Niels Grarup

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/251523/publications.pdf

Version: 2024-02-01

249 papers	32,611 citations	8755 75 h-index	5120 166 g-index
285 all docs	285 docs citations	285 times ranked	41374 citing authors

#	Article	IF	Citations
1	Richness of human gut microbiome correlates with metabolic markers. Nature, 2013, 500, 541-546.	27.8	3,641
2	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	21.4	1,982
3	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. Nature Genetics, 2008, 40, 638-645.	21.4	1,683
4	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	21.4	1,631
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	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
7	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615
8	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	21.4	591
9	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
10	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. Nature Genetics, 2015, 47, 1449-1456.	21.4	529
11	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
12	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. Nature Genetics, 2014, 46, 357-363.	21.4	428
13	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	3.5	419
14	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	27.8	406
15	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	21.4	402
16	Greenlandic Inuit show genetic signatures of diet and climate adaptation. Science, 2015, 349, 1343-1347.	12.6	397
17	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	28.9	388
18	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	21.4	365

#	Article	IF	Citations
19	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
20	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	28.9	353
21	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
22	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
23	A common Greenlandic TBC1D4 variant confers muscle insulin resistance and type 2 diabetes. Nature, 2014, 512, 190-193.	27.8	338
24	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
25	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2017, 5, 97-105.	11.4	298
26	Resequencing of 200 human exomes identifies an excess of low-frequency non-synonymous coding variants. Nature Genetics, 2010, 42, 969-972.	21.4	297
27	Impact of Type 2 Diabetes Susceptibility Variants on Quantitative Glycemic Traits Reveals Mechanistic Heterogeneity. Diabetes, 2014, 63, 2158-2171.	0.6	297
28	Identification of low-frequency and rare sequence variants associated with elevated or reduced risk of type 2 diabetes. Nature Genetics, 2014, 46, 294-298.	21.4	294
29	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. Nature Genetics, 2015, 47, 1282-1293.	21.4	294
30	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
31	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. Human Molecular Genetics, 2016, 25, 389-403.	2.9	275
32	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
33	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
34	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	27.8	248
35	A genome-wide association study in the Japanese population identifies susceptibility loci for type 2 diabetes at UBE2E2 and C2CD4A-C2CD4B. Nature Genetics, 2010, 42, 864-868.	21.4	245
36	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	12.8	245

#	Article	IF	Citations
37	Studies of Association of Variants Near the HHEX, CDKN2A/B, and IGF2BP2 Genes With Type 2 Diabetes and Impaired Insulin Release in 10,705 Danish Subjects. Diabetes, 2007, 56, 3105-3111.	0.6	230
38	Human pancreatic islet three-dimensional chromatin architecture provides insights into the genetics of type 2 diabetes. Nature Genetics, 2019, 51, 1137-1148.	21.4	208
39	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	2.5	197
40	Common Type 2 Diabetes Risk Gene Variants Associate with Gestational Diabetes. Journal of Clinical Endocrinology and Metabolism, 2009, 94, 145-150.	3.6	194
41	Genome-wide association study identifies a sequence variant within the DAB2IP gene conferring susceptibility to abdominal aortic aneurysm. Nature Genetics, 2010, 42, 692-697.	21.4	181
42	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. Nature Communications, 2018, 9, 4455.	12.8	181
43	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
44	Estimation of allele frequency and association mapping using next-generation sequencing data. BMC Bioinformatics, 2011, 12, 231.	2.6	170
45	FGF21 Is a Sugar-Induced Hormone Associated with Sweet Intake and Preference in Humans. Cell Metabolism, 2017, 25, 1045-1053.e6.	16.2	169
46	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
47	Gene Ã— Physical Activity Interactions in Obesity: Combined Analysis of 111,421 Individuals of European Ancestry. PLoS Genetics, 2013, 9, e1003607.	3.5	168
48	Genetic susceptibility to type 2 diabetes and obesity: from genome-wide association studies to rare variants and beyond. Diabetologia, 2014, 57, 1528-1541.	6.3	162
49	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
50	Loss-of-function variants in ADCY3 increase risk of obesity and type 2 diabetes. Nature Genetics, 2018, 50, 172-174.	21.4	156
51	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	12.8	153
52	Association Testing of Novel Type 2 Diabetes Risk Alleles in the JAZF1, CDC123/CAMK1D, TSPAN8, THADA, ADAMTS9, and NOTCH2 Loci With Insulin Release, Insulin Sensitivity, and Obesity in a Population-Based Sample of 4,516 Glucose-Tolerant Middle-Aged Danes. Diabetes, 2008, 57, 2534-2540.	0.6	151
53	Apolipoprotein(a) Genetic Sequence Variants Associated With Systemic Atherosclerosis and Coronary Atherosclerotic Burden But Not With Venous Thromboembolism. Journal of the American College of Cardiology, 2012, 60, 722-729.	2.8	149
54	Genome-wide association studies in the Japanese population identify seven novel loci for type 2 diabetes. Nature Communications, 2016, 7, 10531.	12.8	149

