

Cecilia M Lindgren

List of Publications by Year in descending order

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Version: 2024-02-01

269
papers

91,860
citations

1457

107
h-index

460

272
g-index

316
all docs

316
docs citations

316
times ranked

79930
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. <i>Nature</i> , 2007, 447, 661-678.	13.7	8,895
2	PGC-1 α -responsive genes involved in oxidative phosphorylation are coordinately downregulated in human diabetes. <i>Nature Genetics</i> , 2003, 34, 267-273.	9.4	8,185
3	A Common Variant in the FTO Gene Is Associated with Body Mass Index and Predisposes to Childhood and Adult Obesity. <i>Science</i> , 2007, 316, 889-894.	6.0	3,884
4	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
5	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013, 45, 1274-1283.	9.4	2,641
6	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	9.4	2,634
7	A comprehensive 1000 Genomes ² -based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , 2015, 47, 1121-1130.	9.4	2,054
8	Replication of Genome-Wide Association Signals in UK Samples Reveals Risk Loci for Type 2 Diabetes. <i>Science</i> , 2007, 316, 1336-1341.	6.0	2,040
9	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010, 42, 105-116.	9.4	1,982
10	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	9.4	1,818
11	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	13.7	1,789
12	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012, 44, 981-990.	9.4	1,748
13	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. <i>Nature Genetics</i> , 2008, 40, 638-645.	9.4	1,683
14	The common PPAR γ Pro12Ala polymorphism is associated with decreased risk of type 2 diabetes. <i>Nature Genetics</i> , 2000, 26, 76-80.	9.4	1,672
15	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. <i>Nature Genetics</i> , 2010, 42, 579-589.	9.4	1,631
16	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. <i>Nature Genetics</i> , 2009, 41, 25-34.	9.4	1,572
17	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. <i>Nature Genetics</i> , 2018, 50, 1505-1513.	9.4	1,331
18	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	13.7	1,328

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19	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. <i>Nature Genetics</i> , 2007, 39, 1329-1337.	9.4	1,298
20	Common variants near MC4R are associated with fat mass, weight and risk of obesity. <i>Nature Genetics</i> , 2008, 40, 768-775.	9.4	1,179
21	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. <i>Nature Genetics</i> , 2018, 50, 524-537.	9.4	1,124
22	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014, 46, 234-244.	9.4	959
23	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	13.7	952
24	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	9.4	924
25	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010, 42, 949-960.	9.4	836
26	Common variants associated with plasma triglycerides and risk for coronary artery disease. <i>Nature Genetics</i> , 2013, 45, 1345-1352.	9.4	754
27	Meta-analysis of genome-wide association studies for body fat distribution in 694,649 individuals of European ancestry. <i>Human Molecular Genetics</i> , 2019, 28, 166-174.	1.4	752
28	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , 2012, 44, 991-1005.	9.4	746
29	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , 2017, 541, 81-86.	13.7	743
30	Genome-wide association analysis identifies 20 loci that influence adult height. <i>Nature Genetics</i> , 2008, 40, 575-583.	9.4	742
31	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. <i>Nature</i> , 2010, 464, 713-720.	13.7	737
32	Mapping cis- and trans-regulatory effects across multiple tissues in twins. <i>Nature Genetics</i> , 2012, 44, 1084-1089.	9.4	701
33	Variants in MTNR1B influence fasting glucose levels. <i>Nature Genetics</i> , 2009, 41, 77-81.	9.4	662
34	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017, 66, 2888-2902.	0.3	615
35	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013, 45, 501-512.	9.4	578
36	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018, 50, 1225-1233.	9.4	552

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37	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	9.4	549
38	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	13.7	544
39	Localization of type 1 diabetes susceptibility to the MHC class I genes HLA-B and HLA-A. <i>Nature</i> , 2007, 450, 887-892.	13.7	493
40	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , 2017, 49, 403-415.	9.4	492
41	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. <i>Nature Communications</i> , 2020, 11, 163.	5.8	466
42	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. <i>PLoS Genetics</i> , 2009, 5, e1000508.	1.5	453
43	The Metabochip, a Custom Genotyping Array for Genetic Studies of Metabolic, Cardiovascular, and Anthropometric Traits. <i>PLoS Genetics</i> , 2012, 8, e1002793.	1.5	448
44	A brief history of human disease genetics. <i>Nature</i> , 2020, 577, 179-189.	13.7	441
45	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. <i>Nature Genetics</i> , 2014, 46, 357-363.	9.4	428
46	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. <i>PLoS Genetics</i> , 2012, 8, e1002607.	1.5	419
47	The Architecture of Gene Regulatory Variation across Multiple Human Tissues: The MuTHER Study. <i>PLoS Genetics</i> , 2011, 7, e1002003.	1.5	392
48	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012, 490, 267-272.	13.7	383
49	A common variant of HMGA2 is associated with adult and childhood height in the general population. <i>Nature Genetics</i> , 2007, 39, 1245-1250.	9.4	373
50	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. <i>PLoS Genetics</i> , 2013, 9, e1003500.	1.5	371
51	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015, 47, 1415-1425.	9.4	365
52	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018, 50, 559-571.	9.4	356
53	A genome-wide association meta-analysis identifies new childhood obesity loci. <i>Nature Genetics</i> , 2012, 44, 526-531.	9.4	352
54	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. <i>PLoS Genetics</i> , 2014, 10, e1004494.	1.5	351

