Ruth J F Loos

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537	77,772 citations	129	273
papers		h-index	g-index
610	96,900	13.8	6.94
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
537	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, 889-94	33.3	3294
536	Biological, clinical and population relevance of 95 loci for blood lipids. <i>Nature</i> , 2010 , 466, 707-13	50.4	2742
535	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015 , 518, 197-206	50.4	2687
534	The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2020 , 581, 434-443	50.4	2278
533	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010 , 42, 937-48	36.3	2267
532	Correlates of physical activity: why are some people physically active and others not?. <i>Lancet, The</i> , 2012 , 380, 258-71	40	2206
531	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013 , 45, 1274-1283	36.3	1904
530	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010 , 42, 105-16	36.3	1673
529	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011 , 478, 103-9	50.4	1564
528	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010 , 467, 832-8	50.4	1514
527	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012 , 44, 981-90	36.3	1482
526	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. <i>Nature Genetics</i> , 2009 , 41, 25-34	36.3	1368
525	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014 , 46, 1173-86	36.3	1339
524	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , 2015 , 47, 1121-1130	36.3	1290
523	Common genetic determinants of vitamin D insufficiency: a genome-wide association study. <i>Lancet, The,</i> 2010 , 376, 180-8	40	1183
522	Common variants near MC4R are associated with fat mass, weight and risk of obesity. <i>Nature Genetics</i> , 2008 , 40, 768-75	36.3	1048
521	Genome-wide association study identifies eight loci associated with blood pressure. <i>Nature Genetics</i> , 2009 , 41, 666-76	36.3	970

520	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015 , 518, 187-196	50.4	920
519	Conditional and joint multiple-SNP analysis of GWAS summary statistics identifies additional variants influencing complex traits. <i>Nature Genetics</i> , 2012 , 44, 369-75, S1-3	36.3	813
518	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014 , 46, 234-44	36.3	784
517	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, 949-60	36.3	724
516	Loss-of-function mutations in APOC3, triglycerides, and coronary disease. <i>New England Journal of Medicine</i> , 2014 , 371, 22-31	59.2	721
515	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016 , 536, 41-47	50.4	704
514	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	36.3	675
513	Genome-wide association analysis identifies 20 loci that influence adult height. <i>Nature Genetics</i> , 2008 , 40, 575-83	36.3	654
512	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	36.3	621
511	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. <i>Nature Genetics</i> , 2012 , 44, 659-69	36.3	615
510	Common variants associated with plasma triglycerides and risk for coronary artery disease. <i>Nature Genetics</i> , 2013 , 45, 1345-52	36.3	597
509	Causal relationship between obesity and vitamin D status: bi-directional Mendelian randomization analysis of multiple cohorts. <i>PLoS Medicine</i> , 2013 , 10, e1001383	11.6	592
508	Variants in MTNR1B influence fasting glucose levels. <i>Nature Genetics</i> , 2009 , 41, 77-81	36.3	584
507	Rapid infancy weight gain and subsequent obesity: systematic reviews and hopeful suggestions. <i>Acta Paediatrica, International Journal of Paediatrics</i> , 2006 , 95, 904-8	3.1	552
506	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. <i>Nature Genetics</i> , 2010 , 42, 142-8	36.3	527
505	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. <i>Nature Genetics</i> , 2010 , 42, 436-40	36.3	521
504	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2013 , 45, 145-54	36.3	505
503	Obesity. <i>Nature Reviews Disease Primers</i> , 2017 , 3, 17034	51.1	464

