

# Ruth J F Loos

## List of Publications by Year in descending order

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529  
papers

110,548  
citations

293

139  
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239

304  
g-index

610  
all docs

610  
docs citations

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times ranked

86197  
citing authors

#	ARTICLE	IF	CITATIONS
1	The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2020, 581, 434-443.	13.7	6,140
2	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
3	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
4	Biological, clinical and population relevance of 95 loci for blood lipids. <i>Nature</i> , 2010, 466, 707-713.	13.7	3,249
5	Correlates of physical activity: why are some people physically active and others not?. <i>Lancet</i> , The, 2012, 380, 258-271.	6.3	2,874
6	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013, 45, 1274-1283.	9.4	2,641
7	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
8	A comprehensive 1000 Genomesâ€based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , 2015, 47, 1121-1130.	9.4	2,054
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	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011, 478, 103-109.	13.7	1,855
11	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
12	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	13.7	1,789
13	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
14	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
15	Common genetic determinants of vitamin D insufficiency: a genome-wide association study. <i>Lancet</i> , The, 2010, 376, 180-188.	6.3	1,385
16	Conditional and joint multiple-SNP analysis of GWAS summary statistics identifies additional variants influencing complex traits. <i>Nature Genetics</i> , 2012, 44, 369-375.	9.4	1,338
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	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
20	Genome-wide association study identifies eight loci associated with blood pressure. <i>Nature Genetics</i> , 2009, 41, 666-676.	9.4	1,104
21	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021, 590, 290-299.	13.7	1,069
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	Loss-of-Function Mutations in <i>APOC3</i> , Triglycerides, and Coronary Disease. <i>New England Journal of Medicine</i> , 2014, 371, 22-31.	13.9	936
25	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
26	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
27	Obesity. <i>Nature Reviews Disease Primers</i> , 2017, 3, 17034.	18.1	766
28	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycaemic traits and insulin resistance. <i>Nature Genetics</i> , 2012, 44, 659-669.	9.4	762
29	Common variants associated with plasma triglycerides and risk for coronary artery disease. <i>Nature Genetics</i> , 2013, 45, 1345-1352.	9.4	754
30	Causal Relationship between Obesity and Vitamin D Status: Bi-Directional Mendelian Randomization Analysis of Multiple Cohorts. <i>PLoS Medicine</i> , 2013, 10, e1001383.	3.9	753
31	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
32	Large-scale association analyses identify new loci influencing glycaemic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , 2012, 44, 991-1005.	9.4	746
33	Genome-wide association analysis identifies 20 loci that influence adult height. <i>Nature Genetics</i> , 2008, 40, 575-583.	9.4	742
34	Rapid infancy weight gain and subsequent obesity: Systematic reviews and hopeful suggestions. <i>Acta Paediatrica, International Journal of Paediatrics</i> , 2006, 95, 904-908.	0.7	684
35	Genetic analyses of diverse populations improves discovery for complex traits. <i>Nature</i> , 2019, 570, 514-518.	13.7	679
36	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2013, 45, 145-154.	9.4	675

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37	Variants in MTNR1B influence fasting glucose levels. <i>Nature Genetics</i> , 2009, 41, 77-81.	9.4	662
38	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017, 66, 2888-2902.	0.3	615
39	A structural variation reference for medical and population genetics. <i>Nature</i> , 2020, 581, 444-451.	13.7	614
40	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. <i>Nature Genetics</i> , 2010, 42, 142-148.	9.4	591
41	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. <i>Nature Genetics</i> , 2010, 42, 436-440.	9.4	581
42	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
43	Association analyses based on false discovery rate implicate new loci for coronary artery disease. <i>Nature Genetics</i> , 2017, 49, 1385-1391.	9.4	571
44	Genomic Risk Prediction of Coronary Artery Disease in 480,000 Adults. <i>Journal of the American College of Cardiology</i> , 2018, 72, 1883-1893.	1.2	557
45	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018, 50, 1225-1233.	9.4	552
46	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
47	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	13.7	548
48	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	13.7	544
49	Genome-wide association study identifies five loci associated with lung function. <i>Nature Genetics</i> , 2010, 42, 36-44.	9.4	518
50	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. <i>Nature Genetics</i> , 2011, 43, 1131-1138.	9.4	501
51	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
52	The bigger picture of FTO—the first GWAS-identified obesity gene. <i>Nature Reviews Endocrinology</i> , 2014, 10, 51-61.	4.3	490
53	Variability in the Heritability of Body Mass Index: A Systematic Review and Meta-Regression. <i>Frontiers in Endocrinology</i> , 2012, 3, 29.	1.5	489
54	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766.	9.4	470