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55	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. <i>PLoS Genetics</i> , 2018, 14, e1007813.	1.5	341
56	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	9.4	341
57	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	1.5	331
58	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. <i>Nature Genetics</i> , 2019, 51, 51-62.	9.4	328
59	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. <i>Nature Metabolism</i> , 2020, 2, 1135-1148.	5.1	327
60	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , 2018, 103, 691-706.	2.6	326
61	Mosaic loss of chromosome Y in peripheral blood is associated with shorter survival and higher risk of cancer. <i>Nature Genetics</i> , 2014, 46, 624-628.	9.4	320
62	Genome-wide association of polycystic ovary syndrome implicates alterations in gonadotropin secretion in European ancestry populations. <i>Nature Communications</i> , 2015, 6, 7502.	5.8	314
63	The impact of low-frequency and rare variants on lipid levels. <i>Nature Genetics</i> , 2015, 47, 589-597.	9.4	310
64	Identification of an imprinted master trans regulator at the KLF14 locus related to multiple metabolic phenotypes. <i>Nature Genetics</i> , 2011, 43, 561-564.	9.4	289
65	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018, 50, 26-41.	9.4	286
66	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016, 48, 1462-1472.	9.4	284
67	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. <i>Nature Genetics</i> , 2017, 49, 946-952.	9.4	279
68	Common Variation in the <i>FTO</i> Gene Alters Diabetes-Related Metabolic Traits to the Extent Expected Given Its Effect on BMI. <i>Diabetes</i> , 2008, 57, 1419-1426.	0.3	277
69	MHC2TA is associated with differential MHC molecule expression and susceptibility to rheumatoid arthritis, multiple sclerosis and myocardial infarction. <i>Nature Genetics</i> , 2005, 37, 486-494.	9.4	276
70	Global microRNA expression profiles in insulin target tissues in a spontaneous rat model of type 2 diabetes. <i>Diabetologia</i> , 2010, 53, 1099-1109.	2.9	261
71	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016, 48, 1151-1161.	9.4	261
72	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. <i>Nature Genetics</i> , 2022, 54, 560-572.	9.4	250

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73	Genetics and epigenetics of obesity. <i>Maturitas</i> , 2011, 69, 41-49.	1.0	245
74	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016, 7, 10495.	5.8	245
75	GWAS identifies 14 loci for device-measured physical activity and sleep duration. <i>Nature Communications</i> , 2018, 9, 5257.	5.8	241
76	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015, 20, 647-656.	4.1	235
77	Type 2 diabetes: new genes, new understanding. <i>Trends in Genetics</i> , 2008, 24, 613-621.	2.9	229
78	Variants in <i>ADCY5</i> and near <i>CCNL1</i> are associated with fetal growth and birth weight. <i>Nature Genetics</i> , 2010, 42, 430-435.	9.4	223
79	Integrated Genetic and Epigenetic Analysis Identifies Haplotype-Specific Methylation in the <i>FTO</i> Type 2 Diabetes and Obesity Susceptibility Locus. <i>PLoS ONE</i> , 2010, 5, e14040.	1.1	215
80	Strong Genetic Evidence of <i>DCDC2</i> as a Susceptibility Gene for Dyslexia. <i>American Journal of Human Genetics</i> , 2006, 78, 52-62.	2.6	211
81	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. <i>PLoS ONE</i> , 2012, 7, e29202.	1.1	197
82	Mapping of 79 loci for 83 plasma protein biomarkers in cardiovascular disease. <i>PLoS Genetics</i> , 2017, 13, e1006706.	1.5	194
83	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. <i>American Journal of Human Genetics</i> , 2014, 94, 233-245.	2.6	193
84	The Genetics of Obesity. <i>Current Diabetes Reports</i> , 2010, 10, 498-505.	1.7	192
85	The Genetic and Epigenetic Basis of Type 2 Diabetes and Obesity. <i>Clinical Pharmacology and Therapeutics</i> , 2012, 92, 707-715.	2.3	191
86	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. <i>PLoS Medicine</i> , 2013, 10, e1001474.	3.9	178
87	The miRNA Profile of Human Pancreatic Islets and Beta-Cells and Relationship to Type 2 Diabetes Pathogenesis. <i>PLoS ONE</i> , 2013, 8, e55272.	1.1	178
88	Genomewide Linkage Analysis of Stature in Multiple Populations Reveals Several Regions with Evidence of Linkage to Adult Height. <i>American Journal of Human Genetics</i> , 2001, 69, 106-116.	2.6	177
89	Genetic evidence that raised sex hormone binding globulin (SHBG) levels reduce the risk of type 2 diabetes. <i>Human Molecular Genetics</i> , 2010, 19, 535-544.	1.4	176
90	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. <i>Nature Communications</i> , 2015, 6, 5897.	5.8	173