502	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013 , 45, 501-12	36.3	437
501	Genome-wide association study identifies five loci associated with lung function. <i>Nature Genetics</i> , 2010 , 42, 36-44	36.3	430
500	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. <i>Nature Genetics</i> , 2011 , 43, 1131-8	36.3	415
499	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017 , 66, 28	8& 29 0	2 414
498	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017 , 542, 186-190	50.4	412
497	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014 , 514, 92-97	50.4	401
496	The metabochip, a custom genotyping array for genetic studies of metabolic, cardiovascular, and anthropometric traits. <i>PLoS Genetics</i> , 2012 , 8, e1002793	6	395
495	Genome-wide association scan meta-analysis identifies three Loci influencing adiposity and fat distribution. <i>PLoS Genetics</i> , 2009 , 5, e1000508	6	393
494	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018 , 50, 1412-1425	36.3	386
493	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	11.6	379
492	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. <i>Nature Genetics</i> , 2010 , 42, 1077-85	36.3	372
491	Association analyses based on false discovery rate implicate new loci for coronary artery disease. <i>Nature Genetics</i> , 2017 , 49, 1385-1391	36.3	361
490	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, 2153-65	5.8	356
489	The bigger picture of FTO: the first GWAS-identified obesity gene. <i>Nature Reviews Endocrinology</i> , 2014 , 10, 51-61	15.2	353
488	Variability in the heritability of body mass index: a systematic review and meta-regression. <i>Frontiers in Endocrinology</i> , 2012 , 3, 29	5.7	351
487	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011 , 43, 1005-11	36.3	338
486	New gene functions in megakaryopoiesis and platelet formation. <i>Nature</i> , 2011 , 480, 201-8	50.4	330
485	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	6	326

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484	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. <i>Science</i> , 2016 , 351, 1166-71	33.3	325
483	Coding Variation in ANGPTL4, LPL, and SVEP1 and the Risk of Coronary Disease. <i>New England Journal of Medicine</i> , 2016 , 374, 1134-44	59.2	325
482	Genetic variants influencing circulating lipid levels and risk of coronary artery disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2010 , 30, 2264-76	9.4	318
481	Common variants at 10 genomic loci influence hemoglobin A(C) levels via glycemic and nonglycemic pathways. <i>Diabetes</i> , 2010 , 59, 3229-39	0.9	314
480	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , 2017 , 49, 403-415	36.3	313
479	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. <i>Nature Genetics</i> , 2011 , 43, 1082-90	36.3	313
478	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017 , 49, 1758-	1 36 .6	310
477	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012 , 490, 267-72	50.4	304
476	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016 , 7, 10023	17.4	295
475	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015 , 47, 1415-25	36.3	292
474	LDL-cholesterol concentrations: a genome-wide association study. <i>Lancet, The</i> , 2008 , 371, 483-91	40	292
473	Genetic analyses of diverse populations improves discovery for complex traits. <i>Nature</i> , 2019 , 570, 514-5	5 15 80.4	291
472	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, 2624-34	0.9	285
471	Genomic Risk Prediction of Coronary Artery Disease in 480,000 Adults: Implications for Primary Prevention. <i>Journal of the American College of Cardiology</i> , 2018 , 72, 1883-1893	15.1	285
470	Quality control and conduct of genome-wide association meta-analyses. <i>Nature Protocols</i> , 2014 , 9, 1192	2-28.8	278
469	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018 , 50, 1225-1233	36.3	277
468	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	6	277
467	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021 , 590, 290-299	50.4	268

466	Genetic variation in LIN28B is associated with the timing of puberty. <i>Nature Genetics</i> , 2009 , 41, 729-33	36.3	258
465	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	5.6	258
464	Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , 2012 , 492, 369-75	50.4	257
463	Genome-wide association study of blood pressure extremes identifies variant near UMOD associated with hypertension. <i>PLoS Genetics</i> , 2010 , 6, e1001177	6	255
462	Glycogen synthase kinase-3beta 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, 41340-9	5.4	253
461	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	36.3	251
460	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. <i>Nature Genetics</i> , 2011 , 43, 753-60	36.3	237
459	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, 223-32	11	233
458	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	36.3	232
457	Genome-wide SNP and CNV analysis identifies common and low-frequency variants associated with severe early-onset obesity. <i>Nature Genetics</i> , 2013 , 45, 513-7	36.3	231
456	A structural variation reference for medical and population genetics. <i>Nature</i> , 2020 , 581, 444-451	50.4	223
455	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	11.6	223
454	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018 , 50, 559-571	36.3	221
453	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	6	220
452	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013 , 45, 621-31	36.3	219
451	Genome-wide association and genetic functional studies identify autism susceptibility candidate 2 gene (AUTS2) in the regulation of alcohol consumption. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 7119-24	11.5	218
450	FTO: the first gene contributing to common forms of human obesity. <i>Obesity Reviews</i> , 2008 , 9, 246-50	10.6	218
449	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019 , 51, 957-972	36.3	217

