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	Metabolomic differences in lung function metrics: evidence from two cohorts. Thorax, 2022, 77, 919-928.	5.6	2
2	Associations Between Glycemic Traits and Colorectal Cancer: A Mendelian Randomization Analysis. Journal of the National Cancer Institute, 2022, 114, 740-752.	6.3	35
3	Evidence for Shared Genetic Aetiology Between Schizophrenia, Cardiometabolic, and Inflammation-Related Traits: Genetic Correlation and Colocalization Analyses. Schizophrenia Bulletin Open, 2022, 3, sgac001.	1.7	19
4	Physical activity attenuates but does not eliminate coronary heart disease risk amongst adults with risk factors: EPIC-CVD case-cohort study. European Journal of Preventive Cardiology, 2022, 29, 1618-1629.	1.8	8
5	Metabolomic profiling reveals extensive adrenal suppression due to inhaled corticosteroid therapy in asthma. Nature Medicine, 2022, 28, 814-822.	30.7	37
6	Multiâ€phenotype analyses of hemostatic traits with cardiovascular events reveal novel genetic associations. Journal of Thrombosis and Haemostasis, 2022, 20, 1331-1349.	3.8	12
7	Transcriptional, epigenetic and metabolic signatures in cardiometabolic syndrome defined by extreme phenotypes. Clinical Epigenetics, 2022, 14, 39.	4.1	6
8	Genetically Determined Reproductive Aging and Coronary Heart Disease: A Bidirectional 2-sample Mendelian Randomization. Journal of Clinical Endocrinology and Metabolism, 2022, 107, e2952-e2961.	3.6	13
9	Genetic Landscape of the ACE2 Coronavirus Receptor. Circulation, 2022, 145, 1398-1411.	1.6	20
10	Identification of Rare Loss-of-Function Genetic Variation Regulating Body Fat Distribution. Journal of Clinical Endocrinology and Metabolism, 2022, 107, 1065-1077.	3.6	12
11	Development and validation of a metabolite score for red meat intake: an observational cohort study and randomized controlled dietary intervention. American Journal of Clinical Nutrition, 2022, 116, 511-522.	4.7	8
12	Genome-wide studies reveal factors associated with circulating uromodulin and its relationships to complex diseases. JCI Insight, 2022, 7, .	5.0	12
13	Whole-exome sequencing identifies rare genetic variants associated with human plasma metabolites. American Journal of Human Genetics, 2022, 109, 1038-1054.	6.2	17
14	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
15	Detection and characterization of male sex chromosome abnormalities in the UK Biobank study. Genetics in Medicine, 2022, 24, 1909-1919.	2.4	14
16	Genomic analysis of diet composition finds novel loci and associations with health and lifestyle. Molecular Psychiatry, 2021, 26, 2056-2069.	7.9	79
17	Plasma Vitamin C and Type 2 Diabetes: Genome-Wide Association Study and Mendelian Randomization Analysis in European Populations. Diabetes Care, 2021, 44, 98-106.	8.6	68
18	rs641738C>T near MBOAT7 is associated with liver fat, ALT and fibrosis in NAFLD: A meta-analysis. Journal of Hepatology, 2021, 74, 20-30.	3.7	77