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91	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	13.7	173
92	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, 14977.	5.8	169
93	Mosaic Loss of Chromosome Y in Blood Is Associated with Alzheimer Disease. <i>American Journal of Human Genetics</i> , 2016, 98, 1208-1219.	2.6	164
94	Smoking is associated with mosaic loss of chromosome Y. <i>Science</i> , 2015, 347, 81-83.	6.0	163
95	Genome-wide physical activity interactions in adiposity – A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	1.5	158
96	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , 2016, 7, 10494.	5.8	153
97	Rare variants in <i>PPARG</i> with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 13127-13132.	3.3	152
98	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. <i>Nature Communications</i> , 2017, 8, 16015.	5.8	149
99	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 2017, 8, 80.	5.8	147
100	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. <i>Journal of the American College of Cardiology</i> , 2019, 73, 58-66.	1.2	147
101	Type 2 Diabetes Risk Alleles Are Associated With Reduced Size at Birth. <i>Diabetes</i> , 2009, 58, 1428-1433.	0.3	135
102	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019, 10, 4130.	5.8	133
103	Genomewide Search for Type 2 Diabetes Mellitus Susceptibility Loci in Finnish Families: The Botnia Study. <i>American Journal of Human Genetics</i> , 2002, 70, 509-516.	2.6	132
104	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. <i>American Journal of Human Genetics</i> , 2017, 100, 865-884.	2.6	131
105	Common variants at 12q15 and 12q24 are associated with infant head circumference. <i>Nature Genetics</i> , 2012, 44, 532-538.	9.4	130
106	Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. <i>Lancet Neurology</i> , The, 2016, 15, 695-707.	4.9	130
107	Common variants at 6q22 and 17q21 are associated with intracranial volume. <i>Nature Genetics</i> , 2012, 44, 539-544.	9.4	126
108	Association of variants in the fat mass and obesity associated (FTO) gene with polycystic ovary syndrome. <i>Diabetologia</i> , 2008, 51, 1153-1158.	2.9	121

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109	Mendelian Randomization Studies Do Not Support a Causal Role for Reduced Circulating Adiponectin Levels in Insulin Resistance and Type 2 Diabetes. <i>Diabetes</i> , 2013, 62, 3589-3598.	0.3	116
110	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. <i>Nature Genetics</i> , 2017, 49, 125-130.	9.4	116
111	Interactions between Glutathione <i>S</i> -Transferase P1, Tumor Necrosis Factor, and Traffic-Related Air Pollution for Development of Childhood Allergic Disease. <i>Environmental Health Perspectives</i> , 2008, 116, 1077-1084.	2.8	115
112	Causal relationships between obesity and the leading causes of death in women and men. <i>PLoS Genetics</i> , 2019, 15, e1008405.	1.5	113
113	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. <i>Nature Communications</i> , 2019, 10, 29.	5.8	113
114	Insights Into the Molecular Mechanism for Type 2 Diabetes Susceptibility at the <i>KCNQ1</i> Locus From Temporal Changes in Imprinting Status in Human Islets. <i>Diabetes</i> , 2013, 62, 987-992.	0.3	112
115	Haplotypes of G Protein-coupled Receptor 154 Are Associated with Childhood Allergy and Asthma. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2005, 171, 1089-1095.	2.5	111
116	Large-Scale Zygosity Testing Using Single Nucleotide Polymorphisms. <i>Twin Research and Human Genetics</i> , 2007, 10, 604-625.	0.3	110
117	Variants in the Calpain-10 Gene Predispose to Insulin Resistance and Elevated Free Fatty Acid Levels. <i>Diabetes</i> , 2002, 51, 2658-2664.	0.3	109
118	Adiposity-Related Heterogeneity in Patterns of Type 2 Diabetes Susceptibility Observed in Genome-Wide Association Data. <i>Diabetes</i> , 2009, 58, 505-510.	0.3	109
119	Clinical and Genetic Correlates of Growth Differentiation Factor 15 in the Community. <i>Clinical Chemistry</i> , 2012, 58, 1582-1591.	1.5	106
120	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. <i>Journal of Clinical Investigation</i> , 2017, 127, 1798-1812.	3.9	106
121	MicroRNA-125a is over-expressed in insulin target tissues in a spontaneous rat model of Type 2 Diabetes. <i>BMC Medical Genomics</i> , 2009, 2, 54.	0.7	105
122	Genome Wide Association Identifies Common Variants at the <i>SERPINA6/SERPINA1</i> Locus Influencing Plasma Cortisol and Corticosteroid Binding Globulin. <i>PLoS Genetics</i> , 2014, 10, e1004474.	1.5	105
123	Genome-wide association study of toxic metals and trace elements reveals novel associations. <i>Human Molecular Genetics</i> , 2015, 24, 4739-4745.	1.4	104
124	Mouse-Human Experimental Epigenetic Analysis Unmasks Dietary Targets and Genetic Liability for Diabetic Phenotypes. <i>Cell Metabolism</i> , 2015, 21, 138-149.	7.2	98
125	Meta-analysis of sex-specific genome-wide association studies. <i>Genetic Epidemiology</i> , 2010, 34, 846-853.	0.6	96
126	Identification and Functional Characterization of <i>G6PC2</i> Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the <i>G6PC2-ABCB11</i> Locus. <i>PLoS Genetics</i> , 2015, 11, e1004876.	1.5	95

