Harald Grallert

List of Publications by Year
in descending order

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	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
2	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
3	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
4	Systematic identification of trans eQTLs as putative drivers of known disease associations. Nature Genetics, 2013, 45, 1238-1243.	21.4	1,544
5	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. Nature Genetics, 2018, 50, 1505-1513.	21.4	1,331
6	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
7	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. Nature, 2017, 541, 81-86.	27.8	743
8	DNA methylation and body-mass index: a genome-wide analysis. Lancet, The, 2014, 383, 1990-1998.	13.7	686
9	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615
10	Connecting genetic risk to disease end points through the human blood plasma proteome. Nature Communications, 2017, 8, 14357.	12.8	460
11	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426
12	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
13	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	21.4	365
14	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	21.4	356
15	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. PLoS Medicine, 2017, 14, e1002383.	8.4	341
16	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
17	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	3.5	331
18	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	6.2	326

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19	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	21.4	310
20	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. Genome Biology, 2016, 17, 255.	8.8	251
21	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	12.8	245
22	Gender-specific pathway differences in the human serum metabolome. Metabolomics, 2015, 11, 1815-1833.	3.0	218
23	Targeted Metabolomics Identifies Reliable and Stable Metabolites in Human Serum and Plasma Samples. PLoS ONE, 2014, 9, e89728.	2.5	196
24	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
25	Characterization of whole-genome autosomal differences of DNA methylation between men and women. Epigenetics and Chromatin, 2015, 8, 43.	3.9	176
26	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
27	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
28	A genomeâ€wide approach to children's aggressive behavior: *The EAGLE consortium*. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2016, 171, 562-572.	1.7	153
29	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	12.8	153
30	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	12.8	147
31	Genetic variation at MECOM, TERT, JAK2 and HBS1L-MYB predisposes to myeloproliferative neoplasms. Nature Communications, 2015, 6, 6691.	12.8	145
32	Characterization of missing values in untargeted MS-based metabolomics data and evaluation of missing data handling strategies. Metabolomics, 2018, 14, 128.	3.0	138
33	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	21.4	131
34	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. Diabetes, 2016, 65, 803-817.	0.6	131
35	Genome-wide methylation data mirror ancestry information. Epigenetics and Chromatin, 2017, 10, 1.	3.9	120
36	Cell Specific eQTL Analysis without Sorting Cells. PLoS Genetics, 2015, 11, e1005223.	3.5	115

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37	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. Cell, 2014, 156, 343-358.	28.9	113
38	Genome-wide association study of kidney function decline in individuals of European descent. Kidney International, 2015, 87, 1017-1029.	5.2	113
39	A novel common variant in DCST2 is associated with length in early life and height in adulthood. Human Molecular Genetics, 2015, 24, 1155-1168.	2.9	109
40	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	12.8	108
41	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. PLoS Genetics, 2015, 11, e1005035.	3.5	107
42	The stool microbiota of insulin resistant women with recent gestational diabetes, a high risk group for type 2 diabetes. Scientific Reports, 2015, 5, 13212.	3.3	105
43	Genome-wide association study in 8,956 German individuals identifies influence of ABO histo-blood groups on gut microbiome. Nature Genetics, 2021, 53, 147-155.	21.4	101
44	Genome-wide association study identifies inversion in the *CTRB1-CTRB2* locus to modify risk for alcoholic and non-alcoholic chronic pancreatitis. Gut, 2018, 67, 1855-1863.	12.1	97
45	Exome-wide association study reveals novel susceptibility genes to sporadic dilated cardiomyopathy. PLoS ONE, 2017, 12, e0172995.	2.5	92
46	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. European Heart Journal, 2012, 33, 238-251.	2.2	89
47	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
48	GWAS on longitudinal growth traits reveals different genetic factors influencing infant, child, and adult BMI. Science Advances, 2019, 5, eaaw3095.	10.3	86
49	Association between DNA Methylation in Whole Blood and Measures of Glucose Metabolism: KORA F4 Study. PLoS ONE, 2016, 11, e0152314.	2.5	81
50	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. PLoS Genetics, 2014, 10, e1004508.	3.5	80
51	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. PLoS Genetics, 2015, 11, e1005230.	3.5	77
52	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
53	Network inference from glycoproteomics data reveals new reactions in the IgG glycosylation pathway. Nature Communications, 2017, 8, 1483.	12.8	67
54	Genome‐wide association study identifies new susceptibility loci for cutaneous lupus erythematosus. Experimental Dermatology, 2015, 24, 510-515.	2.9	66

