Cecilia M Lindgren

List of Publications by Year
in descending order

269	91,860	1457 107	460 272
papers	citations	h-index	g-index

316	316	316	79930
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function. Nature Genetics, 2022, 54, 18-29.	9.4	60
2	Making sense of the linear genome, gene function and TADs. Epigenetics and Chromatin, 2022, 15, 4.	1.8	15
3	Obesity and risk of female reproductive conditions: A Mendelian randomisation study. PLoS Medicine, 2022, 19, e1003679.	3.9	50
4	Evidence From Men for Ovary-independent Effects of Genetic Risk Factors for Polycystic Ovary Syndrome. Journal of Clinical Endocrinology and Metabolism, 2022, 107, e1577-e1587.	1.8	14
5	Multi-ancestry genome-wide association study of gestational diabetes mellitus highlights genetic links with type 2 diabetes. Human Molecular Genetics, 2022, 31, 3377-3391.	1.4	47
6	Broadâ€Spectrum Antidote Discovery by Untangling the Reactivation Mechanism of Nerveâ€Agentâ€Inhibited Acetylcholinesterase. Chemistry - A European Journal, 2022, 28, .	1.7	4
7	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250
8	Transcriptome and fatty-acid signatures of adipocyte hypertrophy and its non-invasive MR-based characterization in human adipose tissue. EBioMedicine, 2022, 79, 104020.	2.7	16
9	Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. Kidney International, 2022, 102, 624-639.	2.6	18
10	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	2.0	17
11	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	6.2	79
12	Sex Differences in the Risk of Coronary Heart Disease Associated With Type 2 Diabetes: A Mendelian Randomization Analysis. Diabetes Care, 2021, 44, 556-562.	4.3	21
13	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	5.8	87
14	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.	7.2	28
15	Colocalization analysis of polycystic ovary syndrome to identify potential disease-mediating genes and proteins. European Journal of Human Genetics, 2021, 29, 1446-1454.	1.4	12
16	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
17	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.	1.6	16
18	Linking the FTO obesity rs1421085 variant circuitry to cellular, metabolic, and organismal phenotypes in vivo. Science Advances, 2021, 7, .	4.7	19

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19	The genomics of heart failure: design and rationale of the HERMES consortium. ESC Heart Failure, 2021, 8, 5531-5541.	1.4	11
20	Response to comment on â€œEvaluating the cardiovascular safety of sclerostin inhibition using evidence from meta-analysis of clinical trials and human geneticsâ€. Science Translational Medicine, 2021, 13, eabf4530.	5.8	1
21	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	5.8	466
22	A Polygenic and Phenotypic Risk Prediction for Polycystic Ovary Syndrome Evaluated by Phenome-Wide Association Studies. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 1918-1936.	1.8	40
23	A brief history of human disease genetics. Nature, 2020, 577, 179-189.	13.7	441
24	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. Nature Metabolism, 2020, 2, 1135-1148.	5.1	327
25	Commentary: Using human genetics to guide the repurposing of medicines. International Journal of Epidemiology, 2020, 49, 1140-1146.	0.9	3
26	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	9.4	91
27	The genetic architecture of sporadic and multiple consecutive miscarriage. Nature Communications, 2020, 11, 5980.	5.8	52
28	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.3	26
29	Machine Learning based histology phenotyping to investigate the epidemiologic and genetic basis of adipocyte morphology and cardiometabolic traits. PLoS Computational Biology, 2020, 16, e1008044.	1.5	16
30	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	5.8	59
31	Evaluating the cardiovascular safety of sclerostin inhibition using evidence from meta-analysis of clinical trials and human genetics. Science Translational Medicine, 2020, 12, .	5.8	68
32	Genome-wide association study of adipocyte lipolysis in the GENetics of adipocyte lipolysis (GENiAL) cohort. Molecular Metabolism, 2020, 34, 85-96.	3.0	11
33	Genome-wide Study Identifies Association between HLA-Bâˆ—55:01 and Self-Reported Penicillin Allergy. American Journal of Human Genetics, 2020, 107, 612-621.	2.6	34
34	Title is missing!. , 2020, 16, e1008044.		0
35	Title is missing!. , 2020, 16, e1008044.		0
36	Title is missing!. , 2020, 16, e1008044.		0

