Lars G Fritsche

List of Publications by Year in Descending Order

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	Global Prevalence of Post COVID-19 Condition or Long COVID: A Meta-Analysis and Systematic Review.. *Journal of Infectious Diseases*, **2022**,	7	30
112	Association of Smoking, Alcohol Consumption, Blood Pressure, Body Mass Index, and Glycemic Risk Factors With Age-Related Macular Degeneration: A Mendelian Randomization Study. *JAMA Ophthalmology*, **2021**,	3.9	2
111	Type 2 diabetes sex-specific effects associated with E167K coding variant in. *IScience*, **2021**, 24, 103196	6.1	1
110	A phenome-wide association study (PheWAS) of COVID-19 outcomes by race using the electronic health records data in Michigan Medicine **2021**,		2
109	A Phenome-Wide Association Study (PheWAS) of COVID-19 Outcomes by Race Using the Electronic Health Records Data in Michigan Medicine. *Journal of Clinical Medicine*, **2021**, 10,	5.1	6
108	A powerful subset-based method identifies gene set associations and improves interpretation in UK Biobank. *American Journal of Human Genetics*, **2021**, 108, 669-681	11	2
107	Genome-wide analysis of 944 133 individuals provides insights into the etiology of haemorrhoidal disease. *Gut*, **2021**,	19.2	2
106	Genome-wide association study of cardiac troponin I in the general population. *Human Molecular Genetics*, **2021**, 30, 2027-2039	5.6	5
105	Assessment of a causal relationship between body mass index and atopic dermatitis. *Journal of Allergy and Clinical Immunology*, **2021**, 147, 400-403	11.5	6
104	Patterns of repeated diagnostic testing for COVID-19 in relation to patient characteristics and outcomes. *Journal of Internal Medicine*, **2021**, 289, 726-737	10.8	6
103	Cluster Analysis and Genotype-Phenotype Assessment of Geographic Atrophy in Age-Related Macular Degeneration: Age-Related Eye Disease Study 2 Report 25. *Ophthalmology Retina*, **2021**, 5, 1061-1073	3.8	2
102	A genome-wide association study with 1,126,563 individuals identifies new risk loci for Alzheimer's disease. *Nature Genetics*, **2021**, 53, 1276-1282	36.3	40
101	On cross-ancestry cancer polygenic risk scores. *PLoS Genetics*, **2021**, 17, e1009670	6	4
100	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. *Cell*, **2021**, 184, 4784-4818.e17	36.1	14
99	Unbiased immune profiling reveals a natural killer cell-peripheral nerve axis in fibromyalgia.. *Pain*, **2021**,	8	2
98	Phenotype risk scores (PheRS) for pancreatic cancer using time-stamped electronic health record data: Discovery and validation in two large biobanks. *Journal of Biomedical Informatics*, **2021**, 113, 103652	10.2	5
97	Characteristics Associated With Racial/Ethnic Disparities in COVID-19 Outcomes in an Academic Health Care System. *JAMA Network Open*, **2020**, 3, e2025197	10.4	97