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127	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. <i>Nature Communications</i> , 2017, 8, 15805.	5.8	95
128	Identification and validation of N-acetyltransferase 2 as an insulin sensitivity gene. <i>Journal of Clinical Investigation</i> , 2015, 125, 1739-1751.	3.9	94
129	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. <i>Nature Genetics</i> , 2020, 52, 1314-1332.	9.4	91
130	A Gene Conferring Susceptibility to Type 2 Diabetes in Conjunction With Obesity Is Located on Chromosome 18p11. <i>Diabetes</i> , 2001, 50, 675-680.	0.3	89
131	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.	9.4	89
132	Neuropeptide S Receptor 1 Gene Polymorphism Is Associated With Susceptibility to Inflammatory Bowel Disease. <i>Gastroenterology</i> , 2007, 133, 808-817.	0.6	87
133	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021, 12, 24.	5.8	87
134	Common variants in HNF-1 β and risk of type 2 diabetes. <i>Diabetologia</i> , 2006, 49, 2882-2891.	2.9	85
135	The Presence of Methylation Quantitative Trait Loci Indicates a Direct Genetic Influence on the Level of DNA Methylation in Adipose Tissue. <i>PLoS ONE</i> , 2013, 8, e55923.	1.1	83
136	Genome-wide association study identifies 48 common genetic variants associated with handedness. <i>Nature Human Behaviour</i> , 2021, 5, 59-70.	6.2	79
137	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. <i>PLoS Genetics</i> , 2015, 11, e1005230.	1.5	77
138	A Common Allele in FGF21 Associated with Sugar Intake Is Associated with Body Shape, Lower Total Body-Fat Percentage, and Higher Blood Pressure. <i>Cell Reports</i> , 2018, 23, 327-336.	2.9	76
139	Variability of gene expression profiles in human blood and lymphoblastoid cell lines. <i>BMC Genomics</i> , 2010, 11, 96.	1.2	75
140	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, 13357.	5.8	74
141	Common Variants in Maturity-Onset Diabetes of the Young Genes and Future Risk of Type 2 Diabetes. <i>Diabetes</i> , 2008, 57, 1738-1744.	0.3	73
142	Genome-wide enrichment analysis between endometriosis and obesity-related traits reveals novel susceptibility loci. <i>Human Molecular Genetics</i> , 2015, 24, 1185-1199.	1.4	71
143	The human GIMAP5 gene has a common polyadenylation polymorphism increasing risk to systemic lupus erythematosus. <i>Journal of Medical Genetics</i> , 2007, 44, 314-321.	1.5	70
144	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. <i>Human Molecular Genetics</i> , 2003, 12, 1865-1873.	1.4	68

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145	Evaluating the cardiovascular safety of sclerostin inhibition using evidence from meta-analysis of clinical trials and human genetics. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	68
146	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. <i>American Journal of Human Genetics</i> , 2016, 99, 636-646.	2.6	67
147	Genome-Wide Association Study of the Modified Stumvoll Insulin Sensitivity Index Identifies <i>BCL2</i> and <i>FAM19A2</i> as Novel Insulin Sensitivity Loci. <i>Diabetes</i> , 2016, 65, 3200-3211.	0.3	67
148	A Genome-Wide Scan in Families With Maturity-Onset Diabetes of the Young: Evidence for Further Genetic Heterogeneity. <i>Diabetes</i> , 2003, 52, 872-881.	0.3	62
149	Meta-Analysis of the <i>INSIG2</i> Association with Obesity Including 74,345 Individuals: Does Heterogeneity of Estimates Relate to Study Design?. <i>PLoS Genetics</i> , 2009, 5, e1000694.	1.5	62
150	Variation in DNA Repair Genes <i>ERCC2</i> , <i>XRCC1</i> , and <i>XRCC3</i> and Risk of Follicular Lymphoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2006, 15, 258-265.	1.1	61
151	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. <i>American Journal of Human Genetics</i> , 2013, 93, 236-248.	2.6	60
152	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function. <i>Nature Genetics</i> , 2022, 54, 18-29.	9.4	60
153	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020, 11, 2542.	5.8	59
154	Sexual dimorphisms in genetic loci linked to body fat distribution. <i>Bioscience Reports</i> , 2017, 37, .	1.1	58
155	Coexpression Network Analysis in Abdominal and Gluteal Adipose Tissue Reveals Regulatory Genetic Loci for Metabolic Syndrome and Related Phenotypes. <i>PLoS Genetics</i> , 2012, 8, e1002505.	1.5	57
156	The influence of menstrual cycle and endometriosis on endometrial methylome. <i>Clinical Epigenetics</i> , 2016, 8, 2.	1.8	57
157	Mechanisms of inactivation of <i>MLH1</i> in hereditary nonpolyposis colorectal carcinoma: a novel approach. <i>Oncogene</i> , 2007, 26, 4541-4549.	2.6	56
158	GWAS Identifies Risk Locus for Erectile Dysfunction and Implicates Hypothalamic Neurobiology and Diabetes in Etiology. <i>American Journal of Human Genetics</i> , 2019, 104, 157-163.	2.6	55
159	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. <i>Nature Communications</i> , 2018, 9, 711.	5.8	54
160	Liver X receptor gene polymorphisms and adipose tissue expression levels in obesity. <i>Pharmacogenetics and Genomics</i> , 2006, 16, 881-889.	0.7	53
161	A powerful approach to sub-phenotype analysis in population-based genetic association studies. <i>Genetic Epidemiology</i> , 2010, 34, 335-343.	0.6	52
162	Evaluation of the genetic overlap between osteoarthritis with body mass index and height using genome-wide association scan data. <i>Annals of the Rheumatic Diseases</i> , 2013, 72, 935-941.	0.5	52