#	Article	IF	Citations
55	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. Nature Communications, 2017, 8, 16015.	12.8	149
56	Natural Selection Affects Multiple Aspects of Genetic Variation at Putatively Neutral Sites across the Human Genome. PLoS Genetics, 2011, 7, e1002326.	3.5	146
57	VariantASGR1Associated with a Reduced Risk of Coronary Artery Disease. New England Journal of Medicine, 2016, 374, 2131-2141.	27.0	137
58	A Genome-Wide Association Study of Diabetic Kidney Disease in Subjects With Type 2 Diabetes. Diabetes, 2018, 67, 1414-1427.	0.6	136
59	G-allele of Intronic rs10830963 in MTNR1B Confers Increased Risk of Impaired Fasting Glycemia and Type 2 Diabetes Through an Impaired Glucose-Stimulated Insulin Release. Diabetes, 2009, 58, 1450-1456.	0.6	125
60	Whole-Exome Sequencing of 2,000 Danish Individuals and the Role of Rare Coding Variants in Type 2 Diabetes. American Journal of Human Genetics, 2013, 93, 1072-1086.	6.2	124
61	Obesity, unfavourable lifestyle and genetic risk of type 2 diabetes: a case-cohort study. Diabetologia, 2020, 63, 1324-1332.	6.3	121
62	Exome sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. Diabetologia, 2013, 56, 298-310.	6.3	119
63	Genetic evidence of a causal effect of insulin resistance on branched-chain amino acid levels. Diabetologia, 2017, 60, 873-878.	6.3	119
64	Cardiolipin Synthesis in Brown and Beige Fat Mitochondria Is Essential for Systemic Energy Homeostasis. Cell Metabolism, 2018, 28, 159-174.e11.	16.2	114
65	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. Cell, 2014, 156, 343-358.	28.9	113
66	Genetic Architecture of Vitamin B12 and Folate Levels Uncovered Applying Deeply Sequenced Large Datasets. PLoS Genetics, 2013, 9, e1003530.	3.5	112
67	Studies of the relationship between the ENPP1 K121Q polymorphism and type 2 diabetes, insulin resistance and obesity in 7,333 Danish white subjects. Diabetologia, 2006, 49, 2097-2104.	6.3	111
68	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. American Journal of Human Genetics, 2019, 104, 112-138.	6.2	106
69	Genome-Wide Population-Based Association Study of Extremely Overweight Young Adults â€“ The GOYA Study. PLoS ONE, 2011, 6, e24303.	2.5	105
70	A Genome-Wide Association Study of IVGTT-Based Measures of First-Phase Insulin Secretion Refines the Underlying Physiology of Type 2 Diabetes Variants. Diabetes, 2017, 66, 2296-2309.	0.6	102
71	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. Science Translational Medicine, 2016, 8, 341ra76.	12.4	100
72	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.	8.6	99

#	Article	IF	Citations
73	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. PLoS Genetics, 2015, 11, e1004876.	3.5	95
74	Novel loci for childhood body mass index and shared heritability with adult cardiometabolic traits. PLoS Genetics, 2020, 16, e1008718.	3.5	95
75	Habitual sleep duration is associated with BMI and macronutrient intake and may be modified by CLOCK genetic variants. American Journal of Clinical Nutrition, 2015, 101, 135-143.	4.7	93
76	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	21.4	91
77	Variants at DGKB/TMEM195, ADRA2A, GLIS3 and C2CD4B loci are associated with reduced glucose-stimulated beta cell function in middle-aged Danish people. Diabetologia, 2010, 53, 1647-1655.	6.3	90
78	Selection in Europeans on Fatty Acid Desaturases Associated with Dietary Changes. Molecular Biology and Evolution, 2017, 34, 1307-1318.	8.9	90
79	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
80	Uncovering the Genetic History of the Present-Day Greenlandic Population. American Journal of Human Genetics, 2015, 96, 54-69.	6.2	85
81	Re-analysis of public genetic data reveals a rare X-chromosomal variant associated with type 2 diabetes. Nature Communications, 2018, 9, 321.	12.8	85
82	Genomewide metaâ€analysis identifies loci associated with <scp>IGF</scp> â€I and <scp>IGFBP</scp> â€3 levels with impact on ageâ€related traits. Aging Cell, 2016, 15, 811-824.	6.7	83
83	Variants Near MC4R Are Associated With Obesity and Influence Obesity-Related Quantitative Traits in a Population of Middle-Aged People: Studies of 14,940 Danes. Diabetes, 2009, 58, 757-764.	0.6	80
84	Dysregulation of a long noncoding RNA reduces leptin leading to a leptin-responsive form of obesity. Nature Medicine, 2019, 25, 507-516.	30.7	79
85	A Common Allele in FGF21 Associated with Sugar Intake Is Associated with Body Shape, Lower Total Body-Fat Percentage, and Higher Blood Pressure. Cell Reports, 2018, 23, 327-336.	6.4	76
86	A trans-ancestral meta-analysis of genome-wide association studies reveals loci associated with childhood obesity. Human Molecular Genetics, 2019, 28, 3327-3338.	2.9	76
87	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
88	Causal relationship between obesity and serum testosterone status in men: A bi-directional mendelian randomization analysis. PLoS ONE, 2017, 12, e0176277.	2.5	72
89	A genetic risk score of 45 coronary artery disease risk variants associates with increased risk of myocardial infarction in 6041 Danish individuals. Atherosclerosis, 2015, 240, 305-310.	0.8	68
90	Lipolysis drives expression of the constitutively active receptor GPR3 to induce adipose thermogenesis. Cell, 2021, 184, 3502-3518.e33.	28.9	68

