

# Harald Grallert

## List of Publications by Year in descending order

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Version: 2024-02-01

119  
papers

24,154  
citations

30070

54  
h-index

18130

120  
g-index

124  
all docs

124  
docs citations

124  
times ranked

34807  
citing authors

#	ARTICLE	IF	CITATIONS
1	Novel associations between inflammation-related proteins and adiposity: A targeted proteomics approach across four population-based studies. <i>Translational Research</i> , 2022, 242, 93-104.	5.0	13
2	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function. <i>Nature Genetics</i> , 2022, 54, 18-29.	21.4	60
3	Extensive identification of genes involved in congenital and structural heart disorders and cardiomyopathy. , 2022, 1, 157-173.		22
4	Epigenome-wide association study of incident type 2 diabetes: a meta-analysis of five prospective European cohorts. <i>Diabetologia</i> , 2022, 65, 763-776.	6.3	28
5	Colocalization analysis of pancreas eQTLs with risk loci from alcoholic and novel non-alcoholic chronic pancreatitis GWAS suggests potential disease causing mechanisms. <i>Pancreatology</i> , 2022, 22, 449-456.	1.1	3
6	A Family and a Genome-Wide Polygenic Risk Score Are Independently Associated With Stroke in a Population-Based Study. <i>Stroke</i> , 2022, 53, 2331-2339.	2.0	4
7	A randomization-based causal inference framework for uncovering environmental exposure effects on human gut microbiota. <i>PLoS Computational Biology</i> , 2022, 18, e1010044.	3.2	8
8	Obesity Genes and Weight Loss During Lifestyle Intervention in Children With Obesity. <i>JAMA Pediatrics</i> , 2021, 175, e205142.	6.2	21
9	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021, 12, 24.	12.8	87
10	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. <i>Human Molecular Genetics</i> , 2021, 30, 393-409.	2.9	32
11	Revealing the role of the human blood plasma proteome in obesity using genetic drivers. <i>Nature Communications</i> , 2021, 12, 1279.	12.8	50
12	Associations between habitual diet, metabolic disease, and the gut microbiota using latent Dirichlet allocation. <i>Microbiome</i> , 2021, 9, 61.	11.1	47
13	Association between Single Nucleotide Polymorphisms and Weight Reduction in Behavioural Interventionsâ€”A Pooled Analysis. <i>Nutrients</i> , 2021, 13, 819.	4.1	12
14	Metabolic syndrome and the plasma proteome: from association to causation. <i>Cardiovascular Diabetology</i> , 2021, 20, 111.	6.8	19
15	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	21.4	341
16	Comparison of genetic risk prediction models to improve prediction of coronary heart disease in two large cohorts of the MONICA/KORA study. <i>Genetic Epidemiology</i> , 2021, 45, 633-650.	1.3	6
17	Synergistic effect of genetic polymorphisms in <i>TLR6</i> and <i>TLR10</i> genes on the risk of pulmonary tuberculosis in a Moldavian population. <i>Innate Immunity</i> , 2021, 27, 365-376.	2.4	5
18	Linking the <i>FTO</i> obesity rs1421085 variant circuitry to cellular, metabolic, and organismal phenotypes in vivo. <i>Science Advances</i> , 2021, 7, .	10.3	19

