Cecilia M Lindgren

List of Publications by Year in Descending Order

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	Making sense of the linear genome, gene function and TADs.. *Epigenetics and Chromatin*, **2022**, 15, 4	5.8	1
275	Obesity and risk of female reproductive conditions: A Mendelian randomisation study.. *PLoS Medicine*, **2022**, 19, e1003679	11.6	1
274	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function.. *Nature Genetics*, **2022**,	36.3	6
273	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. *Nature Genetics*, **2022**,	36.3	7
272	Transcriptome and fatty-acid signatures of adipocyte hypertrophy and its non-invasive MR-based characterization in human adipose tissue.. *EBioMedicine*, **2022**, 79, 104020	8.8	0
271	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. *Communications Biology*, **2022**, 5,	6.7	1
270	Evidence From Men for Ovary-independent Effects of Genetic Risk Factors for Polycystic Ovary Syndrome.. *Journal of Clinical Endocrinology and Metabolism*, **2021**,	5.6	3
269	Response to comment on "Evaluating the cardiovascular safety of sclerostin inhibition using evidence from meta-analysis of clinical trials and human genetics". *Science Translational Medicine*, **2021**, 13, eabf4530	17.5	
268	A regulatory variant at 3q21.1 confers an increased pleiotropic risk for hyperglycemia and altered bone mineral density. *Cell Metabolism*, **2021**, 33, 615-628.e13	24.6	7
267	Colocalization analysis of polycystic ovary syndrome to identify potential disease-mediating genes and proteins. *European Journal of Human Genetics*, **2021**, 29, 1446-1454	5.3	5
266	The trans-ancestral genomic architecture of glycemic traits. *Nature Genetics*, **2021**, 53, 840-860	36.3	44
265	A distribution-centered approach for analyzing human adipocyte size estimates and their association with obesity-related traits and mitochondrial function. *International Journal of Obesity*, **2021**, 45, 2108-2117	5.5	4
264	Linking the obesity rs1421085 variant circuitry to cellular, metabolic, and organismal phenotypes in vivo. *Science Advances*, **2021**, 7,	14.3	4
263	Genome-wide association study identifies 48 common genetic variants associated with handedness. *Nature Human Behaviour*, **2021**, 5, 59-70	12.8	33
262	Sex Differences in the Risk of Coronary Heart Disease Associated With Type 2 Diabetes: A Mendelian Randomization Analysis. *Diabetes Care*, **2021**, 44, 556-562	14.6	4
261	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. *Nature Communications*, **2021**, 12, 24	17.4	30
260	The genomics of heart failure: design and rationale of the HERMES consortium. *ESC Heart Failure*, **2021**,	3.7	1

259	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. *Nature Communications*, **2020**, 11, 2542	17.4	16
258	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
257	Genome-wide association study of adipocyte lipolysis in the GENetics of adipocyte lipolysis (GENiAL) cohort. *Molecular Metabolism*, **2020**, 34, 85-96	8.8	6
256	Genome-wide Study Identifies Association between HLA-B55:01 and Self-Reported Penicillin Allergy. *American Journal of Human Genetics*, **2020**, 107, 612-621	11	17
255	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. *Nature Communications*, **2020**, 11, 163	17.4	140
254	A Polygenic and Phenotypic Risk Prediction for Polycystic Ovary Syndrome Evaluated by Phenome-Wide Association Studies. *Journal of Clinical Endocrinology and Metabolism*, **2020**, 105,	5.6	17
253	A brief history of human disease genetics. *Nature*, **2020**, 577, 179-189	50.4	181
252	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. *Nature Metabolism*, **2020**, 2, 1135-1148	14.6	61
251	Commentary: Using human genetics to guide the repurposing of medicines. *International Journal of Epidemiology*, **2020**, 49, 1140-1146	7.8	2
250	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
249	The genetic architecture of sporadic and multiple consecutive miscarriage. *Nature Communications*, **2020**, 11, 5980	17.4	11
248	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. *Diabetes*, **2020**, 69, 2806-2818	0.9	10
247	Machine Learning based histology phenotyping to investigate the epidemiologic and genetic basis of adipocyte morphology and cardiometabolic traits. *PLoS Computational Biology*, **2020**, 16, e1008044	5	5
246	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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241	Machine Learning based histology phenotyping to investigate the epidemiologic and genetic basis of adipocyte morphology and cardiometabolic traits **2020**, 16, e1008044		
240	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. *Nature Communications*, **2019**, 10, 4130	17.4	43
239	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. *American Journal of Human Genetics*, **2019**, 105, 15-28	11	12
238	A catalog of genetic loci associated with kidney function from analyses of a million individuals. *Nature Genetics*, **2019**, 51, 957-972	36.3	217
237	MicroRNA-196a links human body fat distribution to adipose tissue extracellular matrix composition. *EBioMedicine*, **2019**, 44, 467-475	8.8	12
236	Commentary: Mendelian randomization and women's health. *International Journal of Epidemiology*, **2019**, 48, 830-833	7.8	4
235	Disentangling the genetics of lean mass. *American Journal of Clinical Nutrition*, **2019**, 109, 276-287	7	24
234	Causal relationships between obesity and the leading causes of death in women and men. *PLoS Genetics*, **2019**, 15, e1008405	6	48
233	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
232	Common Genetic Variation in Relation to Brachial Vascular Dimensions and Flow-Mediated Vasodilation. *Circulation Genomic and Precision Medicine*, **2019**, 12, e002409	5.2	2
231	GWAS Identifies Risk Locus for Erectile Dysfunction and Implicates Hypothalamic Neurobiology and Diabetes in Etiology. *American Journal of Human Genetics*, **2019**, 104, 157-163	11	12
230	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
229	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. *Nature Genetics*, **2019**, 51, 51-62	36.3	152
228	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
227	Cerebrospinal fluid lactate and neurological outcome after subarachnoid haemorrhage. *Journal of Clinical Neuroscience*, **2019**, 60, 63-67	2.2	3
226	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
225	Causal relationships between obesity and the leading causes of death in women and men **2019**, 15, e1008405		
224	Causal relationships between obesity and the leading causes of death in women and men **2019**, 15, e1008405		

