Lars G Fritsche

List of Publications by Year
in descending order

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102 papers	27,430 citations	50244 46 h-index	29127 104 g-index
142 all docs	142 docs citations	142 times ranked	44328 citing authors

#	Article	IF	Citations
1	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
2	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.	9.4	1,307
3	A large genome-wide association study of age-related macular degeneration highlights contributions of rare and common variants. Nature Genetics, 2016, 48, 134-143.	9.4	1,167
4	Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies. Nature Genetics, 2018, 50, 1335-1341.	9.4	896
5	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, 3227-3236.	1.4	741
6	Seven new loci associated with age-related macular degeneration. Nature Genetics, 2013, 45, 433-439.	9.4	687
7	Global Prevalence of Post-Coronavirus Disease 2019 (COVID-19) Condition or Long COVID: A Meta-Analysis and Systematic Review. Journal of Infectious Diseases, 2022, 226, 1593-1607.	1.9	559
8	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. Nature Genetics, 2018, 50, 1234-1239.	9.4	547
9	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
10	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. Nature Genetics, 2017, 49, 1752-1757.	9.4	432
11	A genome-wide association study with 1,126,563 individuals identifies new risk loci for Alzheimerâ€™s disease. Nature Genetics, 2021, 53, 1276-1282.	9.4	430
12	Age-Related Macular Degeneration: Genetics and Biology Coming Together. Annual Review of Genomics and Human Genetics, 2014, 15, 151-171.	2.5	394
13	Age-related macular degeneration is associated with an unstable ARMS2 (LOC387715) mRNA. Nature Genetics, 2008, 40, 892-896.	9.4	367
14	Systemic Complement Activation in Age-Related Macular Degeneration. PLoS ONE, 2008, 3, e2593.	1.1	308
15	Retinal transcriptome and eQTL analyses identify genes associated with age-related macular degeneration. Nature Genetics, 2019, 51, 606-610.	9.4	201
16	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. Cell, 2021, 184, 4784-4818.e17.	13.5	188
17	CRX ChIP-seq reveals the cis-regulatory architecture of mouse photoreceptors. Genome Research, 2010, 20, 1512-1525.	2.4	183
18	Characteristics Associated With Racial/Ethnic Disparities in COVID-19 Outcomes in an Academic Health Care System. JAMA Network Open, 2020, 3, e2025197.	2.8	182

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19	Defective complement control of Factor H (Y402H) and FHL-1 in age-related macular degeneration. Molecular Immunology, 2007, 44, 3398-3406.	1.0	181
20	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, 4694-4704.	1.4	178
21	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.	2.6	147
22	Evidence of a causal relationship between body mass index and psoriasis: A mendelian randomization study. PLoS Medicine, 2019, 16, e1002739.	3.9	144
23	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.	9.4	138
24	Evidence of association ofAPOEwith age-related macular degeneration - a pooled analysis of 15 studies. Human Mutation, 2011, 32, 1407-1416.	1.1	130
25	Exome chip meta-analysis identifies novel loci and East Asianâ€“specific coding variants that contribute to lipid levels and coronary artery disease. Nature Genetics, 2017, 49, 1722-1730.	9.4	129
26	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. Journal of the National Cancer Institute, 2019, 111, 146-157.	3.0	129
27	Exploring and visualizing large-scale genetic associations by using PheWeb. Nature Genetics, 2020, 52, 550-552.	9.4	129
28	Scalable generalized linear mixed model for region-based association tests in large biobanks and cohorts. Nature Genetics, 2020, 52, 634-639.	9.4	124
29	In SilicoFunctional Meta-Analysis of 5,962ABCA4Variants in 3,928 Retinal Dystrophy Cases. Human Mutation, 2017, 38, 400-408.	1.1	118
30	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.	4.3	99
31	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. Nature Communications, 2018, 9, 2252.	5.8	99
32	Genome-wide analysis yields new loci associating with aortic valve stenosis. Nature Communications, 2018, 9, 987.	5.8	91
33	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.	1.1	91
34	Protein-altering and regulatory genetic variants near GATA4 implicated in bicuspid aortic valve. Nature Communications, 2017, 8, 15481.	5.8	90
35	No Clinically Significant Association between CFH and ARMS2 Genotypes and Response to Nutritional Supplements. Ophthalmology, 2014, 121, 2173-2180.	2.5	86
36	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.	2.6	86