#	ARTICLE	IF	CITATIONS
163	Large-Scale Genome-Wide Association Studies and Meta-Analyses of Longitudinal Change in Adult Lung Function. <i>PLoS ONE</i> , 2014, 9, e100776.	1.1	52
164	The genetic architecture of sporadic and multiple consecutive miscarriage. <i>Nature Communications</i> , 2020, 11, 5980.	5.8	52
165	Obesity and risk of female reproductive conditions: A Mendelian randomisation study. <i>PLoS Medicine</i> , 2022, 19, e1003679.	3.9	50
166	Extent, Causes, and Consequences of Small RNA Expression Variation in Human Adipose Tissue. <i>PLoS Genetics</i> , 2012, 8, e1002704.	1.5	48
167	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475,000 Individuals. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	48
168	Insights into the Genetic Susceptibility to Type 2 Diabetes from Genome-Wide Association Studies of Obesity-Related Traits. <i>Current Diabetes Reports</i> , 2015, 15, 83.	1.7	47
169	A Low-Frequency Inactivating <i>AKT2</i> Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017, 66, 2019-2032.	0.3	47
170	Multi-ancestry genome-wide association study of gestational diabetes mellitus highlights genetic links with type 2 diabetes. <i>Human Molecular Genetics</i> , 2022, 31, 3377-3391.	1.4	47
171	Mechanisms of Disease: genetic insights into the etiology of type 2 diabetes and obesity. <i>Nature Clinical Practice Endocrinology and Metabolism</i> , 2008, 4, 156-163.	2.9	46
172	MicroRNA Expression in Abdominal and Gluteal Adipose Tissue Is Associated with mRNA Expression Levels and Partly Genetically Driven. <i>PLoS ONE</i> , 2011, 6, e27338.	1.1	46
173	Phenylketonuria screening registry as a resource for population genetic studies. <i>Journal of Medical Genetics</i> , 2005, 42, e60-e60.	1.5	43
174	Chromosome 7p linkage and GPR154 gene association in Italian families with allergic asthma. <i>Clinical and Experimental Allergy</i> , 2007, 37, 83-89.	1.4	43
175	Expression of Phosphofruktokinase in Skeletal Muscle Is Influenced by Genetic Variation and Associated With Insulin Sensitivity. <i>Diabetes</i> , 2014, 63, 1154-1165.	0.3	41
176	A genome wide scan for early onset primary hypertension in Scandinavians. <i>Human Molecular Genetics</i> , 2003, 12, 2077-2081.	1.4	40
177	A Polygenic and Phenotypic Risk Prediction for Polycystic Ovary Syndrome Evaluated by Phenome-Wide Association Studies. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, 1918-1936.	1.8	40
178	Contribution of 32 GWAS-Identified Common Variants to Severe Obesity in European Adults Referred for Bariatric Surgery. <i>PLoS ONE</i> , 2013, 8, e70735.	1.1	39
179	Polymorphisms in the gene encoding the voltage-dependent Ca ²⁺ channel Ca _v 2.3 (<i>CACNA1E</i>) are associated with type 2 diabetes and impaired insulin secretion. <i>Diabetologia</i> , 2007, 50, 2467-2475.	2.9	38
180	Disentangling the genetics of lean mass. <i>American Journal of Clinical Nutrition</i> , 2019, 109, 276-287.	2.2	38

