Cecilia M Lindgren

List of Publications by Citations

276 papers	69,204 citations	99 h-index	263 g-index
316 ext. papers	82,607 ext. citations	15.2 avg, IF	7.5 L-index

#	Paper	IF	Citations
276	Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. *Nature*, **2007**, 447, 661-78	50.4	7801
275	PGC-1alpha-responsive genes involved in oxidative phosphorylation are coordinately downregulated in human diabetes. *Nature Genetics*, **2003**, 34, 267-73	36.3	5810
274	A common variant in the FTO gene is associated with body mass index and predisposes to childhood and adult obesity. *Science*, **2007**, 316, 889-94	33.3	3294
273	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
272	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics*, **2010**, 42, 937-48	36.3	2267
271	Discovery and refinement of loci associated with lipid levels. *Nature Genetics*, **2013**, 45, 1274-1283	36.3	1904
270	Replication of genome-wide association signals in UK samples reveals risk loci for type 2 diabetes. *Science*, **2007**, 316, 1336-41	33.3	1823
269	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. *Nature Genetics*, **2010**, 42, 105-16	36.3	1673
268	Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature*, **2010**, 467, 832-8	50.4	1514
267	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. *Nature Genetics*, **2008**, 40, 638-45	36.3	1496
266	The common PPARgamma Pro12Ala polymorphism is associated with decreased risk of type 2 diabetes. *Nature Genetics*, **2000**, 26, 76-80	36.3	1486
265	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. *Nature Genetics*, **2012**, 44, 981-90	36.3	1482
264	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. *Nature Genetics*, **2010**, 42, 579-89	36.3	1449
263	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. *Nature Genetics*, **2009**, 41, 25-34	36.3	1368
262	Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86	36.3	1339
261	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. *Nature Genetics*, **2015**, 47, 1121-1130	36.3	1290
260	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. *Nature Genetics*, **2007**, 39, 1329-37	36.3	1130

259	Common variants near MC4R are associated with fat mass, weight and risk of obesity. *Nature Genetics*, **2008**, 40, 768-75	36.3	1048
258	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
257	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. *Nature Genetics*, **2014**, 46, 234-44	36.3	784
256	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. *Nature Genetics*, **2010**, 42, 949-60	36.3	724
255	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
254	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	36.3	675
253	Genome-wide association analysis identifies 20 loci that influence adult height. *Nature Genetics*, **2008**, 40, 575-83	36.3	654
252	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. *Nature*, **2010**, 464, 713-20	50.4	639
251	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. *Nature Genetics*, **2012**, 44, 991-1005	36.3	621
250	Common variants associated with plasma triglycerides and risk for coronary artery disease. *Nature Genetics*, **2013**, 45, 1345-52	36.3	597
249	Variants in MTNR1B influence fasting glucose levels. *Nature Genetics*, **2009**, 41, 77-81	36.3	584
248	Mapping cis- and trans-regulatory effects across multiple tissues in twins. *Nature Genetics*, **2012**, 44, 1084-9	36.3	572
247	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. *Nature Genetics*, **2018**, 50, 524-537	36.3	536
246	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. *Nature*, **2017**, 541, 81-86	50.4	511
245	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics*, **2013**, 45, 501-12	36.3	437
244	Localization of type 1 diabetes susceptibility to the MHC class I genes HLA-B and HLA-A. *Nature*, **2007**, 450, 887-92	50.4	421
243	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. *Diabetes*, **2017**, 66, 2888-2902	36.3	414
242	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412