#	Article	IF	Citations
91	Replication and metaâ€analysis of common variants identifies a genomeâ€wide significant locus in migraine. European Journal of Neurology, 2013, 20, 765-772.	3.3	67
92	Genome-Wide Association Study of the Modified Stumvoll Insulin Sensitivity Index Identifies BCL2 and FAM19A2 as Novel Insulin Sensitivity Loci. Diabetes, 2016, 65, 3200-3211.	0.6	67
93	Underlying Genetic Models of Inheritance in Established Type 2 Diabetes Associations. American Journal of Epidemiology, 2009, 170, 537-545.	3.4	63
94	Studies of the CommonDIO2Thr92Ala Polymorphism and Metabolic Phenotypes in 7342 Danish White Subjects. Journal of Clinical Endocrinology and Metabolism, 2007, 92, 363-366.	3.6	62
95	Type 2 diabetes risk alleles near ADCY5, CDKAL1 and HHEX-IDE are associated with reduced birthweight. Diabetologia, 2010, 53, 1908-1916.	6.3	61
96	Type 2 Diabetes Risk Alleles Near BCAR1 and in ANK1 Associate With Decreased Î²-Cell Function Whereas Risk Alleles Near ANKRD55 and GRB14 Associate With Decreased Insulin Sensitivity in the Danish Inter99 Cohort. Journal of Clinical Endocrinology and Metabolism, 2013, 98, E801-E806.	3.6	60
97	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	6.2	60
98	Combined Analyses of 20 Common Obesity Susceptibility Variants. Diabetes, 2010, 59, 1667-1673.	0.6	55
99	Genetic investigations of sudden unexpected deaths in infancy using next-generation sequencing of 100 genes associated with cardiac diseases. European Journal of Human Genetics, 2016, 24, 817-822.	2.8	55
100	The Effect of an Extreme and Prolonged Population Bottleneck on Patterns of Deleterious Variation: Insights from the Greenlandic Inuit. Genetics, 2017, 205, 787-801.	2.9	54
101	Gene???environment interactions in the pathogenesis of type 2 diabetes and metabolism. Current Opinion in Clinical Nutrition and Metabolic Care, 2007, 10, 420-426.	2.5	53
102	Combined analysis of 19 common validated type 2 diabetes susceptibility gene variants shows moderate discriminative value and no evidence of geneâ€“gene interaction. Diabetologia, 2009, 52, 1308-1314.	6.3	53
103	Rare genetic variants previously associated with congenital forms of long QT syndrome have little or no effect on the QT interval. European Heart Journal, 2015, 36, 2523-2529.	2.2	53
104	Variant near ADAMTS9 Known to Associate with Type 2 Diabetes Is Related to Insulin Resistance in Offspring of Type 2 Diabetes Patientsâ€”EUGENE2 Study. PLoS ONE, 2009, 4, e7236.	2.5	53
105	Identification of KCNJ15 as a Susceptibility Gene in Asian Patients with Type 2 Diabetes Mellitus. American Journal of Human Genetics, 2010, 86, 54-64.	6.2	52
106	Gene-Environment Interactions of Circadian-Related Genes for Cardiometabolic Traits. Diabetes Care, 2015, 38, 1456-1466.	8.6	52
107	A glycogene mutation map for discovery of diseases of glycosylation. Glycobiology, 2015, 25, 211-224.	2.5	52
108	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. Nature Communications, 2021, 12, 3505.	12.8	49