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448	Life course variations in the associations between FTO and MC4R gene variants and body size. <i>Human Molecular Genetics</i> , 2010 , 19, 545-52	5.6	206
447	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, 733-45	4.1	206
446	Variants in the fat mass- and obesity-associated (FTO) gene are not associated with obesity in a Chinese Han population. <i>Diabetes</i> , 2008 , 57, 264-8	0.9	206
445	Genetic loci influencing kidney function and chronic kidney disease. <i>Nature Genetics</i> , 2010 , 42, 373-5	36.3	205
444	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	11.6	201
443	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. <i>Nature Genetics</i> , 2014 , 46, 826-36	36.3	199
442	Common variants in CDKAL1, CDKN2A/B, IGF2BP2, SLC30A8, and HHEX/IDE genes are associated with type 2 diabetes and impaired fasting glucose in a Chinese Han population. <i>Diabetes</i> , 2008 , 57, 2834	4-42	199
441	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	6	198
440	Prominent cerebral amyloid angiopathy in transgenic mice overexpressing the london mutant of human APP in neurons. <i>American Journal of Pathology</i> , 2000 , 157, 1283-98	5.8	198
439	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. <i>Nature Genetics</i> , 2013 , 45, 690-6	36.3	192
438	Population genetic differentiation of height and body mass index across Europe. <i>Nature Genetics</i> , 2015 , 47, 1357-62	36.3	186
437	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	36.3	186
436	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016 , 7, 10495	17.4	180
435	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. <i>Nature Genetics</i> , 2017 , 49, 946-952	36.3	176
434	Obesityis it a genetic disorder?. <i>Journal of Internal Medicine</i> , 2003 , 254, 401-25	10.8	174
433	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	36.3	170
432	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. <i>American Journal of Human Genetics</i> , 2014 , 94, 233-45	11	170
431	CUBN is a gene locus for albuminuria. <i>Journal of the American Society of Nephrology: JASN</i> , 2011 , 22, 55.	5±7207	170

430	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015 , 20, 647-656	15.1	167
429	Genetic determinants of common obesity and their value in prediction. <i>Best Practice and Research in Clinical Endocrinology and Metabolism</i> , 2012 , 26, 211-26	6.5	166
428	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, 184-90	7	163
427	Genome-wide meta-analysis of observational studies shows common genetic variants associated with macronutrient intake. <i>American Journal of Clinical Nutrition</i> , 2013 , 97, 1395-402	7	161
426	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, 951-9	7	157
425	Physical activity attenuates the body mass index-increasing influence of genetic variation in the FTO gene. <i>American Journal of Clinical Nutrition</i> , 2009 , 90, 425-8	7	155
424	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. <i>Nature Genetics</i> , 2016 , 48, 1162-70	36.3	152
423	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	6	151
422	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	11	151
421	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. <i>Nature Communications</i> , 2015 , 6, 5897	17.4	147
420	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	15.1	146
419	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, 545-54	11	145
418	The prenatal gut microbiome: are we colonized with bacteria in utero?. <i>Pediatric Obesity</i> , 2017 , 12 Suppl 1, 3-17	4.6	144
417	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, 981-95	10.3	144
416	A genome-wide association study identifies GRK5 and RASGRP1 as type 2 diabetes loci in Chinese Hans. <i>Diabetes</i> , 2013 , 62, 291-8	0.9	142
415	Genetic markers of adult obesity risk are associated with greater early infancy weight gain and growth. <i>PLoS Medicine</i> , 2010 , 7, e1000284	11.6	142
414	A genome-wide association search for type 2 diabetes genes in African Americans. <i>PLoS ONE</i> , 2012 , 7, e29202	3.7	138
413	TCF7L2 polymorphisms modulate proinsulin levels and beta-cell function in a British Europid population. <i>Diabetes</i> , 2007 , 56, 1943-7	0.9	137