241	The metabochip, a custom genotyping array for genetic studies of metabolic, cardiovascular, and anthropometric traits. *PLoS Genetics*, **2012**, 8, e1002793	6	395
240	Genome-wide association scan meta-analysis identifies three Loci influencing adiposity and fat distribution. *PLoS Genetics*, **2009**, 5, e1000508	6	393
239	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. *Nature Genetics*, **2018**, 50, 1412-1425	36.3	386
238	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. *Nature Genetics*, **2014**, 46, 357-63	36.3	351
237	The architecture of gene regulatory variation across multiple human tissues: the MuTHER study. *PLoS Genetics*, **2011**, 7, e1002003	6	336
236	A common variant of HMGA2 is associated with adult and childhood height in the general population. *Nature Genetics*, **2007**, 39, 1245-50	36.3	330
235	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	6	326
234	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. *Nature Genetics*, **2017**, 49, 403-415	36.3	313
233	FTO genotype is associated with phenotypic variability of body mass index. *Nature*, **2012**, 490, 267-72	50.4	304
232	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. *Nature Genetics*, **2015**, 47, 1415-25	36.3	292
231	A genome-wide association meta-analysis identifies new childhood obesity loci. *Nature Genetics*, **2012**, 44, 526-31	36.3	292
230	Multi-ethnic genome-wide association study for atrial fibrillation. *Nature Genetics*, **2018**, 50, 1225-1233	36.3	277
229	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. *PLoS Genetics*, **2013**, 9, e1003500	6	277
228	Common variation in the FTO gene alters diabetes-related metabolic traits to the extent expected given its effect on BMI. *Diabetes*, **2008**, 57, 1419-26	0.9	260
227	Meta-analysis of genome-wide association studies for body fat distribution in 694 649 individuals of European ancestry. *Human Molecular Genetics*, **2019**, 28, 166-174	5.6	258
226	MHC2TA is associated with differential MHC molecule expression and susceptibility to rheumatoid arthritis, multiple sclerosis and myocardial infarction. *Nature Genetics*, **2005**, 37, 486-94	36.3	254
225	Identification of an imprinted master trans regulator at the KLF14 locus related to multiple metabolic phenotypes. *Nature Genetics*, **2011**, 43, 561-4	36.3	253
224	Distribution and medical impact of loss-of-function variants in the Finnish founder population. *PLoS Genetics*, **2014**, 10, e1004494	6	243

223	The impact of low-frequency and rare variants on lipid levels. *Nature Genetics*, **2015**, 47, 589-97	36.3	229
222	Global microRNA expression profiles in insulin target tissues in a spontaneous rat model of type 2 diabetes. *Diabetologia*, **2010**, 53, 1099-109	10.3	227
221	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics*, **2018**, 50, 559-571	36.3	221
220	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	6	220
219	A catalog of genetic loci associated with kidney function from analyses of a million individuals. *Nature Genetics*, **2019**, 51, 957-972	36.3	217
218	Genome-wide association of polycystic ovary syndrome implicates alterations in gonadotropin secretion in European ancestry populations. *Nature Communications*, **2015**, 6, 7502	17.4	214
217	Mosaic loss of chromosome Y in peripheral blood is associated with shorter survival and higher risk of cancer. *Nature Genetics*, **2014**, 46, 624-8	36.3	213
216	Type 2 diabetes: new genes, new understanding. *Trends in Genetics*, **2008**, 24, 613-21	8.5	204
215	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. *Nature Genetics*, **2016**, 48, 1462-1472	36.3	198
214	Integrated genetic and epigenetic analysis identifies haplotype-specific methylation in the FTO type 2 diabetes and obesity susceptibility locus. *PLoS ONE*, **2010**, 5, e14040	3.7	193
213	Genetics and epigenetics of obesity. *Maturitas*, **2011**, 69, 41-9	5	190
212	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
211	Variants in ADCY5 and near CCNL1 are associated with fetal growth and birth weight. *Nature Genetics*, **2010**, 42, 430-5	36.3	184
210	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
209	A brief history of human disease genetics. *Nature*, **2020**, 577, 179-189	50.4	181
208	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180
207	Strong genetic evidence of DCDC2 as a susceptibility gene for dyslexia. *American Journal of Human Genetics*, **2006**, 78, 52-62	11	179
206	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. *Nature Genetics*, **2017**, 49, 946-952	36.3	176