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55	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. <i>PLoS Genetics</i> , 2009, 5, e1000508.	1.5	453
56	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
57	Physical Activity Attenuates the Influence of FTO Variants on Obesity Risk: A Meta-Analysis of 218,166 Adults and 19,268 Children. <i>PLoS Medicine</i> , 2011, 8, e1001116.	3.9	446
58	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 1077-1085.	9.4	445
59	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. <i>Science</i> , 2016, 351, 1166-1171.	6.0	438
60	Coding Variation in <i>ANGPTL4</i> , <i>LPL</i> and <i>SVEP1</i> and the Risk of Coronary Disease. <i>New England Journal of Medicine</i> , 2016, 374, 1134-1144.	13.9	427
61	The genetics of obesity: from discovery to biology. <i>Nature Reviews Genetics</i> , 2022, 23, 120-133.	7.7	425
62	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
63	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016, 7, 10023.	5.8	412
64	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011, 43, 1005-1011.	9.4	403
65	New gene functions in megakaryopoiesis and platelet formation. <i>Nature</i> , 2011, 480, 201-208.	13.7	401
66	Quality control and conduct of genome-wide association meta-analyses. <i>Nature Protocols</i> , 2014, 9, 1192-1212.	5.5	398
67	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11.	13.5	388
68	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. <i>Diabetes</i> , 2010, 59, 3229-3239.	0.3	387
69	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012, 490, 267-272.	13.7	383
70	Prominent Axonopathy in the Brain and Spinal Cord of Transgenic Mice Overexpressing Four-Repeat Human tau Protein. <i>American Journal of Pathology</i> , 1999, 155, 2153-2165.	1.9	379
71	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020, 586, 763-768.	13.7	376
72	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

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73	Genetic Variants Influencing Circulating Lipid Levels and Risk of Coronary Artery Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2010, 30, 2264-2276.	1.1	369
74	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. <i>Nature Genetics</i> , 2011, 43, 1082-1090.	9.4	367
75	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
76	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016, 48, 1171-1184.	9.4	362
77	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
78	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. <i>Cell</i> , 2020, 182, 1198-1213.e14.	13.5	353
79	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	13.7	353
80	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. <i>PLoS Medicine</i> , 2017, 14, e1002383.	3.9	341
81	The trans-ancestral genomic architecture of glycemc traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	9.4	341
82	Genome-Wide Association Identifies Nine Common Variants Associated With Fasting Proinsulin Levels and Provides New Insights Into the Pathophysiology of Type 2 Diabetes. <i>Diabetes</i> , 2011, 60, 2624-2634.	0.3	335
83	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
84	LDL-cholesterol concentrations: a genome-wide association study. <i>Lancet</i> , The, 2008, 371, 483-491.	6.3	329
85	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
86	Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , 2012, 492, 369-375.	13.7	320
87	Genetic variation in LIN28B is associated with the timing of puberty. <i>Nature Genetics</i> , 2009, 41, 729-733.	9.4	317
88	Genome-Wide Association Study of Blood Pressure Extremes Identifies Variant near UMOD Associated with Hypertension. <i>PLoS Genetics</i> , 2010, 6, e1001177.	1.5	312
89	Glycogen Synthase Kinase-3 $\beta$ Phosphorylates Protein Tau and Rescues the Axonopathy in the Central Nervous System of Human Four-repeat Tau Transgenic Mice. <i>Journal of Biological Chemistry</i> , 2000, 275, 41340-41349.	1.6	294
90	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. <i>Nature Genetics</i> , 2013, 45, 76-82.	9.4	293