#	ARTICLE	IF	CITATIONS
181	Global analysis of uniparental disomy using high density genotyping arrays. <i>Journal of Medical Genetics</i> , 2005, 42, 847-851.	1.5	37
182	A Partial Loss-of-Function Variant in <i>AKT2</i> Is Associated With Reduced Insulin-Mediated Glucose Uptake in Multiple Insulin-Sensitive Tissues: A Genotype-Based Callback Positron Emission Tomography Study. <i>Diabetes</i> , 2018, 67, 334-342.	0.3	37
183	Population Structure in Contemporary Sweden—A Chromosomal and Mitochondrial DNA Analysis. <i>Annals of Human Genetics</i> , 2009, 73, 61-73.	0.3	36
184	The Use of Genome-Wide eQTL Associations in Lymphoblastoid Cell Lines to Identify Novel Genetic Pathways Involved in Complex Traits. <i>PLoS ONE</i> , 2011, 6, e22070.	1.1	36
185	Imprinted genes and imprinting control regions show predominant intermediate methylation in adult somatic tissues. <i>Epigenomics</i> , 2016, 8, 789-799.	1.0	35
186	Genome-wide Study Identifies Association between HLA-B*55:01 and Self-Reported Penicillin Allergy. <i>American Journal of Human Genetics</i> , 2020, 107, 612-621.	2.6	34
187	Variability of genome-wide DNA methylation and mRNA expression profiles in reproductive and endocrine disease related tissues. <i>Epigenetics</i> , 2017, 12, 897-908.	1.3	33
188	Genome-wide DNA methylation study identifies genes associated with the cardiovascular biomarker GDF-15. <i>Human Molecular Genetics</i> , 2016, 25, 817-827.	1.4	32
189	G protein-coupled receptor for asthma susceptibility associates with respiratory distress syndrome. <i>Annals of Medicine</i> , 2006, 38, 357-366.	1.5	31
190	Population substructure in Finland and Sweden revealed by the use of spatial coordinates and a small number of unlinked autosomal SNPs. <i>BMC Genetics</i> , 2008, 9, 54.	2.7	31
191	Restriction Site-Specific Methylation Studies of Imprinted Genes with Quantitative Real-Time PCR. <i>Clinical Chemistry</i> , 2008, 54, 491-499.	1.5	31
192	Interaction between early maternal smoking and variants in <i>TNF</i> and <i>GSTP1</i> in childhood wheezing. <i>Clinical and Experimental Allergy</i> , 2010, 40, 458-467.	1.4	31
193	GWAS-identified loci for coronary heart disease are associated with intima-media thickness and plaque presence at the carotid artery bulb. <i>Atherosclerosis</i> , 2015, 239, 304-310.	0.4	31
194	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, 170179.	2.4	31
195	Contribution of Known and Unknown Susceptibility Genes to Early-Onset Diabetes in Scandinavia: Evidence for Heterogeneity. <i>Diabetes</i> , 2002, 51, 1609-1617.	0.3	30
196	Fat depot-specific mRNA expression of novel loci associated with waist-hip ratio. <i>International Journal of Obesity</i> , 2014, 38, 120-125.	1.6	29
197	A regulatory variant at 3q21.1 confers an increased pleiotropic risk for hyperglycemia and altered bone mineral density. <i>Cell Metabolism</i> , 2021, 33, 615-628.e13.	7.2	28
198	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. <i>Diabetes</i> , 2020, 69, 2806-2818.	0.3	26

#	ARTICLE	IF	CITATIONS
199	Frequency of Non-convulsive Seizures and Non-convulsive Status Epilepticus in Subarachnoid Hemorrhage Patients in Need of Controlled Ventilation and Sedation. <i>Neurocritical Care</i> , 2012, 17, 367-373.	1.2	25
200	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. <i>Scientific Reports</i> , 2016, 6, 35278.	1.6	25
201	Simulation of Finnish Population History, Guided by Empirical Genetic Data, to Assess Power of Rare-Variant Tests in Finland. <i>American Journal of Human Genetics</i> , 2014, 94, 710-720.	2.6	24
202	Ranking and characterization of established BMI and lipid associated loci as candidates for gene-environment interactions. <i>PLoS Genetics</i> , 2017, 13, e1006812.	1.5	24
203	Absence of Association Between Asthma and High Serum Immunoglobulin E Associated GPR4 Haplotypes and Adult Atopic Dermatitis. <i>Journal of Investigative Dermatology</i> , 2005, 125, 399-401.	0.3	23
204	MicroRNA-196a links human body fat distribution to adipose tissue extracellular matrix composition. <i>EBioMedicine</i> , 2019, 44, 467-475.	2.7	22
205	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. <i>American Journal of Human Genetics</i> , 2016, 98, 857-868.	2.6	21
206	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. <i>American Journal of Human Genetics</i> , 2019, 105, 15-28.	2.6	21
207	Sex Differences in the Risk of Coronary Heart Disease Associated With Type 2 Diabetes: A Mendelian Randomization Analysis. <i>Diabetes Care</i> , 2021, 44, 556-562.	4.3	21
208	Large-scale meta-analysis highlights the hypothalamic-pituitary-gonadal axis in the genetic regulation of menstrual cycle length. <i>Human Molecular Genetics</i> , 2018, 27, 4323-4332.	1.4	20
209	Linking the <i>FTO</i> obesity rs1421085 variant circuitry to cellular, metabolic, and organismal phenotypes in vivo. <i>Science Advances</i> , 2021, 7, .	4.7	19
210	A quality assessment survey of SNP genotyping laboratories. <i>Human Mutation</i> , 2006, 27, 711-714.	1.1	18
211	Genome-Wide Association Studies of Estimated Fatty Acid Desaturase Activity in Serum and Adipose Tissue in Elderly Individuals: Associations with Insulin Sensitivity. <i>Nutrients</i> , 2018, 10, 1791.	1.7	18
212	Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. <i>Kidney International</i> , 2022, 102, 624-639.	2.6	18
213	The Genetics of Type 2 Diabetes. , 2001, 11, 178-187.		17
214	ADMA Levels and Arginine/ADMA Ratios Reflect Severity of Disease and Extent of Inflammation After Subarachnoid Hemorrhage. <i>Neurocritical Care</i> , 2014, 21, 91-101.	1.2	17
215	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022, 5, .	2.0	17
216	Benefits of statistical molecular design, covariance analysis, and reference models in QSAR: a case study on acetylcholinesterase. <i>Journal of Computer-Aided Molecular Design</i> , 2015, 29, 199-215.	1.3	16