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37	GWAS of thyroid stimulating hormone highlights pleiotropic effects and inverse association with thyroid cancer. Nature Communications, 2020, 11, 3981.	5.8	86
38	Variations in Apolipoprotein E Frequency With Age in a Pooled Analysis of a Large Group of Older People. American Journal of Epidemiology, 2011, 173, 1357-1364.	1.6	85
39	Complement factor H genetic variant and age-related macular degeneration: effect size, modifiers and relationship to disease subtype. International Journal of Epidemiology, 2012, 41, 250-262.	0.9	79
40	Modelling the Genetic Risk in Age-Related Macular Degeneration. PLoS ONE, 2012, 7, e37979.	1.1	79
41	A Subgroup of Age-Related Macular Degeneration is Associated With Mono-Allelic Sequence Variants in theABCA4Gene. , 2012, 53, 2112.		79
42	Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program. Circulation, 2020, 142, 1633-1646.	1.6	78
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.	0.9	73
44	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, 1387-1399.	1.4	70
45	Genome-wide analysis of disease progression in age-related macular degeneration. Human Molecular Genetics, 2018, 27, 929-940.	1.4	67
46	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.	2.6	65
47	A Scalable Bayesian Method for Integrating Functional Information in Genome-wide Association Studies. American Journal of Human Genetics, 2017, 101, 404-416.	2.6	63
48	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.	0.8	57
49	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.	2.6	57
50	UK Biobank Whole-Exome Sequence Binary Phenome Analysis with Robust Region-Based Rare-Variant Test. American Journal of Human Genetics, 2020, 106, 3-12.	2.6	56
51	Sex-specific and pleiotropic effects underlying kidney function identified from GWAS meta-analysis. Nature Communications, 2019, 10, 1847.	5.8	55
52	Bivariate Analysis of Age-Related Macular Degeneration Progression Using Genetic Risk Scores. Genetics, 2017, 206, 119-133.	1.2	46
53	Expanding the spectrum of PTH1R mutations in patients with primary failure of tooth eruption. Clinical Oral Investigations, 2014, 18, 377-384.	1.4	45
54	Assessment of the contribution of CFH and chromosome 10q26 AMD susceptibility loci in a Russian population isolate. British Journal of Ophthalmology, 2007, 91, 576-578.	2.1	39

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55	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	5.8	39
56	Age-related macular degeneration and functional promoter and coding variants of the apolipoprotein E gene. Human Mutation, 2009, 30, 1048-1053.	1.1	36
57	Case-control genetic association study of fibulin-6 (FBLN6orHMCN1) variants in age-related macular degeneration (AMD). Human Mutation, 2007, 28, 406-413.	1.1	34
58	Genotype Imputation in Genomeâ€Wide Association Studies. Current Protocols in Human Genetics, 2013, 78, Unit 1.25.	3.5	34
59	On cross-ancestry cancer polygenic risk scores. PLoS Genetics, 2021, 17, e1009670.	1.5	32
60	Association of Genetic Variants With Response to Antiâ€“Vascular Endothelial Growth Factor Therapy in Age-Related Macular Degeneration. JAMA Ophthalmology, 2018, 136, 875.	1.4	30
61	Association of Smoking, Alcohol Consumption, Blood Pressure, Body Mass Index, and Glycemic Risk Factors With Age-Related Macular Degeneration. JAMA Ophthalmology, 2021, 139, 1299.	1.4	29
62	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.	1.5	28
63	Improving power of association tests using multiple sets of imputed genotypes from distributed reference panels. Genetic Epidemiology, 2017, 41, 744-755.	0.6	27
64	Age-of-onset information helps identify 76 genetic variants associated with allergic disease. PLoS Genetics, 2020, 16, e1008725.	1.5	27
65	Age-related macular degeneration and coronary heart disease: Evaluation ofÂgenetic and environmental associations. European Journal of Medical Genetics, 2013, 56, 72-79.	0.7	25
66	MEPE loss-of-function variant associates with decreased bone mineral density and increased fracture risk. Nature Communications, 2020, 11, 4093.	5.8	24
67	Genome-wide analysis identifies impaired axonogenesis in chronic overlapping pain conditions. Brain, 2022, 145, 1111-1123.	3.7	24
68	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, 1351.	1.0	23
69	Genome-wide analysis of 944 133 individuals provides insights into the etiology of haemorrhoidal disease. Gut, 2021, 70, 1538-1549.	6.1	21
70	A Fast and Accurate Method for Genome-wide Scale Phenome-wide G Ã— E Analysis and Its Application to UK Biobank. American Journal of Human Genetics, 2019, 105, 1182-1192.	2.6	20
71	Mitochondrial genome-wide association study of migraine â€“ the HUNT Study. Cephalalgia, 2020, 40, 625-634.	1.8	19
72	Genes for Good: Engaging the Public in Genetics Research via Social Media. American Journal of Human Genetics, 2019, 105, 65-77.	2.6	16