#	Article	IF	Citations
37	Title is missing!. , 2020, 16, e1008044.		0
38	Title is missing!. , 2020, 16, e1008044.		0
39	Title is missing!. , 2020, 16, e1008044.		0
40	Commentary: Mendelian randomization and womenâ€™s health. International Journal of Epidemiology, 2019, 48, 830-833.	0.9	5
41	Disentangling the genetics of lean mass. American Journal of Clinical Nutrition, 2019, 109, 276-287.	2.2	38
42	Causal relationships between obesity and the leading causes of death in women and men. PLoS Genetics, 2019, 15, e1008405.	1.5	113
43	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	5.8	133
44	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	2.6	21
45	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
46	MicroRNA-196a links human body fat distribution to adipose tissue extracellular matrix composition. EBioMedicine, 2019, 44, 467-475.	2.7	22
47	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
48	Common Genetic Variation in Relation to Brachial Vascular Dimensions and Flow-Mediated Vasodilation. Circulation Genomic and Precision Medicine, 2019, 12, e002409.	1.6	2
49	GWAS Identifies Risk Locus for Erectile Dysfunction and Implicates Hypothalamic Neurobiology and Diabetes in Etiology. American Journal of Human Genetics, 2019, 104, 157-163.	2.6	55
50	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. Nature Communications, 2019, 10, 29.	5.8	113
51	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	9.4	328
52	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. Journal of the American College of Cardiology, 2019, 73, 58-66.	1.2	147
53	Cerebrospinal fluid lactate and neurological outcome after subarachnoid haemorrhage. Journal of Clinical Neuroscience, 2019, 60, 63-67.	0.8	5
54	Meta-analysis of genome-wide association studies for body fat distribution in 694Â649 individuals of European ancestry. Human Molecular Genetics, 2019, 28, 166-174.	1.4	752

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55	Causal relationships between obesity and the leading causes of death in women and men. , 2019, 15, e1008405.		0
56	Causal relationships between obesity and the leading causes of death in women and men. , 2019, 15, e1008405.		0
57	Causal relationships between obesity and the leading causes of death in women and men. , 2019, 15, e1008405.		0
58	Causal relationships between obesity and the leading causes of death in women and men. , 2019, 15, e1008405.		0
59	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	9.4	356
60	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.	2.9	76
61	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. Nature Communications, 2018, 9, 711.	5.8	54
62	Dynamics Determine Signaling in a Multicomponent System Associated with Rheumatoid Arthritis. Journal of Medicinal Chemistry, 2018, 61, 4774-4790.	2.9	2
63	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.	1.4	6
64	A Partial Loss-of-Function Variant in AKT2 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.	0.3	37
65	GWAS identifies 14 loci for device-measured physical activity and sleep duration. Nature Communications, 2018, 9, 5257.	5.8	241
66	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. PLoS Genetics, 2018, 14, e1007813.	1.5	341
67	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, 1791.	1.7	18
68	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.	9.4	1,331
69	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.	2.6	326
70	Noncovalent Inhibitors of Mosquito Acetylcholinesterase 1 with Resistance-Breaking Potency. Journal of Medicinal Chemistry, 2018, 61, 10545-10557.	2.9	14
71	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	9.4	924
72	Large-scale meta-analysis highlights the hypothalamicâ€“pituitaryâ€“gonadal axis in the genetic regulation of menstrual cycle length. Human Molecular Genetics, 2018, 27, 4323-4332.	1.4	20

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73	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	9.4	552
74	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
75	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	9.4	1,124
76	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	9.4	492
77	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
78	Sexual dimorphisms in genetic loci linked to body fat distribution. Bioscience Reports, 2017, 37, .	1.1	58
79	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	9.4	279
80	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	5.8	169
81	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. Nature Genetics, 2017, 49, 125-130.	9.4	116
82	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	5.8	95
83	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	2.6	131
84	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
85	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.	0.3	47
86	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. Nature, 2017, 541, 81-86.	13.7	743
87	New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48
88	The genetic underpinnings of body fat distribution. Expert Review of Endocrinology and Metabolism, 2017, 12, 417-427.	1.2	3
89	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	5.8	147
90	Variability of genome-wide DNA methylation and mRNA expression profiles in reproductive and endocrine disease related tissues. Epigenetics, 2017, 12, 897-908.	1.3	33