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19	N-glycosylation of immunoglobulin G predicts incident hypertension. <i>Journal of Hypertension</i> , 2021, 39, 2527-2533.	0.5	13
20	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	27.8	183
21	Genome-wide association study in 8,956 German individuals identifies influence of ABO histo-blood groups on gut microbiome. <i>Nature Genetics</i> , 2021, 53, 147-155.	21.4	101
22	Human genome diversity data reveal that L564P is the predominant TPC2 variant and a prerequisite for the blond hair associated M484L gain-of-function effect. <i>PLoS Genetics</i> , 2021, 17, e1009236.	3.5	15
23	A Panel of 6 Biomarkers Significantly Improves the Prediction of Type 2 Diabetes in the MONICA/KORA Study Population. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021, 106, 1647-1659.	3.6	11
24	Smoking-related changes in DNA methylation and gene expression are associated with cardio-metabolic traits. <i>Clinical Epigenetics</i> , 2020, 12, 157.	4.1	31
25	Deciphering the Plasma Proteome of Type 2 Diabetes. <i>Diabetes</i> , 2020, 69, 2766-2778.	0.6	34
26	Rare Variants in Specific Lysosomal Genes Are Associated With Parkinson's Disease. <i>Movement Disorders</i> , 2020, 35, 1245-1248.	3.9	37
27	Investigation of Adiposity Measures and Operational Taxonomic unit (OTU) Data Transformation Procedures in Stool Samples from a German Cohort Study Using Machine Learning Algorithms. <i>Microorganisms</i> , 2020, 8, 547.	3.6	1
28	Private variants in PRKN are associated with late-onset Parkinson's disease. <i>Parkinsonism and Related Disorders</i> , 2020, 75, 24-26.	2.2	4
29	Abstract 21: Deciphering the Plasma Proteome of Type 2 Diabetes. <i>Circulation</i> , 2020, 141, .	1.6	1
30	Mouse mutant phenotyping at scale reveals novel genes controlling bone mineral density. <i>PLoS Genetics</i> , 2020, 16, e1009190.	3.5	19
31	Genome-wide Association Study of Change in Fasting Glucose over time in 13,807 non-diabetic European Ancestry Individuals. <i>Scientific Reports</i> , 2019, 9, 9439.	3.3	5
32	Associations between fecal bile acids, neutral sterols, and serum lipids in the KORA FF4 study. <i>Atherosclerosis</i> , 2019, 288, 1-8.	0.8	8
33	CWAS on longitudinal growth traits reveals different genetic factors influencing infant, child, and adult BMI. <i>Science Advances</i> , 2019, 5, eaaw3095.	10.3	86
34	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. <i>American Journal of Human Genetics</i> , 2019, 105, 15-28.	6.2	21
35	Associations between usual food intake and faecal sterols and bile acids: results from the Cooperative Health Research in the Augsburg Region (KORA FF4) study. <i>British Journal of Nutrition</i> , 2019, 122, 309-321.	2.3	9
36	Association of alcohol consumption with allergic disease and asthma: a multi-centre Mendelian randomization analysis. <i>Addiction</i> , 2019, 114, 216-225.	3.3	14

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37	Genetic variation in TLR pathway and the risk of pulmonary tuberculosis in a Moldavian population. <i>Infection, Genetics and Evolution</i> , 2019, 68, 84-90.	2.3	19
38	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor $\alpha$ . <i>JAMA Cardiology</i> , 2018, 3, 463.	6.1	33
39	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018, 50, 559-571.	21.4	356
40	Identification of genetic elements in metabolism by high-throughput mouse phenotyping. <i>Nature Communications</i> , 2018, 9, 288.	12.8	59
41	Genome-wide meta-analysis identifies novel determinants of circulating serum progranulin. <i>Human Molecular Genetics</i> , 2018, 27, 546-558.	2.9	15
42	High-throughput DNA methylation analysis in anorexia nervosa confirms <i>TNXB</i> hypermethylation. <i>World Journal of Biological Psychiatry</i> , 2018, 19, 187-199.	2.6	28
43	Genome-wide association study identifies inversion in the <i>CTRB1-CTRB2</i> locus to modify risk for alcoholic and non-alcoholic chronic pancreatitis. <i>Gut</i> , 2018, 67, 1855-1863.	12.1	97
44	IgG glycosylation and DNA methylation are interconnected with smoking. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 637-648.	2.4	33
45	Metabolite ratios as potential biomarkers for type 2 diabetes: a DIRECT study. <i>Diabetologia</i> , 2018, 61, 117-129.	6.3	32
46	Characterization of missing values in untargeted MS-based metabolomics data and evaluation of missing data handling strategies. <i>Metabolomics</i> , 2018, 14, 128.	3.0	138
47	Genetic variation in TCF7L2 rs7903146 and history of GDM negatively and independently impact on diabetes-associated metabolic traits. <i>Diabetes Research and Clinical Practice</i> , 2018, 146, 251-257.	2.8	11
48	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. <i>Nature Genetics</i> , 2018, 50, 1505-1513.	21.4	1,331
49	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , 2018, 103, 691-706.	6.2	326
50	Genome-Wide Association Study on Immunoglobulin G Glycosylation Patterns. <i>Frontiers in Immunology</i> , 2018, 9, 277.	4.8	66
51	Common eye diseases in older adults of southern Germany: results from the KORA-Age study. <i>Age and Ageing</i> , 2017, 46, 481-486.	1.6	17
52	Connecting genetic risk to disease end points through the human blood plasma proteome. <i>Nature Communications</i> , 2017, 8, 14357.	12.8	460
53	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	21.4	426
54	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, 14977.	12.8	169

