Claudia Langenberg

List of Publications by Year
in descending order

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338	76,616	643 123	693 253
papers	citations	h-index	g-index

408	408	408	67253
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
2	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	27.8	3,249
3	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
4	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	21.4	1,982
5	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. Nature Genetics, 2018, 50, 1112-1121.	21.4	1,835
6	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
7	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	21.4	1,748
8	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. Nature Genetics, 2008, 40, 638-645.	21.4	1,683
9	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	21.4	1,631
10	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	21.4	1,439
11	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. Nature Genetics, 2018, 50, 1505-1513.	21.4	1,331
12	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
13	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	21.4	1,124
14	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	21.4	959
15	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
16	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
17	The interleukin-6 receptor as a target for prevention of coronary heart disease: a mendelian randomisation analysis. Lancet, The, 2012, 379, 1214-1224.	13.7	886
18	Risk thresholds for alcohol consumption: combined analysis of individual-participant data for 599â€˜912 current drinkers in 83 prospective studies. Lancet, The, 2018, 391, 1513-1523.	13.7	858

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19	Type 2 diabetes and incidence of cardiovascular diseases: a cohort study in 1Â·9 million people. Lancet Diabetes and Endocrinology,the, 2015, 3, 105-113.	11.4	838
20	Strengthening the Reporting of Observational Studies in Epidemiology Using Mendelian Randomization. JAMA - Journal of the American Medical Association, 2021, 326, 1614.	7.4	829
21	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669.	21.4	762
22	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	21.4	754
23	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	21.4	746
24	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
25	Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81.	21.4	662
26	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615
27	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	21.4	591
28	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	21.4	578
29	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. Lancet, The, 2015, 385, 351-361.	13.7	562
30	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
31	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
32	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	6.0	528
33	Parental origin of sequence variants associated with complex diseases. Nature, 2009, 462, 868-874.	27.8	521
34	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	21.4	501
35	Use of low-density lipoprotein cholesterol gene score to distinguish patients with polygenic and monogenic familial hypercholesterolaemia: a case-control study. Lancet, The, 2013, 381, 1293-1301.	13.7	485
36	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470

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37	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	12.8	466
38	Integrative genomic analysis implicates limited peripheral adipose storage capacity in the pathogenesis of human insulin resistance. Nature Genetics, 2017, 49, 17-26.	21.4	452
39	Ultra-High-Throughput Clinical Proteomics Reveals Classifiers of COVID-19 Infection. Cell Systems, 2020, 11, 11-24.e4.	6.2	439
40	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	12.6	438
41	Differences in the prospective association between individual plasma phospholipid saturated fatty acids and incident type 2 diabetes: the EPIC-InterAct case-cohort study. Lancet Diabetes and Endocrinology,the, 2014, 2, 810-818.	11.4	431
42	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426
43	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	3.5	419
44	Estimating excess 1-year mortality associated with the COVID-19 pandemic according to underlying conditions and age: a population-based cohort study. Lancet, The, 2020, 395, 1715-1725.	13.7	412
45	Strengthening the reporting of observational studies in epidemiology using mendelian randomisation (STROBE-MR): explanation and elaboration. BMJ, The, 2021, 375, n2233.	6.0	408
46	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	27.8	406
47	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	21.4	402
48	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	27.8	401
49	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. Diabetes, 2010, 59, 3229-3239.	0.6	387
50	Using human genetics to understand the disease impacts of testosterone in men and women. Nature Medicine, 2020, 26, 252-258.	30.7	384
51	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	3.5	371
52	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	21.4	365
53	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
54	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357