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19	A cross-platform approach identifies genetic regulators of human metabolism and health. Nature Genetics, 2021, 53, 54-64.	21.4	117
20	Genome-wide meta-analysis of muscle weakness identifies 15 susceptibility loci in older men and women. Nature Communications, 2021, 12, 654.	12.8	75
21	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
22	Diabetes Mellitus, Glycemic Traits, and Cerebrovascular Disease. Neurology, 2021, 96, e1732-e1742.	1.1	59
23	A Neanderthal OAS1 isoform protects individuals of European ancestry against COVID-19 susceptibility and severity. Nature Medicine, 2021, 27, 659-667.	30.7	188
24	Genetic disruption of serine biosynthesis is a key driver of macular telangiectasia type 2 aetiology and progression. Genome Medicine, 2021, 13, 39.	8.2	15
25	Plasma metabolites to profile pathways in noncommunicable disease multimorbidity. Nature Medicine, 2021, 27, 471-479.	30.7	81
26	The potential shared role of inflammation in insulin resistance and schizophrenia: A bidirectional two-sample mendelian randomization study. PLoS Medicine, 2021, 18, e1003455.	8.4	37
27	Actionable druggable genome-wide Mendelian randomization identifies repurposing opportunities for COVID-19. Nature Medicine, 2021, 27, 668-676.	30.7	120
28	Reply to Unreliability of genotyping arrays for detecting very rare variants in human genetic studies: Example from a recent study of MC4R. Cell, 2021, 184, 1652-1653.	28.9	3
29	Prepubertal Dietary and Plasma Phospholipid Fatty Acids Related to Puberty Timing: Longitudinal Cohort and Mendelian Randomization Analyses. Nutrients, 2021, 13, 1868.	4.1	6
30	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
31	GIGYF1 loss of function is associated with clonal mosaicism and adverse metabolic health. Nature Communications, 2021, 12, 4178.	12.8	20
32	Weight Change and the Onset of Cardiovascular Diseases: Emulating Trials Using Electronic Health Records. Epidemiology, 2021, 32, 744-755.	2.7	19
33	Identification of 371 genetic variants for age at first sex and birth linked to externalising behaviour. Nature Human Behaviour, 2021, 5, 1717-1730.	12.0	62
34	Genetically Predicted Glucose-Dependent Insulinotropic Polypeptide (GIP) Levels and Cardiovascular Disease Risk Are Driven by Distinct Causal Variants in the GIPR Region. Diabetes, 2021, 70, 2706-2719.	0.6	12
35	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
36	Utility of Genetically Predicted Lp(a) (Lipoprotein [a]) and ApoB Levels for Cardiovascular Risk Assessment. Circulation Genomic and Precision Medicine, 2021, 14, e003312.	3.6	6

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37	Mitochondrial DNA variants modulate N-formylmethionine, proteostasis and risk of late-onset human diseases. Nature Medicine, 2021, 27, 1564-1575.	30.7	40
38	586Effects of maternal circulating amino acids on offspring birthweight: a Mendelian randomisation analysis. International Journal of Epidemiology, 2021, 50, .	1.9	1
39	The genomics of heart failure: design and rationale of the HERMES consortium. ESC Heart Failure, 2021, 8, 5531-5541.	3.1	11
40	The blood metabolome of incident kidney cancer: A caseâ€“control study nested within the MetKid consortium. PLoS Medicine, 2021, 18, e1003786.	8.4	16
41	Estimating the Population Benefits of Blood Pressure Lowering: A Wideâ€Angled Mendelian Randomization Study in UK Biobank. Journal of the American Heart Association, 2021, 10, e021098.	3.7	13
42	Identifying adults at high-risk for change in weight and BMI in England: a longitudinal, large-scale, population-based cohort study using electronic health records. Lancet Diabetes and Endocrinology,the, 2021, 9, 681-694.	11.4	37
43	Appetite disinhibition rather than hunger explains genetic effects on adult BMI trajectory. International Journal of Obesity, 2021, 45, 758-765.	3.4	8
44	High-throughput multivariable Mendelian randomization analysis prioritizes apolipoprotein B as key lipid risk factor for coronary artery disease. International Journal of Epidemiology, 2021, 50, 893-901.	1.9	52
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	Strengthening the Reporting of Observational Studies in Epidemiology Using Mendelian Randomization. JAMA - Journal of the American Medical Association, 2021, 326, 1614.	7.4	829
47	MC3R links nutritional state to childhood growth and the timing of puberty. Nature, 2021, 599, 436-441.	27.8	59
48	Mapping the proteo-genomic convergence of human diseases. Science, 2021, 374, eabj1541.	12.6	192
49	Synergistic insights into human health from aptamer- and antibody-based proteomic profiling. Nature Communications, 2021, 12, 6822.	12.8	95
50	Mapping the serum proteome to neurological diseases using whole genome sequencing. Nature Communications, 2021, 12, 7042.	12.8	29
51	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
52	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	7.9	83
53	Autoimmunity plays a role in the onset of diabetes after 40 years of age. Diabetologia, 2020, 63, 266-277.	6.3	15
54	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	12.8	466