223	Causal relationships between obesity and the leading causes of death in women and men **2019**, 15, e1008405		
222	Causal relationships between obesity and the leading causes of death in women and men **2019**, 15, e1008405		
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	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
219	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. *Nature Communications*, **2018**, 9, 711	17.4	35
218	Dynamics Determine Signaling in a Multicomponent System Associated with Rheumatoid Arthritis. *Journal of Medicinal Chemistry*, **2018**, 61, 4774-4790	8.3	0
217	A genome-wide association study of IgM antibody against phosphorylcholine: shared genetics and phenotypic relationship to chronic lymphocytic leukemia. *Human Molecular Genetics*, **2018**, 27, 1809-1818	5.6	3
216	Multi-ethnic genome-wide association study for atrial fibrillation. *Nature Genetics*, **2018**, 50, 1225-1233	36.3	277
215	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
214	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
213	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
212	GWAS identifies 14 loci for device-measured physical activity and sleep duration. *Nature Communications*, **2018**, 9, 5257	17.4	123
211	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
210	Genome-Wide Association Studies of Estimated Fatty Acid Desaturase Activity in Serum and Adipose Tissue in Elderly Individuals: Associations with Insulin Sensitivity. *Nutrients*, **2018**, 10,	6.7	12
209	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
208	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
207	Noncovalent Inhibitors of Mosquito Acetylcholinesterase 1 with Resistance-Breaking Potency. *Journal of Medicinal Chemistry*, **2018**, 61, 10545-10557	8.3	4
206	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

205	Large-scale meta-analysis highlights the hypothalamic-pituitary-gonadal axis in the genetic regulation of menstrual cycle length. *Human Molecular Genetics*, **2018**, 27, 4323-4332	5.6	11
204	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
203	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
202	Sexual dimorphisms in genetic loci linked to body fat distribution. *Bioscience Reports*, **2017**, 37,	4.1	37
201	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
200	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
199	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
198	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. *Nature Communications*, **2017**, 8, 15805	17.4	50
197	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. *American Journal of Human Genetics*, **2017**, 100, 865-884	11	74
196	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. *Diabetes*, **2017**, 66, 2888-2902	8.2	414
195	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
194	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. *Nature*, **2017**, 541, 81-86	50.4	511
193	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475 000 Individuals. *Circulation: Cardiovascular Genetics*, **2017**, 10,		33
192	The genetic underpinnings of body fat distribution. *Expert Review of Endocrinology and Metabolism*, **2017**, 12, 417-427	4.1	2
191	Genetic and epigenetic studies of adiposity and cardiometabolic disease. *Genome Medicine*, **2017**, 9, 82	14.4	10
190	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. *Nature Communications*, **2017**, 8, 80	17.4	88
189	Variability of genome-wide DNA methylation and mRNA expression profiles in reproductive and endocrine disease related tissues. *Epigenetics*, **2017**, 12, 897-908	5.7	19
188	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. *Nature Communications*, **2017**, 8, 16015	17.4	80