#	Article	IF	Citations
109	Studies of the Association of Arg72Pro of Tumor Suppressor Protein p53 with Type 2 Diabetes in a Combined Analysis of 55,521 Europeans. PLoS ONE, 2011, 6, e15813.	2.5	49
110	New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48
111	Physiologic Characterization of Type 2 Diabetesâ€“Related Loci. Current Diabetes Reports, 2010, 10, 485-497.	4.2	47
112	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.6	47
113	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. Genome Biology, 2018, 19, 87.	8.8	47
114	Association of Variants in the Sterol Regulatory Element-Binding Factor 1 (SREBF1) Gene With Type 2 Diabetes, Glycemia, and Insulin Resistance. Diabetes, 2008, 57, 1136-1142.	0.6	43
115	MTNR1B G24E Variant Associates With BMI and Fasting Plasma Glucose in the General Population in Studies of 22,142 Europeans. Diabetes, 2010, 59, 1539-1548.	0.6	43
116	Variation in the peroxisome proliferator-activated receptor Î´ gene in relation to common metabolic traits in 7,495 middle-aged white people. Diabetologia, 2007, 50, 1201-1208.	6.3	42
117	Common Variation in LMNA Increases Susceptibility to Type 2 Diabetes and Associates With Elevated Fasting Glycemia and Estimates of Body Fat and Height in the General Population: Studies of 7,495 Danish Whites. Diabetes, 2007, 56, 694-698.	0.6	41
118	Meta-analysis of rare and common exome chip variants identifies S1PR4 and other loci influencing blood cell traits. Nature Genetics, 2016, 48, 867-876.	21.4	41
119	Estimating the causal effect of body mass index on hay fever, asthma and lung function using Mendelian randomization. Allergy: European Journal of Allergy and Clinical Immunology, 2018, 73, 153-164.	5.7	41
120	Type 2 diabetes risk allele near CENTD2 is associated with decreased glucose-stimulated insulin release. Diabetologia, 2011, 54, 1052-1056.	6.3	39
121	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. Journal of the American Society of Nephrology: JASN, 2017, 28, 981-994.	6.1	39
122	Diabetic microvascular complications are not associated with two polymorphisms in the GLUTâ€‘1 and PCâ€‘1 genes regulating glucose metabolism in Caucasian type 1 diabetic patients. Nephrology Dialysis Transplantation, 2001, 16, 1653-1656.	0.7	35
123	What Is the Contribution of Two Genetic Variants Regulating VEGF Levels to Type 2 Diabetes Risk and to Microvascular Complications?. PLoS ONE, 2013, 8, e55921.	2.5	35
124	Genetic determinants of serum vitamin B12 and their relation to body mass index. European Journal of Epidemiology, 2017, 32, 125-134.	5.7	35
125	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
126	Glucose tolerance, insulin sensitivity and insulin release in European non-diabetic carriers of a polymorphism upstream of CDKN2A and CDKN2B. Diabetologia, 2011, 54, 795-802.	6.3	34

#	Article	IF	Citations
127	The â"250G>A Promoter Variant in Hepatic Lipase Associates with Elevated Fasting Serum High-Density Lipoprotein Cholesterol Modulated by Interaction with Physical Activity in a Study of 16,156 Danish Subjects. Journal of Clinical Endocrinology and Metabolism, 2008, 93, 2294-2299.	3.6	33
128	Association studies of novel obesity-related gene variants with quantitative metabolic phenotypes in a population-based sample of 6,039 Danish individuals. Diabetologia, 2012, 55, 105-113.	6.3	32
129	High Prevalence of Diabetes-Predisposing Variants in MODY Genes Among Danish Women With Gestational Diabetes Mellitus. Journal of the Endocrine Society, 2017, 1, 681-690.	0.2	32
130	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
131	DeepFake electrocardiograms using generative adversarial networks are the beginning of the end for privacy issues in medicine. Scientific Reports, 2021, 11, 21896.	3.3	31
132	The diabetogenic VPS13C/C2CD4A/C2CD4B rs7172432 variant impairs glucose-stimulated insulin response in 5,722 non-diabetic Danish individuals. Diabetologia, 2011, 54, 789-794.	6.3	30
133	A variant in the G6PC2/ABCB11 locus is associated with increased fasting plasma glucose, increased basal hepatic glucose production and increased insulin release after oral and intravenous glucose loads. Diabetologia, 2009, 52, 2122-2129.	6.3	29
134	Discovery of novel heart rate-associated loci using the Exome Chip. Human Molecular Genetics, 2017, 26, 2346-2363.	2.9	29
135	Genome-wide association meta-analysis of 30,000 samples identifies seven novel loci for quantitative ECG traits. European Journal of Human Genetics, 2019, 27, 952-962.	2.8	29
136	A novel rare CUBN variant and three additional genes identified in Europeans with and without diabetes: results from an exome-wide association study of albuminuria. Diabetologia, 2019, 62, 292-305.	6.3	29
137	Skeletal muscle enhancer interactions identify genes controlling whole-body metabolism. Nature Communications, 2020, 11, 2695.	12.8	29
138	The PNPLA3 rs738409 G-Allele Associates with Reduced Fasting Serum Triglyceride and Serum Cholesterol in Danes with Impaired Glucose Regulation. PLoS ONE, 2012, 7, e40376.	2.5	28
139	MTHFR C677T genotype and cardiovascular risk in a general population without mandatory folic acid fortification. European Journal of Nutrition, 2014, 53, 1549-1559.	3.9	28
140	Interactions of Lipid Genetic Risk Scores With Estimates of Metabolic Health in a Danish Population. Circulation: Cardiovascular Genetics, 2015, 8, 465-472.	5.1	28
141	Quality of dietary fat and genetic risk of type 2 diabetes: individual participant data meta-analysis. BMJ: British Medical Journal, 2019, 366, l4292.	2.3	28
142	ExomeChip-Wide Analysis of 95 626 Individuals Identifies 10 Novel Loci Associated With QT and JT Intervals. Circulation Genomic and Precision Medicine, 2018, 11, e001758.	3.6	27
143	Effects of Calcium, Magnesium, and Potassium Concentrations on Ventricular Repolarization in Unselected Individuals. Journal of the American College of Cardiology, 2019, 73, 3118-3131.	2.8	27
144	Do Gene Variants Influencing Adult Adiposity Affect Birth Weight? A Population-Based Study of 24 Loci in 4,744 Danish Individuals. PLoS ONE, 2010, 5, e14190.	2.5	27