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55	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017, 66, 2888-2902.	0.6	615
56	ANGPTL8 (Betatrophin) is Expressed in Visceral Adipose Tissue and Relates to Human Hepatic Steatosis in Two Independent Clinical Collectives. <i>Hormone and Metabolic Research</i> , 2017, 49, 343-349.	1.5	24
57	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , 2017, 541, 81-86.	27.8	743
58	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 2017, 8, 80.	12.8	147
59	Immediate reduction of serum citrulline but no change of steroid profile after initiation of metformin in individuals with type 2 diabetes. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2017, 174, 114-119.	2.5	15
60	Network inference from glycoproteomics data reveals new reactions in the IgG glycosylation pathway. <i>Nature Communications</i> , 2017, 8, 1483.	12.8	67
61	Investigating the causal effect of smoking on hay fever and asthma: a Mendelian randomization meta-analysis in the CARTA consortium. <i>Scientific Reports</i> , 2017, 7, 2224.	3.3	35
62	Genome-wide methylation data mirror ancestry information. <i>Epigenetics and Chromatin</i> , 2017, 10, 1.	3.9	120
63	pulver: an R package for parallel ultra-rapid p-value computation for linear regression interaction terms. <i>BMC Bioinformatics</i> , 2017, 18, 429.	2.6	1
64	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. <i>PLoS Medicine</i> , 2017, 14, e1002383.	8.4	341
65	Genome-wide physical activity interactions in adiposity $\hat{\epsilon}$ . A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	3.5	158
66	Exome-wide association study reveals novel susceptibility genes to sporadic dilated cardiomyopathy. <i>PLoS ONE</i> , 2017, 12, e0172995.	2.5	92
67	Epigenetic Signatures at AQP3 and SOCS3 Engage in Low-Grade Inflammation across Different Tissues. <i>PLoS ONE</i> , 2016, 11, e0166015.	2.5	14
68	Association between DNA Methylation in Whole Blood and Measures of Glucose Metabolism: KORA F4 Study. <i>PLoS ONE</i> , 2016, 11, e0152314.	2.5	81
69	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016, 17, 255.	8.8	251
70	Association of common variants identified by recent genome-wide association studies with obesity in Chinese children: a case-control study. <i>BMC Medical Genetics</i> , 2016, 17, 7.	2.1	35
71	Analysis with the exome array identifies multiple new independent variants in lipid loci. <i>Human Molecular Genetics</i> , 2016, 25, 4094-4106.	2.9	19
72	A genome-wide approach to children's aggressive behavior: <i>The EAGLE consortium</i>. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2016, 171, 562-572.	1.7	153

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73	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, 13357.	12.8	74
74	Characterization of the metabolic profile associated with serum 25-hydroxyvitamin D: a cross-sectional analysis in population-based data. <i>International Journal of Epidemiology</i> , 2016, 45, 1469-1481.	1.9	19
75	Numerous Genes in Loci Associated With Body Fat Distribution Are Linked to Adipose Function. <i>Diabetes</i> , 2016, 65, 433-437.	0.6	50
76	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. <i>Diabetes</i> , 2016, 65, 803-817.	0.6	131
77	High-Fat Diet During Mouse Pregnancy and Lactation Targets GIP-Regulated Metabolic Pathways in Adult Male Offspring. <i>Diabetes</i> , 2016, 65, 574-584.	0.6	14
78	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016, 7, 10495.	12.8	245
79	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , 2016, 7, 10494.	12.8	153
80	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016, 7, 10023.	12.8	412
81	Genetic variants of lipase activity in chronic pancreatitis: Table 1. <i>Gut</i> , 2016, 65, 184-185.	12.1	10
82	Specific Metabolic Markers Are Associated with Future Waist-Gaining Phenotype in Women. <i>PLoS ONE</i> , 2016, 11, e0157733.	2.5	5
83	Extensive alterations of the whole-blood transcriptome are associated with body mass index: results of an mRNA profiling study involving two large population-based cohorts. <i>BMC Medical Genomics</i> , 2015, 8, 65.	1.5	40
84	The stool microbiota of insulin resistant women with recent gestational diabetes, a high risk group for type 2 diabetes. <i>Scientific Reports</i> , 2015, 5, 13212.	3.3	105
85	Genome-wide association study identifies new susceptibility loci for cutaneous lupus erythematosus. <i>Experimental Dermatology</i> , 2015, 24, 510-515.	2.9	66
86	Mitochondrial GWA Analysis of Lipid Profile Identifies Genetic Variants to Be Associated with HDL Cholesterol and Triglyceride Levels. <i>PLoS ONE</i> , 2015, 10, e0126294.	2.5	14
87	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	3.5	331
88	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. <i>PLoS Genetics</i> , 2015, 11, e1005230.	3.5	77
89	Gender-specific pathway differences in the human serum metabolome. <i>Metabolomics</i> , 2015, 11, 1815-1833.	3.0	218
90	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. <i>Nature Communications</i> , 2015, 6, 8658.	12.8	108

