44	Mitochondrial genome-wide association study of migraine - the HUNT Study. <i>Cephalalgia</i> , 2020 , 40, 625-634	6.34	6
43	Age-related macular degeneration with discordant late stage phenotypes in monozygotic twins. <i>Ophthalmic Genetics</i> , 2011 , 32, 237-44	1.2	6

42	LabWAS: Novel findings and study design recommendations from a meta-analysis of clinical labs in two independent biobanks. <i>PLoS Genetics</i> , 2020 , 16, e1009077	6	6
41	Global Biobank Meta-analysis Initiative: powering genetic discovery across human diseases		6
40	The Emerging Landscape of Epidemiological Research Based on Biobanks Linked to Electronic Health Records: Existing Resources, Analytic Challenges and Potential Opportunities		6
39	Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies		6
38	A Phenome-Wide Association Study (PheWAS) of COVID-19 Outcomes by Race Using the Electronic Health Records Data in Michigan Medicine. <i>Journal of Clinical Medicine</i> , 2021 , 10,	5.1	6
37	Assessment of a causal relationship between body mass index and atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2021 , 147, 400-403	11.5	6
36	Patterns of repeated diagnostic testing for COVID-19 in relation to patient characteristics and outcomes. <i>Journal of Internal Medicine</i> , 2021 , 289, 726-737	10.8	6
35	Robust meta-analysis of biobank-based genome-wide association studies with unbalanced binary phenotypes. <i>Genetic Epidemiology</i> , 2019 , 43, 462-476	2.6	5
34	Multicenter cohort association study of SLC2A1 single nucleotide polymorphisms and age-related macular degeneration. <i>Molecular Vision</i> , 2012 , 18, 657-74	2.3	5
33	Heritability of the Fibromyalgia Phenotype Varies by Age. <i>Arthritis and Rheumatology</i> , 2020 , 72, 815-823	9.5	5
32	Genome-wide association study of cardiac troponin I in the general population. <i>Human Molecular Genetics</i> , 2021 , 30, 2027-2039	5.6	5
31	Validating Online Measures of Cognitive Ability in Genes for Good, a Genetic Study of Health and Behavior. <i>Assessment</i> , 2020 , 27, 136-148	3.7	5
30	Phenotype risk scores (PheRS) for pancreatic cancer using time-stamped electronic health record data: Discovery and validation in two large biobanks. <i>Journal of Biomedical Informatics</i> , 2021 , 113, 103652	10.2	5
29	Global Prevalence of Post-Acute Sequelae of COVID-19 (PASC) or Long COVID: A Meta-Analysis and Systematic Review		4
28	Genome-wide association study of 1 million people identifies 111 loci for atrial fibrillation		4
27	MEPE loss-of-function variant associates with decreased bone mineral density and increased fracture risk. <i>Nature Communications</i> , 2020 , 11, 4093	17.4	4
26	On cross-ancestry cancer polygenic risk scores. <i>PLoS Genetics</i> , 2021 , 17, e1009670	6	4
25	An analytic framework for exploring sampling and observation process biases in genome and phenome-wide association studies using electronic health records. <i>Statistics in Medicine</i> , 2020 , 39, 1965-1979	2.3	3

24	Estimation of DNA contamination and its sources in genotyped samples. <i>Genetic Epidemiology</i> , 2019 , 43, 980-995	2.6	3
23	The HUNT Study: a population-based cohort for genetic research		3
22	Common variants in SOX-2 and congenital cataract genes contribute to age-related nuclear cataract. <i>Communications Biology</i> , 2020 , 3, 755	6.7	3
21	Variation in Serum PCSK9 (Proprotein Convertase Subtilisin/Kexin Type 9), Cardiovascular Disease Risk, and an Investigation of Potential Unanticipated Effects of PCSK9 Inhibition. <i>Circulation Genomic and Precision Medicine</i> , 2019 , 12, e002335	5.2	3
20	Interaction analysis under misspecification of main effects: Some common mistakes and simple solutions. <i>Statistics in Medicine</i> , 2020 , 39, 1675-1694	2.3	2
19	Association of Smoking, Alcohol Consumption, Blood Pressure, Body Mass Index, and Glycemic Risk Factors With Age-Related Macular Degeneration: A Mendelian Randomization Study. <i>JAMA Ophthalmology</i> , 2021 ,	3.9	2
18	Geographic distribution of rare variants associated with age-related macular degeneration. <i>Molecular Vision</i> , 2018 , 24, 75-82	2.3	2
17	Evidence of a common causal relationship between body mass index and inflammatory skin disease: a Mendelian Randomization study		2
16	A phenome-wide association study (PheWAS) of COVID-19 outcomes by race using the electronic health records data in Michigan Medicine 2021 ,		2
15	A Modeling Framework for Exploring Sampling and Observation Process Biases in Genome and Phenome-wide Association Studies using Electronic Health Records		2
14	A powerful subset-based method identifies gene set associations and improves interpretation in UK Biobank. <i>American Journal of Human Genetics</i> , 2021 , 108, 669-681	11	2
13	Genome-wide analysis of 944 133 individuals provides insights into the etiology of haemorrhoidal disease. <i>Gut</i> , 2021 ,	19.2	2
12	Cluster Analysis and Genotype-Phenotype Assessment of Geographic Atrophy in Age-Related Macular Degeneration: Age-Related Eye Disease Study 2 Report 25. <i>Ophthalmology Retina</i> , 2021 , 5, 1061-1073	3.8	2
11	Unbiased immune profiling reveals a natural killer cell-peripheral nerve axis in fibromyalgia.. <i>Pain</i> , 2021 ,	8	2
10	Type 2 diabetes sex-specific effects associated with E167K coding variant in. <i>IScience</i> , 2021 , 24, 103196	6.1	1
9	Exploring Various Polygenic Risk Scores for Skin Cancer in the Phenomes of the Michigan Genomics Initiative and the UK Biobank with a Visual Catalog:PRSWeb		1
8	UK-Biobank Whole Exome Sequence Binary Phenome Analysis with Robust Region-based Rare Variant Test		1
7	Cancer PRSweb An Online Repository with Polygenic Risk Scores (PRS) for Major Cancer Traits and Their Phenome-wide Exploration in Two Independent Biobanks		1

6	LabWAS: novel findings and study design recommendations from a meta-analysis of clinical labs in two independent biobanks	1
5	The Effect of Genetic Variants Associated With Age-Related Macular Degeneration Varies With Age <i>2020, 61, 17</i>	1
4	On Cross-ancestry Cancer Polygenic Risk Scores	1
3	Changes in COVID-19-related outcomes and the impacts of the potential risk factors over time: a follow-up analysis	1
2	Genome-wide meta-analysis of iron status biomarkers and the effect of iron on all-cause mortality in HUNT	1
1	A Novel Variant in Gene Causes Extremely Low LDL-C Without Known Adverse Effects. <i>JACC: Case Reports, 2020, 2, 775-779</i>	1.2