205	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. *American Journal of Human Genetics*, **2014**, 94, 233-45	11	170
204	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. *Molecular Psychiatry*, **2015**, 20, 647-656	15.1	167
203	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. *PLoS Genetics*, **2018**, 14, e1007813	6	166
202	The genetic and epigenetic basis of type 2 diabetes and obesity. *Clinical Pharmacology and Therapeutics*, **2012**, 92, 707-15	6.1	162
201	Genomewide linkage analysis of stature in multiple populations reveals several regions with evidence of linkage to adult height. *American Journal of Human Genetics*, **2001**, 69, 106-16	11	153
200	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. *Nature Genetics*, **2019**, 51, 51-62	36.3	152
199	The genetics of obesity. *Current Diabetes Reports*, **2010**, 10, 498-505	5.6	151
198	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	11	151
197	Genetic evidence that raised sex hormone binding globulin (SHBG) levels reduce the risk of type 2 diabetes. *Human Molecular Genetics*, **2010**, 19, 535-44	5.6	150
196	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. *Nature Communications*, **2015**, 6, 5897	17.4	147
195	The miRNA profile of human pancreatic islets and beta-cells and relationship to type 2 diabetes pathogenesis. *PLoS ONE*, **2013**, 8, e55272	3.7	146
194	The role of adiposity in cardiometabolic traits: a Mendelian randomization analysis. *PLoS Medicine*, **2013**, 10, e1001474	11.6	144
193	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. *Nature Communications*, **2020**, 11, 163	17.4	140
192	A genome-wide association search for type 2 diabetes genes in African Americans. *PLoS ONE*, **2012**, 7, e29202	3.7	138
191	Genomewide search for type 2 diabetes mellitus susceptibility loci in Finnish families: the Botnia study. *American Journal of Human Genetics*, **2002**, 70, 509-16	11	127
190	GWAS identifies 14 loci for device-measured physical activity and sleep duration. *Nature Communications*, **2018**, 9, 5257	17.4	123
189	Rare variants in PPARG with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 13127-32	11.5	121
188	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	50.4	119

187	Type 2 diabetes risk alleles are associated with reduced size at birth. *Diabetes*, **2009**, 58, 1428-33	0.9	117
186	Mutagenesis. Smoking is associated with mosaic loss of chromosome Y. *Science*, **2015**, 347, 81-3	33.3	108
185	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. *Nature Communications*, **2016**, 7, 10494	17.4	107
184	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. *Nature Communications*, **2017**, 8, 14977	17.4	105
183	Common variants at 6q22 and 17q21 are associated with intracranial volume. *Nature Genetics*, **2012** , 44, 539-44	36.3	104
182	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. *PLoS Genetics*, **2017**, 13, e1006528	6	103
181	Large-scale zygosity testing using single nucleotide polymorphisms. *Twin Research and Human Genetics*, **2007**, 10, 604-25	2.2	102
180	Mapping of 79 loci for 83 plasma protein biomarkers in cardiovascular disease. *PLoS Genetics*, **2017**, 13, e1006706	6	102
179	Haplotypes of G protein-coupled receptor 154 are associated with childhood allergy and asthma. *American Journal of Respiratory and Critical Care Medicine*, **2005**, 171, 1089-95	10.2	100
178	Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. *Lancet Neurology, The*, **2016**, 15, 695-707	24.1	100
177	Adiposity-related heterogeneity in patterns of type 2 diabetes susceptibility observed in genome-wide association data. *Diabetes*, **2009**, 58, 505-10	0.9	98
176	Variants in the calpain-10 gene predispose to insulin resistance and elevated free fatty acid levels. *Diabetes*, **2002**, 51, 2658-64	0.9	98
175	Association of variants in the fat mass and obesity associated (FTO) gene with polycystic ovary syndrome. *Diabetologia*, **2008**, 51, 1153-8	10.3	97
174	MicroRNA-125a is over-expressed in insulin target tissues in a spontaneous rat model of Type 2 Diabetes. *BMC Medical Genomics*, **2009**, 2, 54	3.7	96
173	Interactions between glutathione S-transferase P1, tumor necrosis factor, and traffic-related air pollution for development of childhood allergic disease. *Environmental Health Perspectives*, **2008**, 116, 1077-84	8.4	96
172	Mendelian randomization studies do not support a causal role for reduced circulating adiponectin levels in insulin resistance and type 2 diabetes. *Diabetes*, **2013**, 62, 3589-98	0.9	95
171	Common variants at 12q15 and 12q24 are associated with infant head circumference. *Nature Genetics*, **2012**, 44, 532-538	36.3	94
170	Mosaic Loss of Chromosome Y in Blood Is Associated with Alzheimer Disease. *American Journal of Human Genetics*, **2016**, 98, 1208-1219	11	90