#	Article	IF	Citations
145	The Type 2 Diabetes Risk Allele of TMEM154-rs6813195 Associates with Decreased Beta Cell Function in a Study of 6,486 Danes. PLoS ONE, 2015, 10, e0120890.	2.5	27
146	Variation and association to diabetes in 2000 full mtDNA sequences mined from an exome study in a Danish population. European Journal of Human Genetics, 2014, 22, 1040-1045.	2.8	26
147	Numerous Brugada syndromeâ€“associated genetic variants have no effect on J-point elevation, syncope susceptibility, malignant cardiac arrhythmia, and all-cause mortality. Genetics in Medicine, 2017, 19, 521-528.	2.4	26
148	The Early Growth Genetics (EGG) and EArly Genetics and Lifecourse Epidemiology (EAGLE) consortia: design, results and future prospects. European Journal of Epidemiology, 2019, 34, 279-300.	5.7	26
149	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.6	26
150	Explaining deep neural networks for knowledge discovery in electrocardiogram analysis. Scientific Reports, 2021, 11, 10949.	3.3	26
151	Genetic variability of the SUR1 promoter in relation to beta-cell function and Type II diabetes mellitus. Diabetologia, 2001, 44, 1330-1334.	6.3	25
152	The KCNMB1 Glu65Lys polymorphism associates with reduced systolic and diastolic blood pressure in the Inter99 study of 5729 Danes. Journal of Hypertension, 2008, 26, 2142-2146.	0.5	25
153	Carriers of the TCF7L2 rs7903146 TT genotype have elevated levels of plasma glucose, serum proinsulin and plasma gastric inhibitory polypeptide (GIP) during a meal test. Diabetologia, 2011, 54, 103-110.	6.3	25
154	Genetics of Type 2 Diabetes: the Power of Isolated Populations. Current Diabetes Reports, 2016, 16, 65.	4.2	25
155	A Splice Region Variant in LDLR Lowers Non-high Density Lipoprotein Cholesterol and Protects against Coronary Artery Disease. PLoS Genetics, 2015, 11, e1005379.	3.5	24
156	The association between candidate migraine susceptibility loci and severe migraine phenotype in a clinical sample. Cephalalgia, 2016, 36, 615-623.	3.9	24
157	Rare coding variants in 35 genes associate with circulating lipid levelsâ€”A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	6.2	24
158	No Interactions Between Previously Associated 2-Hour Glucose Gene Variants and Physical Activity or BMI on 2-Hour Glucose Levels. Diabetes, 2012, 61, 1291-1296.	0.6	23
159	Discovery of Coding Genetic Variants Influencing Diabetes-Related Serum Biomarkers and Their Impact on Risk of Type 2 Diabetes. Journal of Clinical Endocrinology and Metabolism, 2015, 100, E664-E671.	3.6	23
160	Genetic Variations in the Human G Protein-coupled Receptor Class C, Group 6, Member A (GPRC6A) Control Cell Surface Expression and Function. Journal of Biological Chemistry, 2017, 292, 1524-1534.	3.4	23
161	Genetic Variant SCL2A2 Is Associated with Risk of Cardiovascular Disease â€“ Assessing the Individual and Cumulative Effect of 46 Type 2 Diabetes Related Genetic Variants. PLoS ONE, 2012, 7, e50418.	2.5	22
162	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. BMC Cardiovascular Disorders, 2019, 19, 240.	1.7	22