187	Genetic and methylation variation in the CYP2B6 gene is related to circulating p,p'-dde levels in a population-based sample. *Environment International*, **2017**, 98, 212-218	12.9	4
186	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
185	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
184	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. *PLoS Genetics*, **2017**, 13, e1006528	6	103
183	Mapping of 79 loci for 83 plasma protein biomarkers in cardiovascular disease. *PLoS Genetics*, **2017**, 13, e1006706	6	102
182	Ranking and characterization of established BMI and lipid associated loci as candidates for gene-environment interactions. *PLoS Genetics*, **2017**, 13, e1006812	6	13
181	Identification of a novel proinsulin-associated SNP and demonstration that proinsulin is unlikely to be a causal factor in subclinical vascular remodelling using Mendelian randomisation. *Atherosclerosis*, **2017**, 266, 196-204	3.1	2
180	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. *Nature Communications*, **2016**, 7, 13357	17.4	46
179	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
178	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
177	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. *Scientific Reports*, **2016**, 6, 35278	4.9	18
176	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. *Nature Genetics*, **2016**, 48, 1462-1472	36.3	198
175	The influence of menstrual cycle and endometriosis on endometrial methylome. *Clinical Epigenetics* , **2016**, 8, 2	7.7	35
174	Genome-wide DNA methylation study identifies genes associated with the cardiovascular biomarker GDF-15. *Human Molecular Genetics*, **2016**, 25, 817-27	5.6	23
173	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180
172	Testing the role of predicted gene knockouts in human anthropometric trait variation. *Human Molecular Genetics*, **2016**, 25, 2082-2092	5.6	7
171	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. *Nature Communications*, **2016**, 7, 10494	17.4	107
170	Leptin levels after subarachnoid haemorrhage are gender dependent. *SpringerPlus*, **2016**, 5, 667		1

169	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
168	Mosaic Loss of Chromosome Y in Blood Is Associated with Alzheimer Disease. *American Journal of Human Genetics*, **2016**, 98, 1208-1219	11	90
167	Ovarian Physiology and GWAS: Biobanks, Biology, and Beyond. *Trends in Endocrinology and Metabolism*, **2016**, 27, 516-528	8.8	9
166	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
165	Obesity--On or Off?. *New England Journal of Medicine*, **2016**, 374, 1486-8	59.2	6
164	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. *American Journal of Human Genetics*, **2016**, 98, 857-868	11	14
163	Imprinted genes and imprinting control regions show predominant intermediate methylation in adult somatic tissues. *Epigenomics*, **2016**, 8, 789-99	4.4	14
162	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. *American Journal of Human Genetics*, **2016**, 99, 636-646	11	44
161	Blood Metabolomic Predictors of 1-Year Outcome in Subarachnoid Hemorrhage. *Neurocritical Care*, **2015**, 23, 225-32	3.3	5
160	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	50.4	119
159	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
158	The impact of low-frequency and rare variants on lipid levels. *Nature Genetics*, **2015**, 47, 589-97	36.3	229
157	Genome-wide association study of plasma levels of polychlorinated biphenyls disclose an association with the CYP2B6 gene in a population-based sample. *Environmental Research*, **2015**, 140, 95-101	7.9	10
156	Genome-wide enrichment analysis between endometriosis and obesity-related traits reveals novel susceptibility loci. *Human Molecular Genetics*, **2015**, 24, 1185-99	5.6	57
155	Genome-wide association study of toxic metals and trace elements reveals novel associations. *Human Molecular Genetics*, **2015**, 24, 4739-45	5.6	75
154	Genome-wide association of polycystic ovary syndrome implicates alterations in gonadotropin secretion in European ancestry populations. *Nature Communications*, **2015**, 6, 7502	17.4	214
153	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. *Nature Genetics*, **2015**, 47, 1121-1130	36.3	1290
152	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. *Nature Genetics*, **2015**, 47, 1415-25	36.3	292

151	Benefits of statistical molecular design, covariance analysis, and reference models in QSAR: a case study on acetylcholinesterase. *Journal of Computer-Aided Molecular Design*, **2015**, 29, 199-215	4.2	13
150	Mutagenesis. Smoking is associated with mosaic loss of chromosome Y. *Science*, **2015**, 347, 81-3	33.3	108
149	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. *Molecular Psychiatry*, **2015**, 20, 647-656	15.1	167
148	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
147	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. *PLoS Genetics*, **2015**, 11, e1005230	6	59
146	Robust Linear Models for Cis-eQTL Analysis. *PLoS ONE*, **2015**, 10, e0127882	3.7	6
145	Identification and validation of N-acetyltransferase 2 as an insulin sensitivity gene. *Journal of Clinical Investigation*, **2015**, 125, 1739-51	15.9	67
144	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
143	Hydroxyethylene isosteres introduced in type II collagen fragments substantially alter the structure and dynamics of class II MHC A(q)/glycopeptide complexes. *Organic and Biomolecular Chemistry*, **2015**, 13, 6203-16	3.9	4
142	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
141	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
140	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
139	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. *Nature Communications*, **2015**, 6, 5897	17.4	147
138	Mouse-human experimental epigenetic analysis unmasks dietary targets and genetic liability for diabetic phenotypes. *Cell Metabolism*, **2015**, 21, 138-49	24.6	76
137	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
136	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
135	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
134	Genetic variation in the CYP2B6 gene is related to circulating 2,2',4,4'-tetrabromodiphenyl ether (BDE-47) concentrations: an observational population-based study. *Environmental Health*, **2014**, 13, 34	6	8