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91	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. Nature Communications, 2017, 8, 16015.	5.8	149
92	Genetic and methylation variation in the CYP2B6 gene is related to circulating p,pâ€²-dde levels in a population-based sample. Environment International, 2017, 98, 212-218.	4.8	5
93	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
94	Genetic and epigenetic studies of adiposity and cardiometabolic disease. Genome Medicine, 2017, 9, 82.	3.6	13
95	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.	0.4	3
96	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. Journal of Clinical Investigation, 2017, 127, 1798-1812.	3.9	106
97	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	1.5	158
98	Mapping of 79 loci for 83 plasma protein biomarkers in cardiovascular disease. PLoS Genetics, 2017, 13, e1006706.	1.5	194
99	Ranking and characterization of established BMI and lipid associated loci as candidates for gene-environment interactions. PLoS Genetics, 2017, 13, e1006812.	1.5	24
100	Leptin levels after subarachnoid haemorrhage are gender dependent. SpringerPlus, 2016, 5, 667.	1.2	1
101	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
102	Mosaic Loss of Chromosome Y in Blood Is Associated with Alzheimer Disease. American Journal of Human Genetics, 2016, 98, 1208-1219.	2.6	164
103	Ovarian Physiology and GWAS: Biobanks, Biology, and Beyond. Trends in Endocrinology and Metabolism, 2016, 27, 516-528.	3.1	9
104	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.	4.9	130
105	Obesity â€” On or Off?. New England Journal of Medicine, 2016, 374, 1486-1488.	13.9	7
106	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. American Journal of Human Genetics, 2016, 98, 857-868.	2.6	21
107	Imprinted genes and imprinting control regions show predominant intermediate methylation in adult somatic tissues. Epigenomics, 2016, 8, 789-799.	1.0	35
108	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. American Journal of Human Genetics, 2016, 99, 636-646.	2.6	67

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109	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	5.8	74
110	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
111	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.	0.3	67
112	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. Scientific Reports, 2016, 6, 35278.	1.6	25
113	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	9.4	284
114	The influence of menstrual cycle and endometriosis on endometrial methylome. Clinical Epigenetics, 2016, 8, 2.	1.8	57
115	Genome-wide DNA methylation study identifies genes associated with the cardiovascular biomarker GDF-15. Human Molecular Genetics, 2016, 25, 817-827.	1.4	32
116	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
117	Testing the role of predicted gene knockouts in human anthropometric trait variation. Human Molecular Genetics, 2016, 25, 2082-2092.	1.4	10
118	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	5.8	153
119	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.	1.5	331
120	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. PLoS Genetics, 2015, 11, e1005230.	1.5	77
121	Robust Linear Models for Cis-eQTL Analysis. PLoS ONE, 2015, 10, e0127882.	1.1	7
122	Identification and validation of N-acetyltransferase 2 as an insulin sensitivity gene. Journal of Clinical Investigation, 2015, 125, 1739-1751.	3.9	94
123	Insights into the Genetic Susceptibility to Type 2 Diabetes from Genome-Wide Association Studies of Obesity-Related Traits. Current Diabetes Reports, 2015, 15, 83.	1.7	47
124	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, 6203-6216.	1.5	4
125	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
126	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823

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127	GWAS-identified loci for coronary heart disease are associated with intima-media thickness and plaque presence at the carotid artery bulb. Atherosclerosis, 2015, 239, 304-310.	0.4	31
128	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	5.8	173
129	Mouse-Human Experimental Epigenetic Analysis Unmasks Dietary Targets and Genetic Liability for Diabetic Phenotypes. Cell Metabolism, 2015, 21, 138-149.	7.2	98
130	Blood Metabolomic Predictors of 1-Year Outcome in Subarachnoid Hemorrhage. Neurocritical Care, 2015, 23, 225-232.	1.2	8
131	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
132	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.	1.5	95
133	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	9.4	310
134	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.	3.7	10
135	Genome-wide enrichment analysis between endometriosis and obesity-related traits reveals novel susceptibility loci. Human Molecular Genetics, 2015, 24, 1185-1199.	1.4	71
136	Genome-wide association study of toxic metals and trace elements reveals novel associations. Human Molecular Genetics, 2015, 24, 4739-4745.	1.4	104
137	Genome-wide association of polycystic ovary syndrome implicates alterations in gonadotropin secretion in European ancestry populations. Nature Communications, 2015, 6, 7502.	5.8	314
138	A comprehensive 1000 Genomesâ€“based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	9.4	2,054
139	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365
140	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.	1.3	16
141	Smoking is associated with mosaic loss of chromosome Y. Science, 2015, 347, 81-83.	6.0	163
142	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	4.1	235
143	Large-Scale Genome-Wide Association Studies and Meta-Analyses of Longitudinal Change in Adult Lung Function. PLoS ONE, 2014, 9, e100776.	1.1	52
144	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494.	1.5	351