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55	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	21.4	356
56	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
57	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. Nature Genetics, 2019, 51, 481-493.	21.4	350
58	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. PLoS Medicine, 2017, 14, e1002383.	8.4	341
59	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
60	Genome-Wide Association Identifies Nine Common Variants Associated With Fasting Proinsulin Levels and Provides New Insights Into the Pathophysiology of Type 2 Diabetes. Diabetes, 2011, 60, 2624-2634.	0.6	335
61	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	3.5	331
62	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	21.4	328
63	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.	6.2	326
64	Genetic Predisposition to an Impaired Metabolism of the Branched-Chain Amino Acids and Risk of Type 2 Diabetes: A Mendelian Randomisation Analysis. PLoS Medicine, 2016, 13, e1002179.	8.4	324
65	SARS-CoV-2 (COVID-19): What Do We Know About Children? A Systematic Review. Clinical Infectious Diseases, 2020, 71, 2469-2479.	5.8	323
66	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	27.8	320
67	Rare MTNR1B variants impairing melatonin receptor 1B function contribute to type 2 diabetes. Nature Genetics, 2012, 44, 297-301.	21.4	319
68	Association Between Low-Density Lipoprotein Cholesterolâ€“Lowering Genetic Variants and Risk of Type 2 Diabetes. JAMA - Journal of the American Medical Association, 2016, 316, 1383.	7.4	310
69	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2017, 5, 97-105.	11.4	298
70	Impact of Type 2 Diabetes Susceptibility Variants on Quantitative Glycemic Traits Reveals Mechanistic Heterogeneity. Diabetes, 2014, 63, 2158-2171.	0.6	297
71	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. Nature Communications, 2018, 9, 260.	12.8	295
72	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. Nature Genetics, 2011, 43, 753-760.	21.4	289

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73	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
74	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
75	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
76	Plasma protein patterns as comprehensive indicators of health. Nature Medicine, 2019, 25, 1851-1857.	30.7	261
77	Life-Course Genome-wide Association Study Meta-analysis of Total Body BMD and Assessment of Age-Specific Effects. American Journal of Human Genetics, 2018, 102, 88-102.	6.2	252
78	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
79	Prevalence of Angina in Women Versus Men. Circulation, 2008, 117, 1526-1536.	1.6	245
80	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	12.8	245
81	Detailed Physiologic Characterization Reveals Diverse Mechanisms for Novel Genetic Loci Regulating Glucose and Insulin Metabolism in Humans. Diabetes, 2010, 59, 1266-1275.	0.6	237
82	Fruit and vegetable intake and type 2 diabetes: EPIC-InterAct prospective study and meta-analysis. European Journal of Clinical Nutrition, 2012, 66, 1082-1092.	2.9	228
83	The link between family history and risk of type 2 diabetes is not explained by anthropometric, lifestyle or genetic risk factors: the EPIC-InterAct study. Diabetologia, 2013, 56, 60-69.	6.3	224
84	Genetically Determined Height and Coronary Artery Disease. New England Journal of Medicine, 2015, 372, 1608-1618.	27.0	220
85	Circulating 25-hydroxyvitamin D concentration and the risk of type 2 diabetes: results from the European Prospective Investigation into Cancer (EPIC)-Norfolk cohort and updated meta-analysis of prospective studies. Diabetologia, 2012, 55, 2173-2182.	6.3	213
86	Consumption of sweet beverages and type 2 diabetes incidence in European adults: results from EPIC-InterAct. Diabetologia, 2013, 56, 1520-1530.	6.3	212
87	Genome-wide meta-analysis of observational studies shows common genetic variants associated with macronutrient intake. American Journal of Clinical Nutrition, 2013, 97, 1395-1402.	4.7	210
88	Separate and combined associations of obesity and metabolic health with coronary heart disease: a pan-European case-cohort analysis. European Heart Journal, 2018, 39, 397-406.	2.2	209
89	KLB is associated with alcohol drinking, and its gene product Î²-Klotho is necessary for FGF21 regulation of alcohol preference. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14372-14377.	7.1	208
90	Mortality in adults aged 26-54 years related to socioeconomic conditions in childhood and adulthood: post war birth cohort study. BMJ: British Medical Journal, 2002, 325, 1076-1080.	2.3	206