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91	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	27.8	1,328
92	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	27.8	3,823
93	Age- and Sex-Specific Causal Effects of Adiposity on Cardiovascular Risk Factors. <i>Diabetes</i> , 2015, 64, 1841-1852.	0.6	63
94	Cell Specific eQTL Analysis without Sorting Cells. <i>PLoS Genetics</i> , 2015, 11, e1005223.	3.5	115
95	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. <i>PLoS Genetics</i> , 2015, 11, e1005035.	3.5	107
96	The impact of low-frequency and rare variants on lipid levels. <i>Nature Genetics</i> , 2015, 47, 589-597.	21.4	310
97	Genetic variation at MECOM, TERT, JAK2 and HBS1L-MYB predisposes to myeloproliferative neoplasms. <i>Nature Communications</i> , 2015, 6, 6691.	12.8	145
98	Characterization of whole-genome autosomal differences of DNA methylation between men and women. <i>Epigenetics and Chromatin</i> , 2015, 8, 43.	3.9	176
99	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015, 47, 1415-1425.	21.4	365
100	A novel common variant in DCST2 is associated with length in early life and height in adulthood. <i>Human Molecular Genetics</i> , 2015, 24, 1155-1168.	2.9	109
101	Genome-wide association study of kidney function decline in individuals of European descent. <i>Kidney International</i> , 2015, 87, 1017-1029.	5.2	113
102	Targeted Metabolomics Identifies Reliable and Stable Metabolites in Human Serum and Plasma Samples. <i>PLoS ONE</i> , 2014, 9, e89728.	2.5	196
103	Mapping the Genetic Architecture of Gene Regulation in Whole Blood. <i>PLoS ONE</i> , 2014, 9, e93844.	2.5	31
104	A Systematic Evaluation of Short Tandem Repeats in Lipid Candidate Genes: Riding on the SNP-Wave. <i>PLoS ONE</i> , 2014, 9, e102113.	2.5	7
105	Mitochondrial Genetic Variants Identified to Be Associated with BMI in Adults. <i>PLoS ONE</i> , 2014, 9, e105116.	2.5	34
106	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. <i>PLoS Genetics</i> , 2014, 10, e1004508.	3.5	80
107	Genome Wide Meta-analysis Highlights the Role of Genetic Variation in RARRES2 in the Regulation of Circulating Serum Chemerin. <i>PLoS Genetics</i> , 2014, 10, e1004854.	3.5	31
108	Genetic Determinants of Circulating Interleukin-1 Receptor Antagonist Levels and Their Association With Glycemic Traits. <i>Diabetes</i> , 2014, 63, 4343-4359.	0.6	40

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109	DNA methylation and body-mass index: a genome-wide analysis. <i>Lancet</i> , The, 2014, 383, 1990-1998.	13.7	686
110	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. <i>Cell</i> , 2014, 156, 343-358.	28.9	113
111	Genome-wide association analysis identifies six new loci associated with forced vital capacity. <i>Nature Genetics</i> , 2014, 46, 669-677.	21.4	131
112	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	21.4	1,818
113	Comparative analysis of plasma metabolomics response to metabolic challenge tests in healthy subjects and influence of the FTO obesity risk allele. <i>Metabolomics</i> , 2014, 10, 386-401.	3.0	16
114	Mitochondrial DNA Variants in Obesity. <i>PLoS ONE</i> , 2014, 9, e94882.	2.5	26
115	Metabolomics reveals determinants of weight loss during lifestyle intervention in obese children. <i>Metabolomics</i> , 2013, 9, 1157-1167.	3.0	22
116	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013, 45, 1274-1283.	21.4	2,641
117	Systematic identification of trans eQTLs as putative drivers of known disease associations. <i>Nature Genetics</i> , 2013, 45, 1238-1243.	21.4	1,544
118	Development and Application of Genomic Control Methods for Genome-Wide Association Studies Using Non-Additive Models. <i>PLoS ONE</i> , 2013, 8, e81431.	2.5	14
119	Eight genetic loci associated with variation in lipoprotein-associated phospholipase A2 mass and activity and coronary heart disease: meta-analysis of genome-wide association studies from five community-based studies. <i>European Heart Journal</i> , 2012, 33, 238-251.	2.2	89