96	Scalable generalized linear mixed model for region-based association tests in large biobanks and cohorts. *Nature Genetics*, **2020**, 52, 634-639	36.3	41
95	Exploring and visualizing large-scale genetic associations by using PheWeb. *Nature Genetics*, **2020**, 52, 550-552	36.3	41
94	An analytic framework for exploring sampling and observation process biases in genome and phenome-wide association studies using electronic health records. *Statistics in Medicine*, **2020**, 39, 1965-1979	2.3	3
93	Age-of-onset information helps identify 76 genetic variants associated with allergic disease. *PLoS Genetics*, **2020**, 16, e1008725	6	10
92	A Fast and Accurate Method for Genome-Wide Time-to-Event Data Analysis and Its Application to UK Biobank. *American Journal of Human Genetics*, **2020**, 107, 222-233	11	12
91	Interaction analysis under misspecification of main effects: Some common mistakes and simple solutions. *Statistics in Medicine*, **2020**, 39, 1675-1694	2.3	2
90	Mitochondrial genome-wide association study of migraine - the HUNT Study. *Cephalalgia*, **2020**, 40, 625-634	6.1	6
89	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. *Nature Genetics*, **2020**, 52, 494-504	36.3	39
88	LabWAS: Novel findings and study design recommendations from a meta-analysis of clinical labs in two independent biobanks. *PLoS Genetics*, **2020**, 16, e1009077	6	6
87	A Novel Variant in Gene Causes Extremely Low LDL-C Without Known Adverse Effects. *JACC: Case Reports*, **2020**, 2, 775-779	1.2	
86	COVID-19 outcomes, risk factors and associations by race: a comprehensive analysis using electronic health records data in Michigan Medicine **2020**,		20
85	The emerging landscape of health research based on biobanks linked to electronic health records: Existing resources, statistical challenges, and potential opportunities. *Statistics in Medicine*, **2020**, 39, 773-800	2.3	15
84	Heritability of the Fibromyalgia Phenotype Varies by Age. *Arthritis and Rheumatology*, **2020**, 72, 815-823	9.5	5
83	UK Biobank Whole-Exome Sequence Binary Phenome Analysis with Robust Region-Based Rare-Variant Test. *American Journal of Human Genetics*, **2020**, 106, 3-12	11	21
82	Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program. *Circulation*, **2020**, 142, 1633-1646	16.7	24
81	Cancer PRSweb: An Online Repository with Polygenic Risk Scores for Major Cancer Traits and Their Evaluation in Two Independent Biobanks. *American Journal of Human Genetics*, **2020**, 107, 815-836	11	20
80	GWAS of thyroid stimulating hormone highlights pleiotropic effects and inverse association with thyroid cancer. *Nature Communications*, **2020**, 11, 3981	17.4	21
79	MEPE loss-of-function variant associates with decreased bone mineral density and increased fracture risk. *Nature Communications*, **2020**, 11, 4093	17.4	4

78	Common variants in SOX-2 and congenital cataract genes contribute to age-related nuclear cataract. *Communications Biology*, **2020**, 3, 755	6.7	3
77	The Effect of Genetic Variants Associated With Age-Related Macular Degeneration Varies With Age **2020**, 61, 17		1
76	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. *Nature Communications*, **2020**, 11, 6417	17.4	17
75	Validating Online Measures of Cognitive Ability in Genes for Good, a Genetic Study of Health and Behavior. *Assessment*, **2020**, 27, 136-148	3.7	5
74	Prediction of Ankylosing Spondylitis in the HUNT Study by a Genetic Risk Score Combining 110 Single-nucleotide Polymorphisms of Genome-wide Significance. *Journal of Rheumatology*, **2020**, 47, 204-210	4.1	9
73	Evidence of a causal relationship between body mass index and psoriasis: A mendelian randomization study. *PLoS Medicine*, **2019**, 16, e1002739	11.6	77
72	Genes for Good: Engaging the Public in Genetics Research via Social Media. *American Journal of Human Genetics*, **2019**, 105, 65-77	11	8
71	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. *PLoS Genetics*, **2019**, 15, e1008202	6	18
70	Sex-specific and pleiotropic effects underlying kidney function identified from GWAS meta-analysis. *Nature Communications*, **2019**, 10, 1847	17.4	22
69	Robust meta-analysis of biobank-based genome-wide association studies with unbalanced binary phenotypes. *Genetic Epidemiology*, **2019**, 43, 462-476	2.6	5
68	Retinal transcriptome and eQTL analyses identify genes associated with age-related macular degeneration. *Nature Genetics*, **2019**, 51, 606-610	36.3	93
67	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. *Journal of the National Cancer Institute*, **2019**, 111, 146-157	9.7	67
66	Meta-MultiSKAT: Multiple phenotype meta-analysis for region-based association test. *Genetic Epidemiology*, **2019**, 43, 800-814	2.6	7
65	A Fast and Accurate Method for Genome-wide Scale Phenome-wide G E Analysis and Its Application to UK Biobank. *American Journal of Human Genetics*, **2019**, 105, 1182-1192	11	10
64	Estimation of DNA contamination and its sources in genotyped samples. *Genetic Epidemiology*, **2019**, 43, 980-995	2.6	3
63	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. *Nature Genetics*, **2019**, 51, 237-244	36.3	516
62	Variation in Serum PCSK9 (Proprotein Convertase Subtilisin/Kexin Type 9), Cardiovascular Disease Risk, and an Investigation of Potential Unanticipated Effects of PCSK9 Inhibition. *Circulation Genomic and Precision Medicine*, **2019**, 12, e002335	5.2	3
61	Genome-wide analysis yields new loci associating with aortic valve stenosis. *Nature Communications* , **2018**, 9, 987	17.4	56