#	Article	IF	Citations
163	Abdominal adiposity and cardiometabolic risk factors in children and adolescents: a Mendelian randomization analysis. American Journal of Clinical Nutrition, 2019, 110, 1079-1087.	4.7	22
164	GLP-1 Receptor Agonist Treatment in Morbid Obesity and Type 2 Diabetes Due to Pathogenic Homozygous Melanocortin-4 Receptor Mutation: A Case Report. Cell Reports Medicine, 2020, 1, 100006.	6.5	22
165	Genetic analysis of the estrogen-related receptor Î± and studies of association with obesity and type 2 diabetes. International Journal of Obesity, 2007, 31, 365-370.	3.4	21
166	Bioinformatics-Driven Identification and Examination of Candidate Genes for Non-Alcoholic Fatty Liver Disease. PLoS ONE, 2011, 6, e16542.	2.5	21
167	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	6.2	21
168	FUT2â€“ABO epistasis increases the risk of early childhood asthma and Streptococcus pneumoniae respiratory illnesses. Nature Communications, 2020, 11, 6398.	12.8	21
169	Comparative Analyses of QTLs Influencing Obesity and Metabolic Phenotypes in Pigs and Humans. PLoS ONE, 2015, 10, e0137356.	2.5	21
170	Functional and genetic epidemiological characterisation of theFFAR4(GPR120) p.R270H variant in the Danish population. Journal of Medical Genetics, 2016, 53, 616-623.	3.2	20
171	Urinary metabolomics reveals glycemic and coffee associated signatures of thyroid function in two population-based cohorts. PLoS ONE, 2017, 12, e0173078.	2.5	20
172	ADAMTS9 Regulates Skeletal Muscle Insulin Sensitivity Through Extracellular Matrix Alterations. Diabetes, 2019, 68, 502-514.	0.6	20
173	Abdominal visceral and subcutaneous adipose tissue and associations with cardiometabolic risk in Inuit, Africans and Europeans: a cross-sectional study. BMJ Open, 2020, 10, e038071.	1.9	20
174	Identification of Novel Genetic Determinants of Erythrocyte Membrane Fatty Acid Composition among Greenlanders. PLoS Genetics, 2016, 12, e1006119.	3.5	20
175	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	3.6	19
176	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 2018, 3, 4.	1.8	19
177	Genetic Correlation between Body Fat Percentage and Cardiorespiratory Fitness Suggests Common Genetic Etiology. PLoS ONE, 2016, 11, e0166738.	2.5	18
178	PC-1 amino acid variant (K121Q) has no impact on progression of diabetic nephropathy in type 1 diabetic patients. Nephrology Dialysis Transplantation, 2002, 17, 1408-1412.	0.7	17
179	Genetic Determinants of Weight Loss After Bariatric Surgery. Obesity Surgery, 2019, 29, 2554-2561.	2.1	17
180	A genome-wide association study of thyroid stimulating hormone and free thyroxine in Danish children and adolescents. PLoS ONE, 2017, 12, e0174204.	2.5	17

#	Article	IF	Citations
181	Homozygous carriers of the G allele of rs4664447 of the glucagon gene (GCG) are characterised by decreased fasting and stimulated levels of insulin, glucagon and glucagon-like peptide (GLP)-1. Diabetologia, 2011, 54, 2820-2831.	6.3	16
182	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2020, 13, 387-395.	3.6	16
183	Acute metabolic effects of melatoninâ€"A randomized crossover study in healthy young men. Journal of Pineal Research, 2021, 70, e12706.	7.4	15
184	Genetic risk scores for body fat distribution attenuate weight loss in women during dietary intervention. International Journal of Obesity, 2018, 42, 370-375.	3.4	14
185	Hypertension genetic risk score is associated with burden of coronary heart disease among patients referred for coronary angiography. PLoS ONE, 2018, 13, e0208645.	2.5	14
186	Identification of novel high-impact recessively inherited type 2 diabetes risk variants in the Greenlandic population. Diabetologia, 2018, 61, 2005-2015.	6.3	14
187	Association of alcohol consumption with allergic disease and asthma: a multiâ€centre Mendelian randomization analysis. Addiction, 2019, 114, 216-225.	3.3	14
188	The Birth Weight Lowering C-Allele of rs900400 Near LEKR1 and CCNL1 Associates with Elevated Insulin Release following an Oral Glucose Challenge. PLoS ONE, 2011, 6, e27096.	2.5	13
189	ReducedCD300LGmRNA tissue expression, increased intramyocellular lipid content and impaired glucose metabolism in healthy male carriers of Arg82Cys inCD300LG: a novel genometabolic cross-link betweenCD300LGand common metabolic phenotypes. BMJ Open Diabetes Research and Care, 2015, 3, e000095.	2.8	13
190	Sexâ€specific effects of naturally occurring variants in the dopamine receptor D2 locus on insulin secretion and Type 2 diabetes susceptibility. Diabetic Medicine, 2014, 31, 1001-1008.	2.3	12
191	Carriers of aVEGFAenhancer polymorphism selectively binding CHOP/DDIT3 are predisposed to increased circulating levels of thyroid-stimulating hormone. Journal of Medical Genetics, 2017, 54, 166-175.	3.2	12
192	Genetic Susceptibility for Childhood BMI has no Impact on Weight Loss Following Lifestyle Intervention in Danish Children. Obesity, 2018, 26, 1915-1922.	3.0	12
193	Common variants in the hERG (KCNH2) voltage-gated potassium channel are associated with altered fasting and glucose-stimulated plasma incretin and glucagon responses. BMC Genetics, 2018, 19, 15.	2.7	12
194	Haploinsufficiency of ARHGAP42 is associated with hypertension. European Journal of Human Genetics, 2019, 27, 1296-1303.	2.8	12
195	Linking glycemic dysregulation in diabetes to symptoms, comorbidities, and genetics through EHR data mining. ELife, 2019, 8, .	6.0	12
196	Loss of Function Glucose-Dependent Insulinotropic Polypeptide Receptor Variants Are Associated With Alterations in BMI, Bone Strength and Cardiovascular Outcomes. Frontiers in Cell and Developmental Biology, 2021, 9, 749607.	3.7	12
197	Associations of genetic determinants of serum vitamin B12 and folate concentrations with hay fever and asthma: a Mendelian randomization meta-analysis. European Journal of Clinical Nutrition, 2018, 72, 264-271.	2.9	11
198	An adult-based insulin resistance genetic risk score associates with insulin resistance, metabolic traits and altered fat distribution in Danish children and adolescents who are overweight or obese. Diabetologia, 2018, 61, 1769-1779.	6.3	11