169	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. *Nature Communications*, **2017**, 8, 80	17.4	88
168	Insights into the molecular mechanism for type 2 diabetes susceptibility at the KCNQ1 locus from temporal changes in imprinting status in human islets. *Diabetes*, **2013**, 62, 987-92	0.9	87
167	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. *Journal of the American College of Cardiology*, **2019**, 73, 58-66	15.1	86
166	A gene conferring susceptibility to type 2 diabetes in conjunction with obesity is located on chromosome 18p11. *Diabetes*, **2001**, 50, 675-80	0.9	83
165	Clinical and genetic correlates of growth differentiation factor 15 in the community. *Clinical Chemistry*, **2012**, 58, 1582-91	5.5	81
164	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. *Nature Genetics*, **2017**, 49, 125-130	36.3	80
163	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. *Nature Communications*, **2017**, 8, 16015	17.4	80
162	Neuropeptide s receptor 1 gene polymorphism is associated with susceptibility to inflammatory bowel disease. *Gastroenterology*, **2007**, 133, 808-17	13.3	79
161	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	6	76
160	Mouse-human experimental epigenetic analysis unmasks dietary targets and genetic liability for diabetic phenotypes. *Cell Metabolism*, **2015**, 21, 138-49	24.6	76
159	Common variants in HNF-1 alpha and risk of type 2 diabetes. *Diabetologia*, **2006**, 49, 2882-91	10.3	76
158	Genome-wide association study of toxic metals and trace elements reveals novel associations. *Human Molecular Genetics*, **2015**, 24, 4739-45	5.6	75
157	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. *American Journal of Human Genetics*, **2017**, 100, 865-884	11	74
156	Genome wide association identifies common variants at the SERPINA6/SERPINA1 locus influencing plasma cortisol and corticosteroid binding globulin. *PLoS Genetics*, **2014**, 10, e1004474	6	71
155	The presence of methylation quantitative trait loci indicates a direct genetic influence on the level of DNA methylation in adipose tissue. *PLoS ONE*, **2013**, 8, e55923	3.7	71
154	Meta-analysis of sex-specific genome-wide association studies. *Genetic Epidemiology*, **2010**, 34, 846-53	2.6	69
153	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. *Journal of Clinical Investigation*, **2017**, 127, 1798-1812	15.9	68
152	Identification and validation of N-acetyltransferase 2 as an insulin sensitivity gene. *Journal of Clinical Investigation*, **2015**, 125, 1739-51	15.9	67