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91	The life course prospective design: an example of benefits and problems associated with study longevity. Social Science and Medicine, 2003, 57, 2193-2205.	3.8	202
92	Association of Adiponectin with Coronary Heart Disease and Mortality: The Rancho Bernardo Study. American Journal of Epidemiology, 2006, 165, 164-174.	3.4	197
93	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	2.5	197
94	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	12.8	192
95	Human Gain-of-Function MC4R Variants Show Signaling Bias and Protect against Obesity. Cell, 2019, 177, 597-607.e9.	28.9	192
96	Mapping the proteo-genomic convergence of human diseases. Science, 2021, 374, eabj1541.	12.6	192
97	Stratifying Type 2 Diabetes Cases by BMI Identifies Genetic Risk Variants in LAMA1 and Enrichment for Risk Variants in Lean Compared to Obese Cases. PLoS Genetics, 2012, 8, e1002741.	3.5	190
98	A Neanderthal OAS1 isoform protects individuals of European ancestry against COVID-19 susceptibility and severity. Nature Medicine, 2021, 27, 659-667.	30.7	188
99	Age at Menopause, Reproductive Life Span, and Type 2 Diabetes Risk. Diabetes Care, 2013, 36, 1012-1019.	8.6	186
100	Validity of a short questionnaire to assess physical activity in 10 European countries. European Journal of Epidemiology, 2012, 27, 15-25.	5.7	185
101	Genetic Evidence for a Normal-Weight â€œMetabolically Obeseâ€•Phenotype Linking Insulin Resistance, Hypertension, Coronary Artery Disease, and Type 2 Diabetes. Diabetes, 2014, 63, 4369-4377.	0.6	185
102	The amount and type of dairy product intake and incident type 2 diabetes: results from the EPIC-InterAct Study. American Journal of Clinical Nutrition, 2012, 96, 382-390.	4.7	183
103	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
104	Gene-Lifestyle Interaction and Type 2 Diabetes: The EPIC InterAct Case-Cohort Study. PLoS Medicine, 2014, 11, e1001647.	8.4	180
105	Genetic evidence that raised sex hormone binding globulin (SHBG) levels reduce the risk of type 2 diabetes. Human Molecular Genetics, 2010, 19, 535-544.	2.9	176
106	Mediterranean Diet and Type 2 Diabetes Risk in the European Prospective Investigation Into Cancer and Nutrition (EPIC) Study. Diabetes Care, 2011, 34, 1913-1918.	8.6	176
107	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
108	Design and cohort description of the InterAct Project: an examination of the interaction of genetic and lifestyle factors on the incidence of type 2 diabetes in the EPIC Study. Diabetologia, 2011, 54, 2272-2282.	6.3	169

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109	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
110	Gene Ã— Physical Activity Interactions in Obesity: Combined Analysis of 111,421 Individuals of European Ancestry. PLoS Genetics, 2013, 9, e1003607.	3.5	168
111	A Central Role for GRB10 in Regulation of Islet Function in Man. PLoS Genetics, 2014, 10, e1004235.	3.5	164
112	Association between circulating 25-hydroxyvitamin D and incident type 2 diabetes: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2015, 3, 35-42.	11.4	164
113	Genetic Markers of Adult Obesity Risk Are Associated with Greater Early Infancy Weight Gain and Growth. PLoS Medicine, 2010, 7, e1000284.	8.4	158
114	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
115	Common Genetic Variants Highlight the Role of Insulin Resistance and Body Fat Distribution in Type 2 Diabetes, Independent of Obesity. Diabetes, 2014, 63, 4378-4387.	0.6	153
116	Associations between Potentially Modifiable Risk Factors and Alzheimer Disease: A Mendelian Randomization Study. PLoS Medicine, 2015, 12, e1001841.	8.4	153
117	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	12.8	153
118	Association of Genetic Variants Related to Gluteofemoral vs Abdominal Fat Distribution With Type 2 Diabetes, Coronary Disease, and Cardiovascular Risk Factors. JAMA - Journal of the American Medical Association, 2018, 320, 2553.	7.4	152
119	Association of Plasma Phospholipid n-3 and n-6 Polyunsaturated Fatty Acids with Type 2 Diabetes: The EPIC-InterAct Case-Cohort Study. PLoS Medicine, 2016, 13, e1002094.	8.4	150
120	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. Nature Communications, 2017, 8, 16015.	12.8	149
121	A Genome-Wide Association Study Reveals Variants in ARL15 that Influence Adiponectin Levels. PLoS Genetics, 2009, 5, e1000768.	3.5	148
122	Long-Term Risk of Incident Type 2 Diabetes and Measures of Overall and Regional Obesity: The EPIC-InterAct Case-Cohort Study. PLoS Medicine, 2012, 9, e1001230.	8.4	147
123	Age at Menarche and Type 2 Diabetes Risk. Diabetes Care, 2013, 36, 3526-3534.	8.6	147
124	Genome-wide Association Study for Vitamin D Levels Reveals 69 Independent Loci. American Journal of Human Genetics, 2020, 106, 327-337.	6.2	144
125	Dietary Protein Intake and Incidence of Type 2 Diabetes in Europe: The EPIC-InterAct Case-Cohort Study. Diabetes Care, 2014, 37, 1854-1862.	8.6	141
126	Characterization of missing values in untargeted MS-based metabolomics data and evaluation of missing data handling strategies. Metabolomics, 2018, 14, 128.	3.0	138