412	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	36.3	136
411	Genome-wide association studies identify CHRNA5/3 and HTR4 in the development of airflow obstruction. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2012 , 186, 622-32	10.2	131
410	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019 , 570, 71-76	50.4	129
409	A genome-wide association study reveals variants in ARL15 that influence adiponectin levels. <i>PLoS Genetics</i> , 2009 , 5, e1000768	6	129
408	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020 , 586, 763-768	50.4	127
407	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 Chairman Nature</i> 2016, 104, 271.0	7	125
406	A central role for GRB10 in regulation of islet function in man. <i>PLoS Genetics</i> , 2014 , 10, e1004235	6	124
405	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019 , 51, 1459-1474	36.3	122
404	FTO genetic variants, dietary intake and body mass index: insights from 177,330 individuals. <i>Human Molecular Genetics</i> , 2014 , 23, 6961-72	5.6	120
403	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015 , 523, 459-4	6 3 0.4	119
402	Developments in obesity genetics in the era of genome-wide association studies. <i>Journal of Nutrigenetics and Nutrigenomics</i> , 2011 , 4, 222-38		113
401	Genetic susceptibility to obesity and related traits in childhood and adolescence: influence of loci identified by genome-wide association studies. <i>Diabetes</i> , 2010 , 59, 2980-8	0.9	113
400	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. <i>Diabetes Care</i> , 2010 , 33, 2684-91	14.6	112
	Effect of five genetic variants associated with lung function on the risk of chronic obstructive lung		
399	disease, and their joint effects on lung function. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2011 , 184, 786-95	10.2	112
399 398	disease, and their joint effects on lung function. American Journal of Respiratory and Critical Care	10.2	108
	disease, and their joint effects on lung function. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2011 , 184, 786-95 Genome-wide joint meta-analysis of SNP and SNP-by-smoking interaction identifies novel loci for		
398	disease, and their joint effects on lung function. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2011 , 184, 786-95 Genome-wide joint meta-analysis of SNP and SNP-by-smoking interaction identifies novel loci for pulmonary function. <i>PLoS Genetics</i> , 2012 , 8, e1003098 Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature</i>	6	108

394	Heritability of objectively assessed daily physical activity and sedentary behavior. <i>American Journal of Clinical Nutrition</i> , 2013 , 98, 1317-25	7	104
393	Recent progress in the genetics of common obesity. <i>British Journal of Clinical Pharmacology</i> , 2009 , 68, 811-29	3.8	104
392	Birth weight and body composition in young women: a prospective twin study. <i>American Journal of Clinical Nutrition</i> , 2002 , 75, 676-82	7	103
391	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017 , 13, e1006528	6	103
390	Birth weight and body composition in young adult mena prospective twin study. <i>International Journal of Obesity</i> , 2001 , 25, 1537-45	5.5	102
389	Trend in obesity prevalence in European adult cohort populations during follow-up since 1996 and their predictions to 2015. <i>PLoS ONE</i> , 2011 , 6, e27455	3.7	100
388	Genome-wide linkage scan for the metabolic syndrome in the HERITAGE Family Study. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2003 , 88, 5935-43	5.6	98
387	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. <i>Diabetes</i> , 2016 , 65, 803-17	0.9	96
386	Common variants in ZNF365 are associated with both mammographic density and breast cancer risk. <i>Nature Genetics</i> , 2011 , 43, 185-7	36.3	96
385	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020 , 182, 1214-1231.e11	56.2	96
384	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, 3589-98	0.9	95
383	Type 2 Diabetes Variants Disrupt Function of SLC16A11 through Two Distinct Mechanisms. <i>Cell</i> , 2017 , 170, 199-212.e20	56.2	94
382	Calcium intake is associated with adiposity in Black and White men and White women of the HERITAGE Family Study. <i>Journal of Nutrition</i> , 2004 , 134, 1772-8	4.1	93
381	Common breast cancer susceptibility variants in LSP1 and RAD51L1 are associated with mammographic density measures that predict breast cancer risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012 , 21, 1156-66	4	92
380	Melanocortin-4 receptor gene and physical activity in the QuBec Family Study. <i>International Journal of Obesity</i> , 2005 , 29, 420-8	5.5	92
379	Advances in exercise, fitness, and performance genomics. <i>Medicine and Science in Sports and Exercise</i> , 2010 , 42, 835-46	1.2	91
378	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	6	90
377	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 2017 , 8, 80	17.4	88