151	Variability of gene expression profiles in human blood and lymphoblastoid cell lines. *BMC Genomics*, **2010**, 11, 96	4.5	64
150	Common variants in maturity-onset diabetes of the young genes and future risk of type 2 diabetes. *Diabetes*, **2008**, 57, 1738-44	0.9	63
149	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. *Nature Metabolism*, **2020**, 2, 1135-1148	14.6	61
148	A meta-analysis of four European genome screens (GIFT Consortium) shows evidence for a novel region on chromosome 17p11.2-q22 linked to type 2 diabetes. *Human Molecular Genetics*, **2003**, 12, 1865-73	5.6	60
147	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. *PLoS Genetics*, **2015**, 11, e1005230	6	59
146	The human GIMAP5 gene has a common polyadenylation polymorphism increasing risk to systemic lupus erythematosus. *Journal of Medical Genetics*, **2007**, 44, 314-21	5.8	58
145	Genome-wide enrichment analysis between endometriosis and obesity-related traits reveals novel susceptibility loci. *Human Molecular Genetics*, **2015**, 24, 1185-99	5.6	57
144	A genome-wide scan in families with maturity-onset diabetes of the young: evidence for further genetic heterogeneity. *Diabetes*, **2003**, 52, 872-81	0.9	55
143	Meta-analysis of the INSIG2 association with obesity including 74,345 individuals: does heterogeneity of estimates relate to study design?. *PLoS Genetics*, **2009**, 5, e1000694	6	54
142	Variation in DNA repair genes ERCC2, XRCC1, and XRCC3 and risk of follicular lymphoma. *Cancer Epidemiology Biomarkers and Prevention*, **2006**, 15, 258-65	4	54
141	Coexpression network analysis in abdominal and gluteal adipose tissue reveals regulatory genetic loci for metabolic syndrome and related phenotypes. *PLoS Genetics*, **2012**, 8, e1002505	6	52
140	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. *Nature Communications*, **2019**, 10, 29	17.4	51
139	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. *Nature Communications*, **2017**, 8, 15805	17.4	50
138	Meta-analysis of gene-level associations for rare variants based on single-variant statistics. *American Journal of Human Genetics*, **2013**, 93, 236-48	11	49
137	Mechanisms of inactivation of MLH1 in hereditary nonpolyposis colorectal carcinoma: a novel approach. *Oncogene*, **2007**, 26, 4541-9	9.2	49
136	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	10.6	48
135	Causal relationships between obesity and the leading causes of death in women and men. *PLoS Genetics*, **2019**, 15, e1008405	6	48
134	Genome-Wide Association Study of the Modified Stumvoll Insulin Sensitivity Index Identifies BCL2 and FAM19A2 as Novel Insulin Sensitivity Loci. *Diabetes*, **2016**, 65, 3200-11	0.9	47

133	Liver X receptor gene polymorphisms and adipose tissue expression levels in obesity. *Pharmacogenetics and Genomics*, **2006**, 16, 881-9	1.9	47
132	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. *Nature Communications*, **2016**, 7, 13357	17.4	46
131	The trans-ancestral genomic architecture of glycemic traits. *Nature Genetics*, **2021**, 53, 840-860	36.3	44
130	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. *American Journal of Human Genetics*, **2016**, 99, 636-646	11	44
129	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
128	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. *Nature Communications*, **2019**, 10, 4130	17.4	43
127	Extent, causes, and consequences of small RNA expression variation in human adipose tissue. *PLoS Genetics*, **2012**, 8, e1002704	6	43
126	Large-scale genome-wide association studies and meta-analyses of longitudinal change in adult lung function. *PLoS ONE*, **2014**, 9, e100776	3.7	42
125	Phenylketonuria screening registry as a resource for population genetic studies. *Journal of Medical Genetics*, **2005**, 42, e60	5.8	42
124	MicroRNA expression in abdominal and gluteal adipose tissue is associated with mRNA expression levels and partly genetically driven. *PLoS ONE*, **2011**, 6, e27338	3.7	39
123	A powerful approach to sub-phenotype analysis in population-based genetic association studies. *Genetic Epidemiology*, **2010**, 34, 335-43	2.6	39
122	Chromosome 7p linkage and GPR154 gene association in Italian families with allergic asthma. *Clinical and Experimental Allergy*, **2007**, 37, 83-9	4.1	39
121	Insights into the Genetic Susceptibility to Type 2 Diabetes from Genome-Wide Association Studies of Obesity-Related Traits. *Current Diabetes Reports*, **2015**, 15, 83	5.6	38
120	Sexual dimorphisms in genetic loci linked to body fat distribution. *Bioscience Reports*, **2017**, 37,	4.1	37
119	Mechanisms of disease: genetic insights into the etiology of type 2 diabetes and obesity. *Nature Clinical Practice Endocrinology and Metabolism*, **2008**, 4, 156-63		36
118	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. *Nature Communications*, **2018**, 9, 711	17.4	35
117	The influence of menstrual cycle and endometriosis on endometrial methylome. *Clinical Epigenetics* , **2016**, 8, 2	7.7	35
116	Evaluation of the genetic overlap between osteoarthritis with body mass index and height using genome-wide association scan data. *Annals of the Rheumatic Diseases*, **2013**, 72, 935-41	2.4	35