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91	Genetic variation near <i>IRS1</i> associates with reduced adiposity and an impaired metabolic profile. <i>Nature Genetics</i> , 2011, 43, 753-760.	9.4	289
92	Association of Low-Frequency and Rare Coding-Sequence Variants with Blood Lipids and Coronary Heart Disease in 56,000 Whites and Blacks. <i>American Journal of Human Genetics</i> , 2014, 94, 223-232.	2.6	287
93	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
94	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013, 45, 621-631.	9.4	282
95	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. <i>Nature Genetics</i> , 2014, 46, 826-836.	9.4	281
96	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
97	Genome-wide SNP and CNV analysis identifies common and low-frequency variants associated with severe early-onset obesity. <i>Nature Genetics</i> , 2013, 45, 513-517.	9.4	278
98	Set points, settling points and some alternative models: theoretical options to understand how genes and environments combine to regulate body adiposity. <i>DMM Disease Models and Mechanisms</i> , 2011, 4, 733-745.	1.2	266
99	<i>FTO</i> : the first gene contributing to common forms of human obesity. <i>Obesity Reviews</i> , 2008, 9, 246-250.	3.1	263
100	Genome-wide association and genetic functional studies identify autism susceptibility candidate 2 gene ( <i>AUTS2</i> ) in the regulation of alcohol consumption. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 7119-7124.	3.3	258
101	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. <i>Nature Genetics</i> , 2017, 49, 416-425.	9.4	257
102	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	9.4	251
103	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
104	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019, 570, 71-76.	13.7	248
105	Genetic loci influencing kidney function and chronic kidney disease. <i>Nature Genetics</i> , 2010, 42, 373-375.	9.4	246
106	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016, 7, 10495.	5.8	245
107	Meta-Analysis of Genome-Wide Scans for Human Adult Stature Identifies Novel Loci and Associations with Measures of Skeletal Frame Size. <i>PLoS Genetics</i> , 2009, 5, e1000445.	1.5	237
108	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015, 20, 647-656.	4.1	235

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109	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. <i>Nature Genetics</i> , 2013, 45, 690-696.	9.4	232
110	Physical Activity Attenuates the Genetic Predisposition to Obesity in 20,000 Men and Women from EPIC-Norfolk Prospective Population Study. <i>PLoS Medicine</i> , 2010, 7, e1000332.	3.9	230
111	Life course variations in the associations between FTO and MC4R gene variants and body size. <i>Human Molecular Genetics</i> , 2010, 19, 545-552.	1.4	227
112	Population genetic differentiation of height and body mass index across Europe. <i>Nature Genetics</i> , 2015, 47, 1357-1362.	9.4	227
113	Common Variants in <i>CDKAL1</i> , <i>CDKN2A/B</i> , <i>IGF2BP2</i> , <i>SLC30A8</i> , and <i>HHEX/IDE</i> Genes Are Associated With Type 2 Diabetes and Impaired Fasting Glucose in a Chinese Han Population. <i>Diabetes</i> , 2008, 57, 2834-2842.	0.3	226
114	Variants in the Fat Mass and Obesity-Associated ( <i>FTO</i> ) Gene Are Not Associated With Obesity in a Chinese Han Population. <i>Diabetes</i> , 2008, 57, 264-268.	0.3	223
115	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. <i>Nature Genetics</i> , 2016, 48, 1162-1170.	9.4	223
116	Identification of new susceptibility loci for type 2 diabetes and shared etiological pathways with coronary heart disease. <i>Nature Genetics</i> , 2017, 49, 1450-1457.	9.4	218
117	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2017, 69, 823-836.	1.2	214
118	Prominent Cerebral Amyloid Angiopathy in Transgenic Mice Overexpressing the London Mutant of Human APP in Neurons. <i>American Journal of Pathology</i> , 2000, 157, 1283-1298.	1.9	213
119	The prenatal gut microbiome: are we colonized with bacteria <i>in utero</i> ? <i>Pediatric Obesity</i> , 2017, 12, 3-17.	1.4	211
120	Genome-wide meta-analysis of observational studies shows common genetic variants associated with macronutrient intake. <i>American Journal of Clinical Nutrition</i> , 2013, 97, 1395-1402.	2.2	210
121	Obesity - is it a genetic disorder?. <i>Journal of Internal Medicine</i> , 2003, 254, 401-425.	2.7	208
122	CUBN Is a Gene Locus for Albuminuria. <i>Journal of the American Society of Nephrology: JASN</i> , 2011, 22, 555-570.	3.0	208
123	Use of >100,000 NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium whole genome sequences improves imputation quality and detection of rare variant associations in admixed African and Hispanic/Latino populations. <i>PLoS Genetics</i> , 2019, 15, e1008500.	1.5	203
124	Genetic determinants of common obesity and their value in prediction. <i>Best Practice and Research in Clinical Endocrinology and Metabolism</i> , 2012, 26, 211-226.	2.2	198
125	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. <i>PLoS ONE</i> , 2012, 7, e29202.	1.1	197
126	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