#	Article	IF	Citations
199	Increased frequency of rare missense PPP1R3B variants among Danish patients with type 2 diabetes. PLoS ONE, 2019, 14, e0210114.	2.5	11
200	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	1.8	11
201	Diabetes in Population Isolates: Lessons from Greenland. Review of Diabetic Studies, 2015, 12, 320-329.	1.3	11
202	Common variants in LEPR, IL6, AMD1, and NAMPT do not associate with risk of juvenile and childhood obesity in Danes: a caseâ€“control study. BMC Medical Genetics, 2015, 16, 105.	2.1	10
203	The genetic history of Greenlandic-European contact. Current Biology, 2021, 31, 2214-2219.e4.	3.9	9
204	Abdominal and gluteofemoral fat depots show opposing associations with postprandial lipemia. American Journal of Clinical Nutrition, 2021, 114, 1467-1475.	4.7	9
205	Loss of Sucrase-Isomaltase Function Increases Acetate Levels and Improves Metabolic Health in Greenlandic Cohorts. Gastroenterology, 2022, 162, 1171-1182.e3.	1.3	9
206	Studies of the variability of the hepatocyte nuclear factor-1Î² (HNF-1Î² / TCF2) and the dimerization cofactor of HNF-1 (DcoH / PCBD) genes in relation to type 2 diabetes mellitus and Î²-cell function. Human Mutation, 2001, 18, 356-357.	2.5	8
207	Genome-wide association studies of human adiposity: Zooming in on synapses. Molecular and Cellular Endocrinology, 2015, 418, 90-100.	3.2	8
208	Identification of novel LEPR mutations in Pakistani families with morbid childhood obesity. BMC Medical Genetics, 2018, 19, 199.	2.1	8
209	Genome-wide study of early and severe childhood asthma identifies interaction between CDHR3 and GSDMB. Journal of Allergy and Clinical Immunology, 2022, 150, 622-630.	2.9	8
210	The effect of diabetes and the common diabetogenic TBC1D4 p.Arg684Ter variant on cardiovascular risk in Inuit in Greenland. Scientific Reports, 2020, 10, 22081.	3.3	7
211	Recessive Genome-Wide Meta-analysis Illuminates Genetic Architecture of Type 2 Diabetes. Diabetes, 2022, 71, 554-565.	0.6	7
212	Blood Pressure Levels in Male Carriers of Arg82Cys in CD300LG. PLoS ONE, 2014, 9, e109646.	2.5	6
213	Genetic and phenotypic correlations between surrogate measures of insulin release obtained from OGTT data. Diabetologia, 2015, 58, 1006-1012.	6.3	6
214	A functional IFN-Î»4-generating DNA polymorphism could protect older asthmatic women from aeroallergen sensitization and associate with clinical features of asthma. Scientific Reports, 2017, 7, 10500.	3.3	6
215	Association studies of genetic scores of serum vitamin B12 and folate levels with symptoms of depression and anxiety in two danish population studies. European Journal of Clinical Nutrition, 2017, 71, 1054-1060.	2.9	6
216	Genetic determinants of glycated hemoglobin levels in the Greenlandic Inuit population. European Journal of Human Genetics, 2018, 26, 868-875.	2.8	6