115	The use of genome-wide eQTL associations in lymphoblastoid cell lines to identify novel genetic pathways involved in complex traits. *PLoS ONE*, **2011**, 6, e22070	3.7	35
114	Contribution of 32 GWAS-identified common variants to severe obesity in European adults referred for bariatric surgery. *PLoS ONE*, **2013**, 8, e70735	3.7	34
113	Polymorphisms in the gene encoding the voltage-dependent Ca(2+) channel Ca (V)2.3 (CACNA1E) are associated with type 2 diabetes and impaired insulin secretion. *Diabetologia*, **2007**, 50, 2467-75	10.3	34
112	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475 000 Individuals. *Circulation: Cardiovascular Genetics*, **2017**, 10,		33
111	Global analysis of uniparental disomy using high density genotyping arrays. *Journal of Medical Genetics*, **2005**, 42, 847-51	5.8	33
110	Genome-wide association study identifies 48 common genetic variants associated with handedness. *Nature Human Behaviour*, **2021**, 5, 59-70	12.8	33
109	Population structure in contemporary Sweden--a Y-chromosomal and mitochondrial DNA analysis. *Annals of Human Genetics*, **2009**, 73, 61-73	2.2	32
108	A genome wide scan for early onset primary hypertension in Scandinavians. *Human Molecular Genetics*, **2003**, 12, 2077-81	5.6	30
107	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. *Nature Communications*, **2021**, 12, 24	17.4	30
106	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. *Diabetes*, **2017**, 66, 2019-2032	0.9	29
105	Population substructure in Finland and Sweden revealed by the use of spatial coordinates and a small number of unlinked autosomal SNPs. *BMC Genetics*, **2008**, 9, 54	2.6	29
104	Interaction between early maternal smoking and variants in TNF and GSTP1 in childhood wheezing. *Clinical and Experimental Allergy*, **2010**, 40, 458-67	4.1	28
103	Contribution of known and unknown susceptibility genes to early-onset diabetes in scandinavia: evidence for heterogeneity. *Diabetes*, **2002**, 51, 1609-17	0.9	28
102	Evaluating the cardiovascular safety of sclerostin inhibition using evidence from meta-analysis of clinical trials and human genetics. *Science Translational Medicine*, **2020**, 12,	17.5	27
101	Restriction site-specific methylation studies of imprinted genes with quantitative real-time PCR. *Clinical Chemistry*, **2008**, 54, 491-9	5.5	27
100	G protein-coupled receptor for asthma susceptibility associates with respiratory distress syndrome. *Annals of Medicine*, **2006**, 38, 357-66	1.5	27
99	GWAS-identified loci for coronary heart disease are associated with intima-media thickness and plaque presence at the carotid artery bulb. *Atherosclerosis*, **2015**, 239, 304-10	3.1	26
98	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. *Nature Genetics*, **2020**, 52, 1314-1332	36.3	26

97	Expression of phosphofructokinase in skeletal muscle is influenced by genetic variation and associated with insulin sensitivity. *Diabetes*, **2014**, 63, 1154-65	0.9	25
96	Disentangling the genetics of lean mass. *American Journal of Clinical Nutrition*, **2019**, 109, 276-287	7	24
95	Genome-wide DNA methylation study identifies genes associated with the cardiovascular biomarker GDF-15. *Human Molecular Genetics*, **2016**, 25, 817-27	5.6	23
94	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
93	Fat depot-specific mRNA expression of novel loci associated with waist-hip ratio. *International Journal of Obesity*, **2014**, 38, 120-5	5.5	22
92	Frequency of non-convulsive seizures and non-convulsive status epilepticus in subarachnoid hemorrhage patients in need of controlled ventilation and sedation. *Neurocritical Care*, **2012**, 17, 367-73	3.3	22
91	A Partial Loss-of-Function Variant in Is Associated With Reduced Insulin-Mediated Glucose Uptake in Multiple Insulin-Sensitive Tissues: A Genotype-Based Callback Positron Emission Tomography Study. *Diabetes*, **2018**, 67, 334-342	0.9	22
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7 Machine Learning based histology phenotyping to investigate the epidemiologic and genetic basis of adipocyte morphology and cardiometabolic traits **2020**, 16, e1008044

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4 Causal relationships between obesity and the leading causes of death in women and men **2019**, 15, e1008405

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