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55	Functional Screening of Candidate Causal Genes for Insulin Resistance in Human Preadipocytes and Adipocytes. Circulation Research, 2020, 126, 330-346.	4.5	49
56	The association between circulating 25-hydroxyvitamin D metabolites and type 2 diabetes in European populations: AÂmeta-analysis and Mendelian randomisation analysis. PLoS Medicine, 2020, 17, e1003394.	8.4	45
57	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
58	Genome-wide association analysis of type 2 diabetes in the EPIC-InterAct study. Scientific Data, 2020, 7, 393.	5.3	19
59	Insights into genetic variants associated with NASH-fibrosis from metabolite profiling. Human Molecular Genetics, 2020, 29, 3451-3463.	2.9	27
60	Integrating Genetics and the Plasma Proteome to Predict the Risk of Type 2 Diabetes. Current Diabetes Reports, 2020, 20, 60.	4.2	5
61	Meta-analysis investigating the role of interleukin-6 mediated inflammation in type 2 diabetes. EBioMedicine, 2020, 61, 103062.	6.1	46
62	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.6	26
63	Genetic architecture of host proteins involved in SARS-CoV-2 infection. Nature Communications, 2020, 11, 6397.	12.8	71
64	SARS-CoV-2 (COVID-19): What Do We Know About Children? A Systematic Review. Clinical Infectious Diseases, 2020, 71, 2469-2479.	5.8	323
65	Ultra-High-Throughput Clinical Proteomics Reveals Classifiers of COVID-19 Infection. Cell Systems, 2020, 11, 11-24.e4.	6.2	439
66	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
67	Exome Sequencing Identifies Genes and Gene Sets Contributing to Severe Childhood Obesity, Linking PHIP Variants to Repressed POMC Transcription. Cell Metabolism, 2020, 31, 1107-1119.e12.	16.2	38
68	Genome-wide association study of adipocyte lipolysis in the GENetics of adipocyte lipolysis (GENiAL) cohort. Molecular Metabolism, 2020, 34, 85-96.	6.5	11
69	Genome-wide Association Study for Vitamin D Levels Reveals 69 Independent Loci. American Journal of Human Genetics, 2020, 106, 327-337.	6.2	144
70	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
71	Using human genetics to understand the disease impacts of testosterone in men and women. Nature Medicine, 2020, 26, 252-258.	30.7	384
72	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	1.8	3