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376	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. <i>Cell</i> , 2020 , 182, 1198-1213.e14	56.2	88
375	Comment on "A common genetic variant is associated with adult and childhood obesity". <i>Science</i> , 2007 , 315, 187; author reply 187	33.3	87
374	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. Journal of the American College of Cardiology, 2019 , 73, 58-66	15.1	86
373	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. <i>Hypertension</i> , 2017 ,	8.5	85
372	Genome-wide association study identifies multiple loci associated with both mammographic density and breast cancer risk. <i>Nature Communications</i> , 2014 , 5, 5303	17.4	84
371	Association of genetic Loci with glucose levels in childhood and adolescence: a meta-analysis of over 6,000 children. <i>Diabetes</i> , 2011 , 60, 1805-12	0.9	83
370	Anthropometry, carbohydrate and lipid metabolism in the East Flanders Prospective Twin Survey: heritabilities. <i>Diabetologia</i> , 2007 , 50, 2107-16	10.3	83
369	Recovery of trait heritability from whole genome sequence data		83
368	Pleiotropic genes for metabolic syndrome and inflammation. <i>Molecular Genetics and Metabolism</i> , 2014 , 112, 317-38	3.7	81
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365	Genetic and environmental influences on height from infancy to early adulthood: An individual-based pooled analysis of 45 twin cohorts. <i>Scientific Reports</i> , 2016 , 6, 28496	4.9	80
364	Gene-age interactions in blood pressure regulation: a large-scale investigation with the CHARGE, Global BPgen, and ICBP Consortia. <i>American Journal of Human Genetics</i> , 2014 , 95, 24-38	11	80
363	Association between birth weight and visceral fat in adults. <i>American Journal of Clinical Nutrition</i> , 2010 , 92, 347-52	7	75
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360	Genomewide meta-analysis identifies loci associated with IGF-I and IGFBP-3 levels with impact on age-related traits. <i>Aging Cell</i> , 2016 , 15, 811-24	9.9	71
359	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. <i>Scientific Reports</i> , 2017 , 7, 45040	4.9	70

358	NIH working group report-using genomic information to guide weight management: From universal to precision treatment. <i>Obesity</i> , 2016 , 24, 14-22	8	70
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356	The ADRB3 Trp64Arg variant and BMI: a meta-analysis of 44 833 individuals. <i>International Journal of Obesity</i> , 2008 , 32, 1240-9	5.5	69
355	Gene dietary pattern interactions in obesity: analysis of up to 68 317 adults of European ancestry. <i>Human Molecular Genetics</i> , 2015 , 24, 4728-38	5.6	68
354	Length of gestation and birthweight in dizygotic twins. <i>Lancet, The</i> , 2001 , 358, 560-1	40	68
353	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program		68
352	Associations between common variants in GC and DHCR7/NADSYN1 and vitamin D concentration in Chinese Hans. <i>Human Genetics</i> , 2012 , 131, 505-12	6.3	67
351	Progress in the genetics of common obesity and type 2 diabetes. <i>Expert Reviews in Molecular Medicine</i> , 2010 , 12, e7	6.7	67
350	Birth weight and blood pressure in young adults: a prospective twin study. <i>Circulation</i> , 2001 , 104, 1633-	-8 16.7	67
349	Dietary Intake, FTO Genetic Variants, and Adiposity: A Combined Analysis of Over 16,000 Children and Adolescents. <i>Diabetes</i> , 2015 , 64, 2467-76	0.9	66
348	The genetic epidemiology of melanocortin 4 receptor variants. <i>European Journal of Pharmacology</i> , 2011 , 660, 156-64	5.3	65
347	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. <i>American Journal of Human Genetics</i> , 2016 , 99, 40-55	11	61
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345	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019 , 51, 636-648	36.3	59
344	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018 , 102, 375-400	11	59
343	Common variants in or near FGF5, CYP17A1 and MTHFR genes are associated with blood pressure and hypertension in Chinese Hans. <i>Journal of Hypertension</i> , 2011 , 29, 70-5	1.9	59
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341	Association of variants in the PCSK1 gene with obesity in the EPIC-Norfolk study. <i>Human Molecular Genetics</i> , 2009 , 18, 3496-501	5.6	58