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73	Unbiased immune profiling reveals a natural killer cell-peripheral nerve axis in fibromyalgia. Pain, 2022, 163, e821-e836.	2.0	16
74	Heritability of the Fibromyalgia Phenotype Varies by Age. Arthritis and Rheumatology, 2020, 72, 815-823.	2.9	15
75	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.	2.5	15
76	LabWAS: Novel findings and study design recommendations from a meta-analysis of clinical labs in two independent biobanks. PLoS Genetics, 2020, 16, e1009077.	1.5	14
77	Assessment of a causal relationship between body mass index and atopic dermatitis. Journal of Allergy and Clinical Immunology, 2021, 147, 400-403.	1.5	13
78	Patterns of repeated diagnostic testing for COVIDâ€19 in relation to patient characteristics and outcomes. Journal of Internal Medicine, 2021, 289, 726-737.	2.7	13
79	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.	1.0	12
80	An analytic framework for exploring sampling and observation process biases in genome and phenomeâ€wide association studies using electronic health records. Statistics in Medicine, 2020, 39, 1965-1979.	0.8	12
81	Estimation of DNA contamination and its sources in genotyped samples. Genetic Epidemiology, 2019, 43, 980-995.	0.6	11
82	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.	1.6	11
83	Genome-wide association study of cardiac troponin I in the general population. Human Molecular Genetics, 2021, 30, 2027-2039.	1.4	11
84	Genome-wide meta-analysis of iron status biomarkers and the effect of iron on all-cause mortality in HUNT. Communications Biology, 2022, 5, .	2.0	11
85	Common variants in SOX-2 and congenital cataract genes contribute to age-related nuclear cataract. Communications Biology, 2020, 3, 755.	2.0	10
86	Type 2 diabetes sex-specific effects associated with E167K coding variant in TM6SF2. IScience, 2021, 24, 103196.	1.9	10
87	Metaâ€MultiSKAT: Multiple phenotype metaâ€analysis for regionâ€based association test. Genetic Epidemiology, 2019, 43, 800-814.	0.6	9
88	Developing and validating a multivariable prediction model which predicts progression of intermediate to late age-related macular degenerationâ€”the PINNACLE trial protocol. Eye, 2023, 37, 1275-1283.	1.1	9
89	A powerful subset-based method identifies gene set associations and improves interpretation in UK Biobank. American Journal of Human Genetics, 2021, 108, 669-681.	2.6	8
90	Age-related macular degeneration with discordant late stage phenotypes in monozygotic twins. Ophthalmic Genetics, 2011, 32, 237-244.	0.5	7

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91	Robust metaâ€analysis of biobankâ€based genomeâ€wide association studies with unbalanced binary phenotypes. Genetic Epidemiology, 2019, 43, 462-476.	0.6	7
92	Validating Online Measures of Cognitive Ability in Genes for Good, a Genetic Study of Health and Behavior. Assessment, 2020, 27, 136-148.	1.9	7
93	Polygenic Liability to Depression Is Associated With Multiple Medical Conditions in the Electronic Health Record: Phenome-wide Association Study of 46,782 Individuals. Biological Psychiatry, 2022, 92, 923-931.	0.7	7
94	Cluster Analysis and Genotypeâ€“Phenotype Assessment of Geographic Atrophy in Age-Related Macular Degeneration. Ophthalmology Retina, 2021, 5, 1061-1073.	1.2	6
95	Changes in COVID-19-related outcomes, potential risk factors and disparities over time. Epidemiology and Infection, 2021, 149, .	1.0	5
96	Multicenter cohort association study of SLC2A1 single nucleotide polymorphisms and age-related macular degeneration. Molecular Vision, 2012, 18, 657-74.	1.1	5
97	The Effect of Genetic Variants Associated With Age-Related Macular Degeneration Varies With Age. , 2020, 61, 17.		4
98	Interaction analysis under misspecification of main effects: Some common mistakes and simple solutions. Statistics in Medicine, 2020, 39, 1675-1694.	0.8	4
99	Geographic distribution of rare variants associated with age-related macular degeneration. Molecular Vision, 2018, 24, 75-82.	1.1	4
100	Understanding the Patterns of Serological Testing for COVID-19 Pre- and Post-Vaccination Rollout in Michigan. Journal of Clinical Medicine, 2021, 10, 4341.	1.0	3
101	Imbalance of complement regulatory proteins CFHR1, CFHR3 and factor H influences risk for age related macular degeneration (AMD). Molecular Immunology, 2010, 47, 2211-2211.	1.0	0
102	A Novel Variant in APOB Gene Causes Extremely Low LDL-C Without Known Adverse Effects. JACC: Case Reports, 2020, 2, 775-779.	0.3	0