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145	Genome Wide Association Identifies Common Variants at the SERPINA6/SERPINA1 Locus Influencing Plasma Cortisol and Corticosteroid Binding Globulin. PLoS Genetics, 2014, 10, e1004474.	1.5	105
146	Genome-Wide Association Studies of Obesity. , 2014, , 33-53.		2
147	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, 13127-13132.	3.3	152
148	Here and now â€“ there and then: Narrative time and space in intercountry adopteesâ€™ stories about background, origin and roots. Qualitative Social Work, 2014, 13, 539-554.	0.9	5
149	Genome-Wide Association Studies of Obesity and Related Traits. Frontiers in Diabetes, 2014, , 58-70.	0.4	0
150	Fat depot-specific mRNA expression of novel loci associated with waistâ€“hip ratio. International Journal of Obesity, 2014, 38, 120-125.	1.6	29
151	ADMA Levels and Arginine/ADMA Ratios Reflect Severity of Disease and Extent of Inflammation After Subarachnoid Hemorrhage. Neurocritical Care, 2014, 21, 91-101.	1.2	17
152	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	2.6	193
153	Mosaic loss of chromosome Y in peripheral blood is associated with shorter survival and higher risk of cancer. Nature Genetics, 2014, 46, 624-628.	9.4	320
154	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
155	Genetic variation in the CYP2B6 Gene is related to circulating 2,2â€™,4,4â€™-tetrabromodiphenyl ether (BDE-47) concentrations: an observational population-based study. Environmental Health, 2014, 13, 34.	1.7	10
156	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959
157	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. Nature Genetics, 2014, 46, 357-363.	9.4	428
158	Expression of Phosphofructokinase in Skeletal Muscle Is Influenced by Genetic Variation and Associated With Insulin Sensitivity. Diabetes, 2014, 63, 1154-1165.	0.3	41
159	Genetic variation in the CYP1A1 gene is related to circulating PCB118 levels in a population-based sample. Environmental Research, 2014, 133, 135-140.	3.7	11
160	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, 710-720.	2.6	24
161	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. American Journal of Human Genetics, 2013, 93, 236-248.	2.6	60
162	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	9.4	2,641

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163	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	9.4	754
164	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
165	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, 987-992.	0.3	112
166	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	1.5	371
167	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. PLoS Medicine, 2013, 10, e1001474.	3.9	178
168	Assessing association between protein truncating variants and quantitative traits. Bioinformatics, 2013, 29, 2419-2426.	1.8	12
169	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.	1.1	83
170	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, 935-941.	0.5	52
171	Mendelian Randomization Studies Do Not Support a Causal Role for Reduced Circulating Adiponectin Levels in Insulin Resistance and Type 2 Diabetes. Diabetes, 2013, 62, 3589-3598.	0.3	116
172	Contribution of 32 GWAS-Identified Common Variants to Severe Obesity in European Adults Referred for Bariatric Surgery. PLoS ONE, 2013, 8, e70735.	1.1	39
173	The miRNA Profile of Human Pancreatic Islets and Beta-Cells and Relationship to Type 2 Diabetes Pathogenesis. PLoS ONE, 2013, 8, e55272.	1.1	178
174	Abstract 050: Meta-analysis of Genetic Associations in up to 339,224 Individuals Identify 66 New Loci for Bmi, Confirming a Neuronal Contribution to Body Weight Regulation and Implicating Several Novel Pathways. Circulation, 2013, 127, .	1.6	0
175	Extent, Causes, and Consequences of Small RNA Expression Variation in Human Adipose Tissue. PLoS Genetics, 2012, 8, e1002704.	1.5	48
176	The Metabochip, a Custom Genotyping Array for Genetic Studies of Metabolic, Cardiovascular, and Anthropometric Traits. PLoS Genetics, 2012, 8, e1002793.	1.5	448
177	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.	1.5	419
178	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	9.4	746
179	Common variants at 6q22 and 17q21 are associated with intracranial volume. Nature Genetics, 2012, 44, 539-544.	9.4	126
180	Common variants at 12q15 and 12q24 are associated with infant head circumference. Nature Genetics, 2012, 44, 532-538.	9.4	130

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181	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	9.4	1,748
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