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127	Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. <i>PLoS Genetics</i> , 2014, 10, e1004517.	1.5	191
128	Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. <i>American Journal of Human Genetics</i> , 2013, 93, 545-554.	2.6	189
129	Cumulative effects and predictive value of common obesity-susceptibility variants identified by genome-wide association studies. <i>American Journal of Clinical Nutrition</i> , 2010, 91, 184-190.	2.2	185
130	Physical activity attenuates the body mass indexâ€™s increasing influence of genetic variation in the FTO gene. <i>American Journal of Clinical Nutrition</i> , 2009, 90, 425-428.	2.2	182
131	Obesity genes identified in genome-wide association studies are associated with adiposity measures and potentially with nutrient-specific food preference. <i>American Journal of Clinical Nutrition</i> , 2009, 90, 951-959.	2.2	179
132	Genetic and environmental effects on body mass index from infancy to the onset of adulthood: an individual-based pooled analysis of 45 twin cohorts participating in the COllaborative project of Development of Anthropometrical measures in Twins (CODATwins) study. <i>American Journal of Clinical Nutrition</i> , 2016, 104, 371-379.	2.2	175
133	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
134	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	13.7	173
135	Association of genetic variation in FTO with risk of obesity and type 2 diabetes with data from 96,551 East and South Asians. <i>Diabetologia</i> , 2012, 55, 981-995.	2.9	171
136	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
137	A Genome-Wide Association Study Identifies <i>GRK5</i> and <i>RASGRP1</i> as Type 2 Diabetes Loci in Chinese Hans. <i>Diabetes</i> , 2013, 62, 291-298.	0.3	166
138	Genome-Wide Association Studies Identify <i>CHRNA5</i> and <i>HTR4</i> in the Development of Airflow Obstruction. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2012, 186, 622-632.	2.5	164
139	A Central Role for GRB10 in Regulation of Islet Function in Man. <i>PLoS Genetics</i> , 2014, 10, e1004235.	1.5	164
140	Genetic Markers of Adult Obesity Risk Are Associated with Greater Early Infancy Weight Gain and Growth. <i>PLoS Medicine</i> , 2010, 7, e1000284.	3.9	158
141	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	1.5	158
142	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. <i>Nature Genetics</i> , 2022, 54, 263-273.	9.4	156
143	TCF7L2 Polymorphisms Modulate Proinsulin Levels and Î²-Cell Function in a British European Population. <i>Diabetes</i> , 2007, 56, 1943-1947.	0.3	154
144	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , 2016, 7, 10494.	5.8	153

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145	A Genome-Wide Association Study Reveals Variants in ARL15 that Influence Adiponectin Levels. PLoS Genetics, 2009, 5, e1000768.	1.5	148
146	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	5.8	147
147	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. Journal of the American College of Cardiology, 2019, 73, 58-66.	1.2	147
148	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nature Genetics, 2020, 52, 969-983.	9.4	146
149	FTO genetic variants, dietary intake and body mass index: insights from 177 330 individuals. Human Molecular Genetics, 2014, 23, 6961-6972.	1.4	143
150	Transcript expression-aware annotation improves rare variant interpretation. Nature, 2020, 581, 452-458.	13.7	142
151	Developments in Obesity Genetics in the Era of Genome-Wide Association Studies. Journal of Nutrigenetics and Nutrigenomics, 2011, 4, 222-238.	1.8	134
152	Genetic and environmental influences on height from infancy to early adulthood: An individual-based pooled analysis of 45 twin cohorts. Scientific Reports, 2016, 6, 28496.	1.6	133
153	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. Diabetes, 2016, 65, 803-817.	0.3	131
154	Genome-Wide Joint Meta-Analysis of SNP and SNP-by-Smoking Interaction Identifies Novel Loci for Pulmonary Function. PLoS Genetics, 2012, 8, e1003098.	1.5	130
155	Effect of Five Genetic Variants Associated with Lung Function on the Risk of Chronic Obstructive Lung Disease, and Their Joint Effects on Lung Function. American Journal of Respiratory and Critical Care Medicine, 2011, 184, 786-795.	2.5	128
156	Birth weight and body composition in young adult men—a prospective twin study. International Journal of Obesity, 2001, 25, 1537-1545.	1.6	127
157	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.	4.3	127
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270	Advances in Exercise, Fitness, and Performance Genomics in 2015. <i>Medicine and Science in Sports and Exercise</i> , 2016, 48, 1906-1916.	0.2	52