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73	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	1.8	4
74	Genome-wide meta-analysis of macronutrient intake of 91,114 European ancestry participants from the cohorts for heart and aging research in genomic epidemiology consortium. Molecular Psychiatry, 2019, 24, 1920-1932.	7.9	44
75	Estimated Substitution of Tea or Coffee for Sugar-Sweetened Beverages Was Associated with Lower Type 2 Diabetes Incidence in Caseâ€“Cohort Analysis across 8 European Countries in the EPIC-InterAct Study. Journal of Nutrition, 2019, 149, 1985-1993.	2.9	24
76	Metabolomics Analytics Workflow for Epidemiological Research: Perspectives from the Consortium of Metabolomics Studies (COMETS). Metabolites, 2019, 9, 145.	2.9	30
77	Quality of dietary fat and genetic risk of type 2 diabetes: individual participant data meta-analysis. BMJ: British Medical Journal, 2019, 366, l4292.	2.3	28
78	Interleukin-18 as a drug repositioning opportunity for inflammatory bowel disease: A Mendelian randomization study. Scientific Reports, 2019, 9, 9386.	3.3	25
79	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. BMC Cardiovascular Disorders, 2019, 19, 240.	1.7	22
80	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
81	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
82	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
83	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
84	Regional fat depot masses are influenced by protein-coding gene variants. PLoS ONE, 2019, 14, e0217644.	2.5	9
85	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	6.2	21
86	Generalizability of a Diabetes-Associated Country-Specific Exploratory Dietary Pattern Is Feasible Across European Populations. Journal of Nutrition, 2019, 149, 1047-1055.	2.9	6
87	MicroRNA-196a links human body fat distribution to adipose tissue extracellular matrix composition. EBioMedicine, 2019, 44, 467-475.	6.1	22
88	Liver Function and Risk of Type 2 Diabetes: Bidirectional Mendelian Randomization Study. Diabetes, 2019, 68, 1681-1691.	0.6	79
89	Consumption of Meat, Fish, Dairy Products, and Eggs and Risk of Ischemic Heart Disease. Circulation, 2019, 139, 2835-2845.	1.6	103
90	Human Gain-of-Function MC4R Variants Show Signaling Bias and Protect against Obesity. Cell, 2019, 177, 597-607.e9.	28.9	192

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91	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
92	Association of Plasma Vitamin D Metabolites With Incident Type 2 Diabetes: EPIC-InterAct Case-Cohort Study. Journal of Clinical Endocrinology and Metabolism, 2019, 104, 1293-1303.	3.6	25
93	Assessing the causal association of glycine with risk of cardio-metabolic diseases. Nature Communications, 2019, 10, 1060.	12.8	85
94	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
95	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
96	The Consortium of Metabolomics Studies (COMETS): Metabolomics in 47 Prospective Cohort Studies. American Journal of Epidemiology, 2019, 188, 991-1012.	3.4	81
97	Association of menopausal characteristics and risk of coronary heart disease: a pan-European caseâ€“cohort analysis. International Journal of Epidemiology, 2019, 48, 1275-1285.	1.9	47
98	Dairy Product Intake and Risk of Type 2 Diabetes in EPIC-InterAct: A Mendelian Randomization Study. Diabetes Care, 2019, 42, 568-575.	8.6	29
99	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
100	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
101	Epigenome-Wide Association Study of Incident Type 2 Diabetes in a British Population: EPIC-Norfolk Study. Diabetes, 2019, 68, 2315-2326.	0.6	77
102	Plasma protein patterns as comprehensive indicators of health. Nature Medicine, 2019, 25, 1851-1857.	30.7	261
103	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
104	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	21.4	328
105	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and AlcoholÂUse. Biological Psychiatry, 2019, 85, 946-955.	1.3	69
106	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
107	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
108	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

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109	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
110	Re-analysis of public genetic data reveals a rare X-chromosomal variant associated with type 2 diabetes. Nature Communications, 2018, 9, 321.	12.8	85
111	Elevated Plasma Levels of 3-Hydroxyisobutyric Acid Are Associated With Incident Type 2 Diabetes. EBioMedicine, 2018, 27, 151-155.	6.1	53
112	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
113	Circulating Fetuin-A and Risk of Type 2 Diabetes: A Mendelian Randomization Analysis. Diabetes, 2018, 67, 1200-1205.	0.6	17
114	Interplay between genetic predisposition, macronutrient intake and type 2 diabetes incidence: analysis within EPIC-InterAct across eight European countries. Diabetologia, 2018, 61, 1325-1332.	6.3	20
115	Interaction of Dietary and Genetic Factors Influencing Body Iron Status and Risk of Type 2 Diabetes Within the EPIC-InterAct Study. Diabetes Care, 2018, 41, 277-285.	8.6	15
116	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
117	Characterization of missing values in untargeted MS-based metabolomics data and evaluation of missing data handling strategies. Metabolomics, 2018, 14, 128.	3.0	138
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	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
120	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
121	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
122	Association of Genetically Enhanced Lipoprotein Lipaseâ€“Mediated Lipolysis and Low-Density Lipoprotein Cholesterolâ€“Lowering Alleles With Risk of Coronary Disease and Type 2 Diabetes. JAMA Cardiology, 2018, 3, 957.	6.1	55
123	Alcohol intake in relation to non-fatal and fatal coronary heart disease and stroke: EPIC-CVD case-cohort study. BMJ: British Medical Journal, 2018, 361, k934.	2.3	70
124	Circulating Selenium and Prostate Cancer Risk: A Mendelian Randomization Analysis. Journal of the National Cancer Institute, 2018, 110, 1035-1038.	6.3	84
125	Prioritising Risk Factors for Type 2 Diabetes: Causal Inference through Genetic Approaches. Current Diabetes Reports, 2018, 18, 40.	4.2	4
126	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