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339	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. <i>PLoS Genetics</i> , 2017 , 13, e1006728	6	58
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330	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. <i>American Journal of Human Genetics</i> , 2019 , 104, 112-138	11	54
329	Evaluating drug targets through human loss-of-function genetic variation. <i>Nature</i> , 2020 , 581, 459-464	50.4	53
328	Genome-wide Study of Atrial Fibrillation Identifies Seven Risk Loci and Highlights Biological Pathways and Regulatory Elements Involved in Cardiac Development. <i>American Journal of Human Genetics</i> , 2018 , 102, 103-115	11	53
327	Genome-wide association study of height-adjusted BMI in childhood identifies functional variant in ADCY3. <i>Obesity</i> , 2014 , 22, 2252-9	8	53
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317	Genetic predisposition to obesity leads to increased risk of type 2 diabetes. <i>Diabetologia</i> , 2011 , 54, 776	-82).3	49
316	The CODATwins Project: The Cohort Description of Collaborative Project of Development of Anthropometrical Measures in Twins to Study Macro-Environmental Variation in Genetic and Environmental Effects on Anthropometric Traits. <i>Twin Research and Human Genetics</i> , 2015 , 18, 348-60	2.2	48
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307	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016 , 7, 13357	17.4	46
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298	Advances in exercise, fitness, and performance genomics in 2012. <i>Medicine and Science in Sports and Exercise</i> , 2013 , 45, 824-31	1.2	44	
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293	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. <i>American Journal of Human Genetics</i> , 2016 , 99, 22-39	11	42	
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280	Strategies for Enriching Variant Coverage in Candidate Disease Loci on a Multiethnic Genotyping Array. <i>PLoS ONE</i> , 2016 , 11, e0167758	3.7	39
279	Two ethnic-specific polymorphisms in the human Agouti-related protein gene are associated with macronutrient intake. <i>American Journal of Clinical Nutrition</i> , 2005 , 82, 1097-101	7	38
278	A genetic study of anteroposterior and vertical facial proportions using model-fitting. <i>Angle Orthodontist</i> , 1998 , 68, 467-70	2.6	38
277	Genome-wide association study of red blood cell traits in Hispanics/Latinos: The Hispanic Community Health Study/Study of Latinos. <i>PLoS Genetics</i> , 2017 , 13, e1006760	6	38
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275	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	3- 9 7	36
274	Advances in Exercise, Fitness, and Performance Genomics in 2015. <i>Medicine and Science in Sports and Exercise</i> , 2016 , 48, 1906-16	1.2	36
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263	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, 1254-60	7	32	
262	Birth weight and creatinine clearance in young adult twins: influence of genetic, prenatal, and maternal factors. <i>Journal of the American Society of Nephrology: JASN</i> , 2005 , 16, 2471-6	12.7	32	
261	Metabolic consequences of obesity and type 2 diabetes: Balancing genes and environment for personalized care. <i>Cell</i> , 2021 , 184, 1530-1544	56.2	32	
260	Association of Genetic Variants With Primary Open-Angle Glaucoma Among Individuals With African Ancestry. <i>JAMA - Journal of the American Medical Association</i> , 2019 , 322, 1682-1691	27.4	31	
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255	Associations of genetic risk score with obesity and related traits and the modifying effect of physical activity in a Chinese Han population. <i>PLoS ONE</i> , 2014 , 9, e91442	3.7	30	
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245	15 years of genome-wide association studies and no signs of slowing down. <i>Nature Communications</i> , 2020 , 11, 5900	17.4	26
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243	Association of current and former smoking with body mass index: A study of smoking discordant twin pairs from 21 twin cohorts. <i>PLoS ONE</i> , 2018 , 13, e0200140	3.7	25
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241	Pleiotropic effects of obesity-susceptibility loci on metabolic traits: a meta-analysis of up to 37,874 individuals. <i>Diabetologia</i> , 2013 , 56, 2134-46	10.3	25
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235	Lamin A/C polymorphisms, type 2 diabetes, and the metabolic syndrome: case-control and quantitative trait studies. <i>Diabetes</i> , 2007 , 56, 884-9	0.9	24
234	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021 ,	50.4	24
233	Acute Kidney Injury in Hospitalized Patients with COVID-19 2020 ,		24