#	ARTICLE	IF	CITATIONS
217	Machine Learning based histology phenotyping to investigate the epidemiologic and genetic basis of adipocyte morphology and cardiometabolic traits. <i>PLoS Computational Biology</i> , 2020, 16, e1008044.	1.5	16
218	A distribution-centered approach for analyzing human adipocyte size estimates and their association with obesity-related traits and mitochondrial function. <i>International Journal of Obesity</i> , 2021, 45, 2108-2117.	1.6	16
219	Transcriptome and fatty-acid signatures of adipocyte hypertrophy and its non-invasive MR-based characterization in human adipose tissue. <i>EBioMedicine</i> , 2022, 79, 104020.	2.7	16
220	Association analysis of the LAG3 and CD4 genes in multiple sclerosis in two independent populations. <i>Journal of Neuroimmunology</i> , 2006, 180, 193-198.	1.1	15
221	Making sense of the linear genome, gene function and TADs. <i>Epigenetics and Chromatin</i> , 2022, 15, 4.	1.8	15
222	Noncovalent Inhibitors of Mosquito Acetylcholinesterase 1 with Resistance-Breaking Potency. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 10545-10557.	2.9	14
223	Identification of MAMDC1 as a Candidate Susceptibility Gene for Systemic Lupus Erythematosus (SLE). <i>PLoS ONE</i> , 2009, 4, e8037.	1.1	14
224	Evidence From Men for Ovary-independent Effects of Genetic Risk Factors for Polycystic Ovary Syndrome. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2022, 107, e1577-e1587.	1.8	14
225	Genetic and epigenetic studies of adiposity and cardiometabolic disease. <i>Genome Medicine</i> , 2017, 9, 82.	3.6	13
226	Assessing association between protein truncating variants and quantitative traits. <i>Bioinformatics</i> , 2013, 29, 2419-2426.	1.8	12
227	Colocalization analysis of polycystic ovary syndrome to identify potential disease-mediating genes and proteins. <i>European Journal of Human Genetics</i> , 2021, 29, 1446-1454.	1.4	12
228	Genetic variation in the CYP1A1 gene is related to circulating PCB118 levels in a population-based sample. <i>Environmental Research</i> , 2014, 133, 135-140.	3.7	11
229	Genome-wide association study of adipocyte lipolysis in the GENetics of adipocyte lipolysis (GENIAL) cohort. <i>Molecular Metabolism</i> , 2020, 34, 85-96.	3.0	11
230	The genomics of heart failure: design and rationale of the HERMES consortium. <i>ESC Heart Failure</i> , 2021, 8, 5531-5541.	1.4	11
231	Haplotype construction of the FRDA gene and evaluation of its role in type II diabetes. <i>European Journal of Human Genetics</i> , 2005, 13, 849-855.	1.4	10
232	Genetic variation in the CYP2B6 Gene is related to circulating 2,2,4,4-tetrabromodiphenyl ether (BDE-47) concentrations: an observational population-based study. <i>Environmental Health</i> , 2014, 13, 34.	1.7	10
233	Genome-wide association study of plasma levels of polychlorinated biphenyls disclose an association with the CYP2B6 gene in a population-based sample. <i>Environmental Research</i> , 2015, 140, 95-101.	3.7	10
234	Testing the role of predicted gene knockouts in human anthropometric trait variation. <i>Human Molecular Genetics</i> , 2016, 25, 2082-2092.	1.4	10