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127	Type 2 diabetesâ€“associated variants of the MT ₂ melatonin receptor affect distinct modes of signaling. Science Signaling, 2018, 11, .	3.6	45
128	Genomic insights into the causes of type 2 diabetes. Lancet, The, 2018, 391, 2463-2474.	13.7	110
129	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
130	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
131	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
132	The current and potential health benefits of the National Health Service Health Check cardiovascular disease prevention programme in England: A microsimulation study. PLoS Medicine, 2018, 15, e1002517.	8.4	27
133	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
134	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
135	Genome-wide association study meta-analysis for quantitative ultrasound parameters of bone identifies five novel loci for broadband ultrasound attenuation. Human Molecular Genetics, 2017, 26, 2791-2802.	2.9	32
136	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
137	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
138	Interaction between genes and macronutrient intake on the risk of developing type 2 diabetes: systematic review and findings from European Prospective Investigation into Cancer (EPIC)-InterAct. American Journal of Clinical Nutrition, 2017, 106, 263-275.	4.7	46
139	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	6.2	131
140	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615
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 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.	0.6	47
143	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. Journal of the American Society of Nephrology: JASN, 2017, 28, 981-994.	6.1	39
144	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470

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145	New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48
146	Genome-wide analysis of health-related biomarkers in the UK Household Longitudinal Study reveals novel associations. Scientific Reports, 2017, 7, 11008.	3.3	88
147	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
148	Plasma Mannose Levels Are Associated with Incident Type 2 Diabetes and Cardiovascular Disease. Cell Metabolism, 2017, 26, 281-283.	16.2	85
149	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. Nature Communications, 2017, 8, 16015.	12.8	149
150	Rare Variant Analysis of Human and Rodent Obesity Genes in Individuals with Severe Childhood Obesity. Scientific Reports, 2017, 7, 4394.	3.3	50
151	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
152	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
153	A combination of plasma phospholipid fatty acids and its association with incidence of type 2 diabetes: The EPIC-InterAct case-cohort study. PLoS Medicine, 2017, 14, e1002409.	8.4	61
154	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
155	Association between plasma phospholipid saturated fatty acids and metabolic markers of lipid, hepatic, inflammation and glycaemic pathways in eight European countries: a cross-sectional analysis in the EPIC-InterAct study. BMC Medicine, 2017, 15, 203.	5.5	47
156	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.	0.8	3
157	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
158	Ranking and characterization of established BMI and lipid associated loci as candidates for gene-environment interactions. PLoS Genetics, 2017, 13, e1006812.	3.5	24
159	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
160	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
161	Mendelian Randomisation study of the influence of eGFR on coronary heart disease. Scientific Reports, 2016, 6, 28514.	3.3	14
162	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

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163	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	21.4	66
164	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	27.8	406
165	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
166	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
167	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
168	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
169	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
170	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.	0.6	67
171	Novel genetic loci associated with long-term deterioration in blood lipid concentrations and coronary artery disease in European adults. International Journal of Epidemiology, 2016, 46, dyw245.	1.9	17
172	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
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174	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. Diabetes, 2016, 65, 803-817.	0.6	131
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