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231	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	5.6	23	
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229	Blood pressure in young adulthood and residential greenness in the early-life environment of twins. <i>Environmental Health</i> , 2017 , 16, 53	6	22	
228	Fine-mapping of lipid regions in global populations discovers ethnic-specific signals and refines previously identified lipid loci. <i>Human Molecular Genetics</i> , 2016 , 25, 5500-5512	5.6	22	
227	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017 , 4, 170179	8.2	22	
226	No interactions between previously associated 2-hour glucose gene variants and physical activity or BMI on 2-hour glucose levels. <i>Diabetes</i> , 2012 , 61, 1291-6	0.9	21	
225	Evidence of genetic predisposition for metabolically healthy obesity and metabolically obese normal weight. <i>Physiological Genomics</i> , 2018 , 50, 169-178	3.6	20	
224	Zygosity Differences in Height and Body Mass Index of Twins From Infancy to Old Age: A Study of the CODATwins Project. <i>Twin Research and Human Genetics</i> , 2015 , 18, 557-70	2.2	20	
223	Advances in exercise, fitness, and performance genomics in 2013. <i>Medicine and Science in Sports and Exercise</i> , 2014 , 46, 851-9	1.2	20	
222	Associations between glucose tolerance, insulin sensitivity and insulin secretion phenotypes and polymorphisms in adiponectin and adiponectin receptor genes in the Quebec Family Study. <i>Diabetic Medicine</i> , 2008 , 25, 400-6	3.5	20	
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217	A joint view on genetic variants for adiposity differentiates subtypes with distinct metabolic implications. <i>Nature Communications</i> , 2018 , 9, 1946	17.4	20	
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215	Influence of dietary protein intake and glycemic index on the association between TCF7L2 HapA and weight gain. <i>American Journal of Clinical Nutrition</i> , 2012 , 95, 1468-76	7	19	