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127	Non-invasive risk scores for prediction of type 2 diabetes (EPIC-InterAct): a validation of existing models. Lancet Diabetes and Endocrinology,the, 2014, 2, 19-29.	11.4	132
128	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. Diabetes, 2016, 65, 803-817.	0.6	131
129	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	6.2	131
130	Evidence of a Causal Association Between Insulinemia and Endometrial Cancer: A Mendelian Randomization Analysis. Journal of the National Cancer Institute, 2015, 107, .	6.3	129
131	Interactions of Dietary Whole-Grain Intake With Fasting Glucose- and Insulin-Related Genetic Loci in Individuals of European Descent: A meta-analysis of 14 cohort studies. Diabetes Care, 2010, 33, 2684-2691.	8.6	127
132	Lower educational level is a predictor of incident type 2 diabetes in European countries: The EPIC-InterAct study. International Journal of Epidemiology, 2012, 41, 1162-1173.	1.9	127
133	Central and total obesity in middle aged men and women in relation to lifetime socioeconomic status: evidence from a national birth cohort. Journal of Epidemiology and Community Health, 2003, 57, 816-822.	3.7	123
134	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	2.7	123
135	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	6.2	123
136	Genetic Evidence for a Link Between Favorable Adiposity and Lower Risk of Type 2 Diabetes, Hypertension, and Heart Disease. Diabetes, 2016, 65, 2448-2460.	0.6	122
137	Plasma urate concentration and risk of coronary heart disease: a Mendelian randomisation analysis. Lancet Diabetes and Endocrinology,the, 2016, 4, 327-336.	11.4	122
138	Actionable druggable genome-wide Mendelian randomization identifies repurposing opportunities for COVID-19. Nature Medicine, 2021, 27, 668-676.	30.7	120
139	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. American Journal of Human Genetics, 2020, 106, 389-404.	6.2	118
140	Differential White Blood Cell Count and Type 2 Diabetes: Systematic Review and Meta-Analysis of Cross-Sectional and Prospective Studies. PLoS ONE, 2010, 5, e13405.	2.5	118
141	Genetic variants associated with mosaic Y chromosome loss highlight cell cycle genes and overlap with cancer susceptibility. Nature Genetics, 2017, 49, 674-679.	21.4	117
142	A cross-platform approach identifies genetic regulators of human metabolism and health. Nature Genetics, 2021, 53, 54-64.	21.4	117
143	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.	0.6	116
144	Dietary Intakes of Individual Flavanols and Flavonols Are Inversely Associated with Incident Type 2 Diabetes in European Populations. Journal of Nutrition, 2014, 144, 335-343.	2.9	115