133	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
132	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. *Nature Genetics*, **2014**, 46, 357-63	36.3	351
131	Expression of phosphofructokinase in skeletal muscle is influenced by genetic variation and associated with insulin sensitivity. *Diabetes*, **2014**, 63, 1154-65	0.9	25
130	Genetic variation in the CYP1A1 gene is related to circulating PCB118 levels in a population-based sample. *Environmental Research*, **2014**, 133, 135-40	7.9	10
129	Simulation of Finnish population history, guided by empirical genetic data, to assess power of rare-variant tests in Finland. *American Journal of Human Genetics*, **2014**, 94, 710-20	11	19
128	Large-scale genome-wide association studies and meta-analyses of longitudinal change in adult lung function. *PLoS ONE*, **2014**, 9, e100776	3.7	42
127	Distribution and medical impact of loss-of-function variants in the Finnish founder population. *PLoS Genetics*, **2014**, 10, e1004494	6	243
126	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
125	Genome-Wide Association Studies of Obesity **2014**, 33-53		2
124	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
123	Here and now there and then: Narrative time and space in intercountry adoptees stories about background, origin and roots. *Qualitative Social Work*, **2014**, 13, 539-554	1.3	3
122	Genome-Wide Association Studies of Obesity and Related Traits. *Frontiers in Diabetes*, **2014**, 58-70	0.6	
121	Fat depot-specific mRNA expression of novel loci associated with waist-hip ratio. *International Journal of Obesity*, **2014**, 38, 120-5	5.5	22
120	ADMA levels and arginine/ADMA ratios reflect severity of disease and extent of inflammation after subarachnoid hemorrhage. *Neurocritical Care*, **2014**, 21, 91-101	3.3	16
119	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
118	Discovery and refinement of loci associated with lipid levels. *Nature Genetics*, **2013**, 45, 1274-1283	36.3	1904
117	Common variants associated with plasma triglycerides and risk for coronary artery disease. *Nature Genetics*, **2013**, 45, 1345-52	36.3	597
116	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

115	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
114	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
113	The role of adiposity in cardiometabolic traits: a Mendelian randomization analysis. *PLoS Medicine*, **2013**, 10, e1001474	11.6	144
112	Assessing association between protein truncating variants and quantitative traits. *Bioinformatics*, **2013**, 29, 2419-26	7.2	9
111	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
110	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
109	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
108	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
107	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
106	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
105	A genome-wide association meta-analysis identifies new childhood obesity loci. *Nature Genetics*, **2012**, 44, 526-31	36.3	292
104	Clinical and genetic correlates of growth differentiation factor 15 in the community. *Clinical Chemistry*, **2012**, 58, 1582-91	5.5	81
103	The genetic and epigenetic basis of type 2 diabetes and obesity. *Clinical Pharmacology and Therapeutics*, **2012**, 92, 707-15	6.1	162
102	FTO genotype is associated with phenotypic variability of body mass index. *Nature*, **2012**, 490, 267-72	50.4	304
101	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
100	Mapping cis- and trans-regulatory effects across multiple tissues in twins. *Nature Genetics*, **2012**, 44, 1084-9	36.3	572
99	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
98	A genome-wide association search for type 2 diabetes genes in African Americans. *PLoS ONE*, **2012**, 7, e29202	3.7	138

97	Extent, causes, and consequences of small RNA expression variation in human adipose tissue. *PLoS Genetics*, **2012**, 8, e1002704	6	43
96	The metabochip, a custom genotyping array for genetic studies of metabolic, cardiovascular, and anthropometric traits. *PLoS Genetics*, **2012**, 8, e1002793	6	395
95	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
94	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
93	Common variants at 6q22 and 17q21 are associated with intracranial volume. *Nature Genetics*, **2012** , 44, 539-44	36.3	104
92	Common variants at 12q15 and 12q24 are associated with infant head circumference. *Nature Genetics*, **2012**, 44, 532-538	36.3	94
91	Genetics and epigenetics of obesity. *Maturitas*, **2011**, 69, 41-9	5	190
90	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
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11	Genome-wide association study provides new insights into the genetic architecture and pathogenesis of heart failure		2
10	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes		4
9	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4
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