60	Genome-wide analysis of disease progression in age-related macular degeneration. *Human Molecular Genetics*, **2018**, 27, 929-940	5.6	37
59	Genome-wide Study of Atrial Fibrillation Identifies Seven Risk Loci and Highlights Biological Pathways and Regulatory Elements Involved in Cardiac Development. *American Journal of Human Genetics*, **2018**, 102, 103-115	11	53
58	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. *Nature Genetics*, **2018**, 50, 1234-1239	36.3	254
57	Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies. *Nature Genetics*, **2018**, 50, 1335-1341	36.3	375
56	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. *Nature Communications*, **2018**, 9, 2252	17.4	71
55	Geographic distribution of rare variants associated with age-related macular degeneration. *Molecular Vision*, **2018**, 24, 75-82	2.3	2
54	First Genome-Wide Association Study of Latent Autoimmune Diabetes in Adults Reveals Novel Insights Linking Immune and Metabolic Diabetes. *Diabetes Care*, **2018**, 41, 2396-2403	14.6	57
53	Association of Polygenic Risk Scores for Multiple Cancers in a Phenome-wide Study: Results from The Michigan Genomics Initiative. *American Journal of Human Genetics*, **2018**, 102, 1048-1061	11	83
52	Association of Genetic Variants With Response to Anti-Vascular Endothelial Growth Factor Therapy in Age-Related Macular Degeneration. *JAMA Ophthalmology*, **2018**, 136, 875-884	3.9	20
51	In Silico Functional Meta-Analysis of 5,962 ABCA4 Variants in 3,928 Retinal Dystrophy Cases. *Human Mutation*, **2017**, 38, 400-408	4.7	82
50	Bivariate Analysis of Age-Related Macular Degeneration Progression Using Genetic Risk Scores. *Genetics*, **2017**, 206, 119-133	4	31
49	Protein-altering and regulatory genetic variants near GATA4 implicated in bicuspid aortic valve. *Nature Communications*, **2017**, 8, 15481	17.4	52
48	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
47	Exome chip meta-analysis identifies novel loci and East Asian-specific coding variants that contribute to lipid levels and coronary artery disease. *Nature Genetics*, **2017**, 49, 1722-1730	36.3	83
46	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. *Nature Genetics*, **2017**, 49, 1752-1757	36.3	256
45	A Scalable Bayesian Method for Integrating Functional Information in Genome-wide Association Studies. *American Journal of Human Genetics*, **2017**, 101, 404-416	11	41
44	Improving power of association tests using multiple sets of imputed genotypes from distributed reference panels. *Genetic Epidemiology*, **2017**, 41, 744-755	2.6	13
43	HDL-cholesterol levels and risk of age-related macular degeneration: a multiethnic genetic study using Mendelian randomization. *International Journal of Epidemiology*, **2017**, 46, 1891-1902	7.8	45

42	A large genome-wide association study of age-related macular degeneration highlights contributions of rare and common variants. *Nature Genetics*, **2016**, 48, 134-43	36.3	769
41	A global reference for human genetic variation. *Nature*, **2015**, 526, 68-74	50.4	8599
40	No clinically significant association between CFH and ARMS2 genotypes and response to nutritional supplements: AREDS report number 38. *Ophthalmology*, **2014**, 121, 2173-80	7.3	76
39	Age-related macular degeneration: genetics and biology coming together. *Annual Review of Genomics and Human Genetics*, **2014**, 15, 151-71	9.7	293
38	Expanding the spectrum of PTH1R mutations in patients with primary failure of tooth eruption. *Clinical Oral Investigations*, **2014**, 18, 377-84	4.2	32
37	Genotype imputation in genome-wide association studies. *Current Protocols in Human Genetics*, **2013**, Chapter 1, Unit 1.25	3.2	29
36	Age-related macular degeneration and coronary heart disease: evaluation of genetic and environmental associations. *European Journal of Medical Genetics*, **2013**, 56, 72-9	2.6	14
35	Seven new loci associated with age-related macular degeneration. *Nature Genetics*, **2013**, 45, 433-9, 439e1-2	36.3	577
34	Modelling the genetic risk in age-related macular degeneration. *PLoS ONE*, **2012**, 7, e37979	3.7	65
33	A subgroup of age-related macular degeneration is associated with mono-allelic sequence variants in the ABCA4 gene **2012**, 53, 2112-8		67
32	Complement factor H genetic variant and age-related macular degeneration: effect size, modifiers and relationship to disease subtype. *International Journal of Epidemiology*, **2012**, 41, 250-62	7.8	70
31	Multicenter cohort association study of SLC2A1 single nucleotide polymorphisms and age-related macular degeneration. *Molecular Vision*, **2012**, 18, 657-74	2.3	5
30	Evidence of association of APOE with age-related macular degeneration: a pooled analysis of 15 studies. *Human Mutation*, **2011**, 32, 1407-16	4.7	99
29	Risk- and non-risk-associated variants at the 10q26 AMD locus influence ARMS2 mRNA expression but exclude pathogenic effects due to protein deficiency. *Human Molecular Genetics*, **2011**, 20, 1387-99	5.6	57
28	Variations in apolipoprotein E frequency with age in a pooled analysis of a large group of older people. *American Journal of Epidemiology*, **2011**, 173, 1357-64	3.8	67
27	Age-related macular degeneration with discordant late stage phenotypes in monozygotic twins. *Ophthalmic Genetics*, **2011**, 32, 237-44	1.2	6
26	CRX ChIP-seq reveals the cis-regulatory architecture of mouse photoreceptors. *Genome Research*, **2010**, 20, 1512-25	9.7	145
25	An imbalance of human complement regulatory proteins CFHR1, CFHR3 and factor H influences risk for age-related macular degeneration (AMD). *Human Molecular Genetics*, **2010**, 19, 4694-704	5.6	153