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55	Genome-Wide Association Study on Immunoglobulin G Glycosylation Patterns. Frontiers in Immunology, 2018, 9, 277.	4.8	66
56	Age- and Sex-Specific Causal Effects of Adiposity on Cardiovascular Risk Factors. Diabetes, 2015, 64, 1841-1852.	0.6	63
57	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function. Nature Genetics, 2022, 54, 18-29.	21.4	60
58	Identification of genetic elements in metabolism by high-throughput mouse phenotyping. Nature Communications, 2018, 9, 288.	12.8	59
59	Numerous Genes in Loci Associated With Body Fat Distribution Are Linked to Adipose Function. Diabetes, 2016, 65, 433-437.	0.6	50
60	Revealing the role of the human blood plasma proteome in obesity using genetic drivers. Nature Communications, 2021, 12, 1279.	12.8	50
61	Associations between habitual diet, metabolic disease, and the gut microbiota using latent Dirichlet allocation. Microbiome, 2021, 9, 61.	11.1	47
62	Genetic Determinants of Circulating Interleukin-1 Receptor Antagonist Levels and Their Association With Glycemic Traits. Diabetes, 2014, 63, 4343-4359.	0.6	40
63	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. BMC Medical Genomics, 2015, 8, 65.	1.5	40
64	Rare Variants in Specific Lysosomal Genes Are Associated With Parkinson's Disease. Movement Disorders, 2020, 35, 1245-1248.	3.9	37
65	Association of common variants identified by recent genome-wide association studies with obesity in Chinese children: a case-control study. BMC Medical Genetics, 2016, 17, 7.	2.1	35
66	Investigating the causal effect of smoking on hay fever and asthma: a Mendelian randomization meta-analysis in the CARTA consortium. Scientific Reports, 2017, 7, 2224.	3.3	35
67	Mitochondrial Genetic Variants Identified to Be Associated with BMI in Adults. PLoS ONE, 2014, 9, e105116.	2.5	34
68	Deciphering the Plasma Proteome of Type 2 Diabetes. Diabetes, 2020, 69, 2766-2778.	0.6	34
69	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor Î±. JAMA Cardiology, 2018, 3, 463.	6.1	33
70	IgG glycosylation and DNA methylation are interconnected with smoking. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 637-648.	2.4	33
71	Metabolite ratios as potential biomarkers for type 2 diabetes: a DIRECT study. Diabetologia, 2018, 61, 117-129.	6.3	32
72	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. Human Molecular Genetics, 2021, 30, 393-409.	2.9	32

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73	Mapping the Genetic Architecture of Gene Regulation in Whole Blood. PLoS ONE, 2014, 9, e93844.	2.5	31
74	Genome Wide Meta-analysis Highlights the Role of Genetic Variation in RARRES2 in the Regulation of Circulating Serum Chemerin. PLoS Genetics, 2014, 10, e1004854.	3.5	31
75	Smoking-related changes in DNA methylation and gene expression are associated with cardio-metabolic traits. Clinical Epigenetics, 2020, 12, 157.	4.1	31
76	High-throughput DNA methylation analysis in anorexia nervosa confirms *TNXB* hypermethylation. World Journal of Biological Psychiatry, 2018, 19, 187-199.	2.6	28
77	Epigenome-wide association study of incident type 2 diabetes: a meta-analysis of five prospective European cohorts. Diabetologia, 2022, 65, 763-776.	6.3	28
78	Mitochondrial DNA Variants in Obesity. PLoS ONE, 2014, 9, e94882.	2.5	26
79	ANGPTL8 (Betatrophin) is Expressed in Visceral Adipose Tissue and Relates to Human Hepatic Steatosis in Two Independent Clinical Collectives. Hormone and Metabolic Research, 2017, 49, 343-349.	1.5	24
80	Metabolomics reveals determinants of weight loss during lifestyle intervention in obese children. Metabolomics, 2013, 9, 1157-1167.	3.0	22
81	Extensive identification of genes involved in congenital and structural heart disorders and cardiomyopathy. , 2022, 1, 157-173.		22
82	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	6.2	21
83	Obesity Genes and Weight Loss During Lifestyle Intervention in Children With Obesity. JAMA Pediatrics, 2021, 175, e205142.	6.2	21
84	Analysis with the exome array identifies multiple new independent variants in lipid loci. Human Molecular Genetics, 2016, 25, 4094-4106.	2.9	19
85	Characterization of the metabolic profile associated with serum 25-hydroxyvitamin D: a cross-sectional analysis in population-based data. International Journal of Epidemiology, 2016, 45, 1469-1481.	1.9	19
86	Genetic variation in TLR pathway and the risk of pulmonary tuberculosis in a Moldavian population. Infection, Genetics and Evolution, 2019, 68, 84-90.	2.3	19
87	Metabolic syndrome and the plasma proteome: from association to causation. Cardiovascular Diabetology, 2021, 20, 111.	6.8	19
88	Linking the *FTO* obesity rs1421085 variant circuitry to cellular, metabolic, and organismal phenotypes in vivo. Science Advances, 2021, 7, .	10.3	19
89	Mouse mutant phenotyping at scale reveals novel genes controlling bone mineral density. PLoS Genetics, 2020, 16, e1009190.	3.5	19
90	Common eye diseases in older adults of southern Germany: results from the KORA-Age study. Age and Ageing, 2017, 46, 481-486.	1.6	17