#	Article	IF	Citations
217	Associations between birth weight and glucose intolerance in adulthood among Greenlandic Inuit. Diabetes Research and Clinical Practice, 2019, 150, 129-137.	2.8	6
218	Estimating narrow-sense heritability using family data from admixed populations. Heredity, 2020, 124, 751-762.	2.6	6
219	Investigating the causal effect of maternal vitamin B12 and folate levels on offspring birthweight. International Journal of Epidemiology, 2021, 50, 179-189.	1.9	6
220	Physical activity attenuates postprandial hyperglycaemia in homozygous TBC1D4 loss-of-function mutation carriers. Diabetologia, 2021, 64, 1795-1804.	6.3	6
221	Impact of rs361072 in the Phosphoinositide 3-Kinase p110Î² Gene on Whole-Body Glucose Metabolism and Subunit Protein Expression in Skeletal Muscle. Diabetes, 2010, 59, 1108-1112.	0.6	5
222	Common variation in oxidative phosphorylation genes is not a major cause of insulin resistance or type 2 diabetes. Diabetologia, 2012, 55, 340-348.	6.3	5
223	Increasing insulin resistance accentuates the effect of triglyceride-associated loci on serum triglycerides during 5 years. Journal of Lipid Research, 2016, 57, 2193-2199.	4.2	5
224	Mendelian randomisation study of the associations of vitamin B12 and folate genetic risk scores with blood pressure and fasting serum lipid levels in three Danish population-based studies. European Journal of Clinical Nutrition, 2016, 70, 613-619.	2.9	5
225	Genetic predisposition to higher body fat yet lower cardiometabolic risk in children and adolescents. International Journal of Obesity, 2019, 43, 2007-2016.	3.4	5
226	Association of genetic variants previously implicated in coronary artery disease with age at onset of coronary artery disease requiring revascularizations. PLoS ONE, 2019, 14, e0211690.	2.5	5
227	Genome-Wide Association Analysis of Pancreatic Beta-Cell Glucose Sensitivity. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 80-90.	3.6	5
228	Sequencing reveals protective and pathogenic effects on development of diabetes of rare GLIS3 variants. PLoS ONE, 2019, 14, e0220805.	2.5	4
229	The derived allele of a novel intergenic variant at chromosome 11 associates with lower body mass index and a favorable metabolic phenotype in Greenlanders. PLoS Genetics, 2020, 16, e1008544.	3.5	4
230	Association of milk intake with hay fever, asthma, and lung function: a Mendelian randomization analysis. European Journal of Epidemiology, 2022, 37, 713-722.	5.7	4
231	An LDLR missense variant poses high risk of familial hypercholesterolemia in 30% of Greenlanders and offers potential of early cardiovascular disease intervention. Human Genetics and Genomics Advances, 2022, 3, 100118.	1.7	4
232	Genetic architecture of obesity and related metabolic traits â€" recent insights from isolated populations. Current Opinion in Genetics and Development, 2018, 50, 74-78.	3.3	3
233	Screening of 31 genes involved in monogenic forms of obesity in 23 Pakistani probands with early-onset childhood obesity: a case report. BMC Medical Genetics, 2019, 20, 152.	2.1	3
234	Genetic determinants of blood pressure traits are associated with carotid arterial thickening and plaque formation in patients with type 2 diabetes. Diabetes and Vascular Disease Research, 2019, 16, 13-21.	2.0	3

#	Article	IF	Citations
235	Genome-wide association study of circulating levels of glucagon during an oral glucose tolerance test. BMC Medical Genomics, 2021, 14, 3.	1.5	3
236	Genetic markers of abdominal obesity and weight loss after gastric bypass surgery. PLoS ONE, 2021, 16, e0252525.	2.5	3
237	Studies of association of AGPAT6variants with type 2 diabetes and related metabolic phenotypes in 12,068 Danes. BMC Medical Genetics, 2013, 14, 113.	2.1	2
238	Genetic risk scores link body fat distribution with specific cardiometabolic profiles. Obesity, 2016, 24, 1778-1785.	3.0	2
239	Polygenic predisposition to breast cancer and the risk of coronary artery disease. International Journal of Cardiology, 2019, 291, 145-151.	1.7	2
240	Prospective Studies Exploring the Possible Impact of an ID3 Polymorphism on Changes in Obesity Measures. Obesity, 2018, 26, 747-754.	3.0	1
241	Genetic Aspects of Non-alcoholic Fatty Liver Disease (NAFLD). , 2019, , 195-206.		1
242	FGL1 as a modulator of plasma Dâ€dimer levels: Exomeâ€wide marker analysis of plasma tPA, PAIâ€1, and Dâ€dimer. Journal of Thrombosis and Haemostasis, 2021, 19, 2019-2028.	3.8	1
243	Insulin resistance genetic risk score and burden of coronary artery disease in patients referred for coronary angiography. PLoS ONE, 2021, 16, e0252855.	2.5	1
244	The Effect of Melatonin on Incretin Hormones: Results From Experimental and Randomized Clinical Studies. Journal of Clinical Endocrinology and Metabolism, 2021, 106, e5109-e5123.	3.6	1
245	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	1.8	1
246	Non-linear interaction between physical activity and polygenic risk score of body mass index in Danish and Russian populations. PLoS ONE, 2021, 16, e0258748.	2.5	1
247	The Arg82Cys Polymorphism of the Protein Nepmucin Implies a Role in HDL Metabolism. Journal of the Endocrine Society, 2022, 6, bvac034.	0.2	1
248	EHMTI-0380. The association of migraine susceptibility loci with severe migraine characteristics in a clinic-based migraine sample. Journal of Headache and Pain, 2014, 15, .	6.0	0
249	P3630Genetic risk score of insulin resistance risk variants is associated with increased risk of coronary artery disease in patients referred to coronary angiography. European Heart Journal, 2018, 39, .	2.2	0