#	ARTICLE	IF	CITATIONS
235	Ovarian Physiology and GWAS: Biobanks, Biology, and Beyond. <i>Trends in Endocrinology and Metabolism</i> , 2016, 27, 516-528.	3.1	9
236	Blood Metabolomic Predictors of 1-Year Outcome in Subarachnoid Hemorrhage. <i>Neurocritical Care</i> , 2015, 23, 225-232.	1.2	8
237	Robust Linear Models for Cis-eQTL Analysis. <i>PLoS ONE</i> , 2015, 10, e0127882.	1.1	7
238	Obesity – On or Off?. <i>New England Journal of Medicine</i> , 2016, 374, 1486-1488.	13.9	7
239	A genome-wide association study of IgM antibody against phosphorylcholine: shared genetics and phenotypic relationship to chronic lymphocytic leukemia. <i>Human Molecular Genetics</i> , 2018, 27, 1809-1818.	1.4	6
240	Characterization of the Annexin I Gene and Evaluation of Its Role in Type 2 Diabetes. <i>Diabetes</i> , 2001, 50, 2402-2405.	0.3	5
241	Here and now – there and then: Narrative time and space in intercountry adoptees’ stories about background, origin and roots. <i>Qualitative Social Work</i> , 2014, 13, 539-554.	0.9	5
242	Genetic and methylation variation in the CYP2B6 gene is related to circulating p,p'-dde levels in a population-based sample. <i>Environment International</i> , 2017, 98, 212-218.	4.8	5
243	Commentary: Mendelian randomization and women’s health. <i>International Journal of Epidemiology</i> , 2019, 48, 830-833.	0.9	5
244	Cerebrospinal fluid lactate and neurological outcome after subarachnoid haemorrhage. <i>Journal of Clinical Neuroscience</i> , 2019, 60, 63-67.	0.8	5
245	Hydroxyethylene isosteres introduced in type II collagen fragments substantially alter the structure and dynamics of class II MHC A^q/glycopeptide complexes. <i>Organic and Biomolecular Chemistry</i> , 2015, 13, 6203-6216.	1.5	4
246	Broad-Spectrum Antidote Discovery by Untangling the Reactivation Mechanism of Nerve-Agent-Inhibited Acetylcholinesterase. <i>Chemistry - A European Journal</i> , 2022, 28, .	1.7	4
247	Lack of Association between Neuropeptide S Receptor 1 Gene (NPSR1) and Eczema in Five European Populations. <i>Acta Dermato-Venereologica</i> , 2008, 89, 115-121.	0.6	4
248	The genetic underpinnings of body fat distribution. <i>Expert Review of Endocrinology and Metabolism</i> , 2017, 12, 417-427.	1.2	3
249	Commentary: Using human genetics to guide the repurposing of medicines. <i>International Journal of Epidemiology</i> , 2020, 49, 1140-1146.	0.9	3
250	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. <i>Atherosclerosis</i> , 2017, 266, 196-204.	0.4	3
251	Genome-Wide Association Studies of Obesity. , 2014, , 33-53.		2
252	Dynamics Determine Signaling in a Multicomponent System Associated with Rheumatoid Arthritis. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 4774-4790.	2.9	2

#	ARTICLE	IF	CITATIONS
253	Common Genetic Variation in Relation to Brachial Vascular Dimensions and Flow-Mediated Vasodilation. <i>Circulation Genomic and Precision Medicine</i> , 2019, 12, e002409.	1.6	2
254	Leptin levels after subarachnoid haemorrhage are gender dependent. <i>SpringerPlus</i> , 2016, 5, 667.	1.2	1
255	Response to comment on "Evaluating the cardiovascular safety of sclerostin inhibition using evidence from meta-analysis of clinical trials and human genetics". <i>Science Translational Medicine</i> , 2021, 13, eabf4530.	5.8	1
256	The genetics of autoimmunity. <i>BioEssays</i> , 2004, 26, 1363-1364.	1.2	0
257	Obesity: is Type II diabetes a foregone conclusion or further dependent on genetic susceptibility?. <i>Diabetes Management</i> , 2011, 1, 413-422.	0.5	0
258	Genome-Wide Association Studies of Obesity and Related Traits. <i>Frontiers in Diabetes</i> , 2014, , 58-70.	0.4	0
259	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. <i>Circulation</i> , 2013, 127, .	1.6	0
260	Title is missing!. , 2020, 16, e1008044.		0
261	Title is missing!. , 2020, 16, e1008044.		0
262	Title is missing!. , 2020, 16, e1008044.		0
263	Title is missing!. , 2020, 16, e1008044.		0
264	Title is missing!. , 2020, 16, e1008044.		0
265	Title is missing!. , 2020, 16, e1008044.		0
266	Causal relationships between obesity and the leading causes of death in women and men. , 2019, 15, e1008405.		0
267	Causal relationships between obesity and the leading causes of death in women and men. , 2019, 15, e1008405.		0
268	Causal relationships between obesity and the leading causes of death in women and men. , 2019, 15, e1008405.		0
269	Causal relationships between obesity and the leading causes of death in women and men. , 2019, 15, e1008405.		0