24	Age-related macular degeneration and functional promoter and coding variants of the apolipoprotein E gene. *Human Mutation*, **2009**, 30, 1048-53	4.7	34
23	CFH, C3 and ARMS2 are significant risk loci for susceptibility but not for disease progression of geographic atrophy due to AMD. *PLoS ONE*, **2009**, 4, e7418	3.7	70
22	Age-related macular degeneration is associated with an unstable ARMS2 (LOC387715) mRNA. *Nature Genetics*, **2008**, 40, 892-6	36.3	320
21	Systemic complement activation in age-related macular degeneration. *PLoS ONE*, **2008**, 3, e2593	3.7	255
20	Case-control genetic association study of fibulin-6 (FBLN6 or HMCN1) variants in age-related macular degeneration (AMD). *Human Mutation*, **2007**, 28, 406-13	4.7	26
19	Assessment of the contribution of CFH and chromosome 10q26 AMD susceptibility loci in a Russian population isolate. *British Journal of Ophthalmology*, **2007**, 91, 576-8	5.5	27
18	Defective complement control of factor H (Y402H) and FHL-1 in age-related macular degeneration. *Molecular Immunology*, **2007**, 44, 3398-406	4.3	154
17	Hypothetical LOC387715 is a second major susceptibility gene for age-related macular degeneration, contributing independently of complement factor H to disease risk. *Human Molecular Genetics*, **2005**, 14, 3227-36	5.6	656
16	The HUNT Study: a population-based cohort for genetic research		3
15	Global Biobank Meta-analysis Initiative: powering genetic discovery across human diseases		6
14	Global Prevalence of Post-Acute Sequelae of COVID-19 (PASC) or Long COVID: A Meta-Analysis and Systematic Review		4
13	The Emerging Landscape of Epidemiological Research Based on Biobanks Linked to Electronic Health Records: Existing Resources, Analytic Challenges and Potential Opportunities		6
12	Evidence of a common causal relationship between body mass index and inflammatory skin disease: a Mendelian Randomization study		2
11	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
10	UK-Biobank Whole Exome Sequence Binary Phenome Analysis with Robust Region-based Rare Variant Test		1
9	Cancer PRSweb an Online Repository with Polygenic Risk Scores (PRS) for Major Cancer Traits and Their Phenome-wide Exploration in Two Independent Biobanks		1
8	LabWAS: novel findings and study design recommendations from a meta-analysis of clinical labs in two independent biobanks		1
7	Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies		6

6	Genome-wide association study of 1 million people identifies 111 loci for atrial fibrillation	4
5	A Modeling Framework for Exploring Sampling and Observation Process Biases in Genome and Phenome-wide Association Studies using Electronic Health Records	2
4	Scalable generalized linear mixed model for region-based association tests in large biobanks and cohorts	7
3	On Cross-ancestry Cancer Polygenic Risk Scores	1
2	Changes in COVID-19-related outcomes and the impacts of the potential risk factors over time: a follow-up analysis	1
1	Genome-wide meta-analysis of iron status biomarkers and the effect of iron on all-cause mortality in HUNT	1