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145	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. Cell, 2014, 156, 343-358.	28.9	113
146	Untargeted Metabolic Profiling Identifies Altered Serum Metabolites of Type 2 Diabetes Mellitus in a Prospective, Nested Case Control Study. Clinical Chemistry, 2015, 61, 487-497.	3.2	113
147	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
148	Birthweight, childhood social class, and change in adult blood pressure in the 1946 British birth cohort. Lancet, The, 2003, 362, 1178-1183.	13.7	110
149	Genomic insights into the causes of type 2 diabetes. Lancet, The, 2018, 391, 2463-2474.	13.7	110
150	The Association Between Dietary Flavonoid and Lignan Intakes and Incident Type 2 Diabetes in European Populations. Diabetes Care, 2013, 36, 3961-3970.	8.6	108
151	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. American Journal of Human Genetics, 2019, 104, 112-138.	6.2	106
152	Type 2 diabetes and incidence of a wide range of cardiovascular diseases: a cohort study in 1Â·9 million people. Lancet, The, 2015, 385, S86.	13.7	105
153	Seropositivity and Higher Immunoglobulin G Antibody Levels Against Cytomegalovirus Are Associated With Mortality in the Population-Based European Prospective Investigation of Cancerâ€“Norfolk Cohort. Clinical Infectious Diseases, 2013, 56, 1421-1427.	5.8	104
154	Association of Genetic Loci With Glucose Levels in Childhood and Adolescence. Diabetes, 2011, 60, 1805-1812.	0.6	103
155	Consumption of Meat, Fish, Dairy Products, and Eggs and Risk of Ischemic Heart Disease. Circulation, 2019, 139, 2835-2845.	1.6	103
156	Integrated Analyses of Microbiome and Longitudinal Metabolome Data Reveal Microbial-Host Interactions on Sulfur Metabolism in Parkinsonâ€™s Disease. Cell Reports, 2019, 29, 1767-1777.e8.	6.4	102
157	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. Science Translational Medicine, 2016, 8, 341ra76.	12.4	100
158	A Mendelian Randomization Study of Circulating Uric Acid and Type 2 Diabetes. Diabetes, 2015, 64, 3028-3036.	0.6	98
159	Synergistic insights into human health from aptamer- and antibody-based proteomic profiling. Nature Communications, 2021, 12, 6822.	12.8	95
160	Social Circumstances and Education: Life Course Origins of Social Inequalities in Metabolic Risk in a Prospective National Birth Cohort. American Journal of Public Health, 2006, 96, 2216-2221.	2.7	94
161	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
162	Influence of height, leg and trunk length on pulse pressure, systolic and diastolic blood pressure. Journal of Hypertension, 2003, 21, 537-543.	0.5	93

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163	Mendelian Randomization Study of B-Type Natriuretic Peptide and Type 2 Diabetes: Evidence of Causal Association from Population Studies. PLoS Medicine, 2011, 8, e1001112.	8.4	92
164	Total Zinc Intake May Modify the Glucose-Raising Effect of a Zinc Transporter (SLC30A8) Variant: A 14-Cohort Meta-analysis. Diabetes, 2011, 60, 2407-2416.	0.6	91
165	Sixty-Five Common Genetic Variants and Prediction of Type 2 Diabetes. Diabetes, 2015, 64, 1830-1840.	0.6	91
166	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	21.4	91
167	No evidence for a causal link between uric acid and type 2 diabetes: a Mendelian randomisation approach. Diabetologia, 2011, 54, 2561-2569.	6.3	89
168	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
169	A truncation mutation in TBC1D4 in a family with acanthosis nigricans and postprandial hyperinsulinemia. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 9350-9355.	7.1	88
170	Genome-wide analysis of health-related biomarkers in the UK Household Longitudinal Study reveals novel associations. Scientific Reports, 2017, 7, 11008.	3.3	88
171	Birthweight, childhood growth, and blood pressure at 43 years in a British birth cohort. International Journal of Epidemiology, 2004, 33, 121-129.	1.9	87
172	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
173	Plasma Mannose Levels Are Associated with Incident Type 2 Diabetes and Cardiovascular Disease. Cell Metabolism, 2017, 26, 281-283.	16.2	85
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175	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
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