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272	Advances in Exercise, Fitness, and Performance Genomics in 2012. <i>Medicine and Science in Sports and Exercise</i> , 2013, 45, 824-831.	0.2	50
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280	Progress in the genetics of common obesity: size matters. <i>Current Opinion in Lipidology</i> , 2008, 19, 113-121.	1.2	47
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290	Anthropometric characteristics of elite female junior rowers. <i>Journal of Sports Sciences</i> , 2001, 19, 195-202.	1.0	42
291	Genetic and environmental influences on adult human height across birth cohorts from 1886 to 1994. <i>ELife</i> , 2016, 5, .	2.8	42
292	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. <i>Kidney International</i> , 2021, 99, 926-939.	2.6	42
293	Association between Mediterranean and Nordic diet scores and changes in weight and waist circumference: influence of FTO and TCF7L2 loci. <i>American Journal of Clinical Nutrition</i> , 2014, 100, 1188-1197.	2.2	41
294	Meta-analysis of rare and common exome chip variants identifies S1PR4 and other loci influencing blood cell traits. <i>Nature Genetics</i> , 2016, 48, 867-876.	9.4	41
295	Genome-wide association study of primary open-angle glaucoma in continental and admixed African populations. <i>Human Genetics</i> , 2018, 137, 847-862.	1.8	40
296	Common SNPs in LEP and LEPR associated with birth weight and type 2 diabetes-related metabolic risk factors in twins. <i>International Journal of Obesity</i> , 2008, 32, 1233-1239.	1.6	39
297	Association Between FTO Variant and Change in Body Weight and Its Interaction With Dietary Factors: The DiOGenes Study. <i>Obesity</i> , 2012, 20, 1669-1674.	1.5	39
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299	Analyses of single nucleotide polymorphisms in selected nutrient-sensitive genes in weight-regain prevention: the DIOGENES study. <i>American Journal of Clinical Nutrition</i> , 2012, 95, 1254-1260.	2.2	38
300	Advances in Exercise, Fitness, and Performance Genomics in 2014. <i>Medicine and Science in Sports and Exercise</i> , 2015, 47, 1105-1112.	0.2	38
301	Genome-wide association of white blood cell counts in Hispanic/Latino Americans: the Hispanic Community Health Study/Study of Latinos. <i>Human Molecular Genetics</i> , 2017, 26, 1193-1204.	1.4	38
302	Evidence of genetic predisposition for metabolically healthy obesity and metabolically obese normal weight. <i>Physiological Genomics</i> , 2018, 50, 169-178.	1.0	38
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304	Implementing genomic screening in diverse populations. <i>Genome Medicine</i> , 2021, 13, 17.	3.6	38
305	Polymorphisms in the leptin and leptin receptor genes in relation to resting metabolic rate and respiratory quotient in the Québec Family Study. <i>International Journal of Obesity</i> , 2006, 30, 183-190.	1.6	36
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308	Blood pressure in young adulthood and residential greenness in the early-life environment of twins. <i>Environmental Health</i> , 2017, 16, 53.	1.7	36
309	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. <i>Science Advances</i> , 2022, 8, eabl6579.	4.7	36
310	Mendelian randomisation analyses find pulmonary factors mediate the effect of height on coronary artery disease. <i>Communications Biology</i> , 2019, 2, 119.	2.0	35
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