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91	Comparative analysis of plasma metabolomics response to metabolic challenge tests in healthy subjects and influence of the FTO obesity risk allele. Metabolomics, 2014, 10, 386-401.	3.0	16
92	Immediate reduction of serum citrulline but no change of steroid profile after initiation of metformin in individuals with type 2 diabetes. Journal of Steroid Biochemistry and Molecular Biology, 2017, 174, 114-119.	2.5	15
93	Genome-wide meta-analysis identifies novel determinants of circulating serum progranulin. Human Molecular Genetics, 2018, 27, 546-558.	2.9	15
94	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. PLoS Genetics, 2021, 17, e1009236.	3.5	15
95	Development and Application of Genomic Control Methods for Genome-Wide Association Studies Using Non-Additive Models. PLoS ONE, 2013, 8, e81431.	2.5	14
96	Mitochondrial GWA Analysis of Lipid Profile Identifies Genetic Variants to Be Associated with HDL Cholesterol and Triglyceride Levels. PLoS ONE, 2015, 10, e0126294.	2.5	14
97	Epigenetic Signatures at AQP3 and SOCS3 Engage in Low-Grade Inflammation across Different Tissues. PLoS ONE, 2016, 11, e0166015.	2.5	14
98	High-Fat Diet During Mouse Pregnancy and Lactation Targets GIP-Regulated Metabolic Pathways in Adult Male Offspring. Diabetes, 2016, 65, 574-584.	0.6	14
99	Association of alcohol consumption with allergic disease and asthma: a multiâ€centre Mendelian randomization analysis. Addiction, 2019, 114, 216-225.	3.3	14
100	N-glycosylation of immunoglobulin G predicts incident hypertension. Journal of Hypertension, 2021, 39, 2527-2533.	0.5	13
101	Novel associations between inflammation-related proteins and adiposity: A targeted proteomics approach across four population-based studies. Translational Research, 2022, 242, 93-104.	5.0	13
102	Association between Single Nucleotide Polymorphisms and Weight Reduction in Behavioural Interventionsâ€"A Pooled Analysis. Nutrients, 2021, 13, 819.	4.1	12
103	Genetic variation in TCF7L2 rs7903146 and history of GDM negatively and independently impact on diabetes-associated metabolic traits. Diabetes Research and Clinical Practice, 2018, 146, 251-257.	2.8	11
104	A Panel of 6 Biomarkers Significantly Improves the Prediction of Type 2 Diabetes in the MONICA/KORA Study Population. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 1647-1659.	3.6	11
105	Genetic variants of lipase activity in chronic pancreatitis: TableÂ1. Gut, 2016, 65, 184-185.	12.1	10
106	Associations between usual food intake and faecal sterols and bile acids: results from the Cooperative Health Research in the Augsburg Region (KORA FF4) study. British Journal of Nutrition, 2019, 122, 309-321.	2.3	9
107	Associations between fecal bile acids, neutral sterols, and serum lipids in the KORA FF4 study. Atherosclerosis, 2019, 288, 1-8.	0.8	8
108	A randomization-based causal inference framework for uncovering environmental exposure effects on human gut microbiota. PLoS Computational Biology, 2022, 18, e1010044.	3.2	8

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109	A Systematic Evaluation of Short Tandem Repeats in Lipid Candidate Genes: Riding on the SNP-Wave. PLoS ONE, 2014, 9, e102113.	2.5	7
110	Comparison of genetic risk prediction models to improve prediction of coronary heart disease in two large cohorts of the MONICA/KORA study. Genetic Epidemiology, 2021, 45, 633-650.	1.3	6
111	Genome-wide Association Study of Change in Fasting Glucose over time in 13,807 non-diabetic European Ancestry Individuals. Scientific Reports, 2019, 9, 9439.	3.3	5
112	Synergistic effect of genetic polymorphisms in *TLR6* and *TLR10* genes on the risk of pulmonary tuberculosis in a Moldavian population. Innate Immunity, 2021, 27, 365-376.	2.4	5
113	Specific Metabolic Markers Are Associated with Future Waist-Gaining Phenotype in Women. PLoS ONE, 2016, 11, e0157733.	2.5	5
114	Private variants in PRKN are associated with late-onset Parkinson's disease. Parkinsonism and Related Disorders, 2020, 75, 24-26.	2.2	4
115	A Family and a Genome-Wide Polygenic Risk Score Are Independently Associated With Stroke in a Population-Based Study. Stroke, 2022, 53, 2331-2339.	2.0	4
116	Colocalization analysis of pancreas eQTLs with risk loci from alcoholic and novel non-alcoholic chronic pancreatitis GWAS suggests potential disease causing mechanisms. Pancreatology, 2022, 22, 449-456.	1.1	3
117	pulver: an R package for parallel ultra-rapid p-value computation for linear regression interaction terms. BMC Bioinformatics, 2017, 18, 429.	2.6	1
118	Investigation of Adiposity Measures and Operational Taxonomic unit (OTU) Data Transformation Procedures in Stool Samples from a German Cohort Study Using Machine Learning Algorithms. Microorganisms, 2020, 8, 547.	3.6	1
119	Abstract 21: Deciphering the Plasma Proteome of Type 2 Diabetes. Circulation, 2020, 141, .	1.6	1