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213	Genetic and environmental variation in educational attainment: an individual-based analysis of 28 twin cohorts. <i>Scientific Reports</i> , 2020 , 10, 12681	4.9	19
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211	Mendelian randomisation analyses find pulmonary factors mediate the effect of height on coronary artery disease. <i>Communications Biology</i> , 2019 , 2, 119	6.7	18
210	Transethnic Evaluation Identifies Low-Frequency Loci Associated With 25-Hydroxyvitamin D Concentrations. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018 , 103, 1380-1392	5.6	18
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204	Fine-mapping of an expanded set of type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps		18
203	A multilevel linear mixed model of the association between candidate genes and weight and body mass index using the Framingham longitudinal family data. <i>BMC Proceedings</i> , 2009 , 3 Suppl 7, S115	2.3	17
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190	The influence of maternal BMI and age in twin pregnancies on insulin resistance in the offspring. <i>Diabetes Care</i> , 2002 , 25, 2191-6	14.6	16
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188	Genome-wide discovery of genetic loci that uncouple excess adiposity from its comorbidities. <i>Nature Metabolism</i> , 2021 , 3, 228-243	14.6	16
187	One size does not fit all. Genomics differentiates among anorexia nervosa, bulimia nervosa, and binge-eating disorder. <i>International Journal of Eating Disorders</i> , 2021 , 54, 785-793	6.3	16
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147	Genetic and environmental causes of tracking in explosive strength during adolescence. <i>Behavior Genetics</i> , 2005 , 35, 551-63	3.2	10
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120	Kidney disease genetic risk variants alter lysosomal beta-mannosidase () expression and disease severity. <i>Science Translational Medicine</i> , 2021 , 13,	17.5	7	
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117	Clonal hematopoiesis in sickle cell disease. <i>Blood</i> , 2021 , 138, 2148-2152	2.2	7	
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103	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data <i>Nature Genetics</i> , 2022 ,	36.3	6
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100	Modelling bivariate ordinal responses smoothly with examples from ophthalmology and genetics. <i>Statistics in Medicine</i> , 2001 , 20, 1825-42	2.3	5
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98	Characterising the loss-of-function impact of 5 lintranslated region variants in whole genome sequence data from 15,708 individuals		5
97	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. <i>Nature Communications</i> , 2021 , 12, 2182	17.4	5
96	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2021 , 108, 874-893	11	5
95	Estimating the causal effect of BMI on mortality risk in people with heart disease, diabetes and cancer using Mendelian randomization. <i>International Journal of Cardiology</i> , 2021 , 330, 214-220	3.2	5
94	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. <i>Nature Communications</i> , 2021 , 12, 3505	17.4	5
93	Host genetic effects in pneumonia. American Journal of Human Genetics, 2021, 108, 194-201	11	5
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91	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. <i>PLoS ONE</i> , 2020 , 15, e0230	08.1/5	4
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89	Theoretical underpinning for the use of twin studies in life course epidemiology 2009 , 57-84		4

88	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes		4
87	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4
86	Tissue-Specific Alteration of Metabolic Pathways Influences Glycemic Regulation		4
85	Genome-wide polygenic risk score for retinopathy of type 2 diabetes. <i>Human Molecular Genetics</i> , 2021 , 30, 952-960	5.6	4
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79	Population-Based Penetrance of Deleterious Clinical Variants <i>JAMA - Journal of the American Medical Association</i> , 2022 , 327, 350-359	27.4	3
78	The Polygenic and Monogenic Basis of Blood Traits and Diseases		3
77	Causal associations between urinary sodium with body mass, shape and composition: a Mendelian randomization study. <i>Scientific Reports</i> , 2020 , 10, 17475	4.9	3
76	Stratification of Type 2 Diabetes by Age of Diagnosis in the UK Biobank Reveals Subgroup-Specific Genetic Associations and Causal Risk Profiles. <i>Diabetes</i> , 2021 , 70, 1816-1825	0.9	3
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73	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential <i>Science Advances</i> , 2022 , 8, eabl6579	14.3	3
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65	MC4R marker associated with stature in children and young adults: a longitudinal study. <i>Journal of Pediatric Endocrinology and Metabolism</i> , 2005 , 18, 859-63	1.6	2
64	Retrospective Determination of Chorion Type in Twins Using a Simple Questionnaire		2
63	Whole-Genome Sequencing Association Analyses of Stroke and Its Subtypes in Ancestrally Diverse Populations From Trans-Omics for Precision Medicine Project. <i>Stroke</i> , 2021 , STROKEAHA120031792	6.7	2
62	Composite trait Mendelian Randomization reveals distinct metabolic and lifestyle consequences of differences in body shape		2
61	Rare coding variants in 35 genes associate with circulating lipid levels 🗈 multi-ancestry analysis of 170,000 exomes		2
60	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		2
59	Serum gamma-glutamyl transferase, a marker of alcohol intake, is associated with telomere length and cardiometabolic risk in young adulthood. <i>Scientific Reports</i> , 2021 , 11, 12407	4.9	2
58	Whole genome sequence analysis of platelet traits in the NHLBI trans-omics for precision medicine initiative. <i>Human Molecular Genetics</i> , 2021 ,	5.6	2
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55	Gestation and Birthweight in Dizygotic Twins: Girls Call the Tune. <i>Twin Research and Human Genetics</i> , 2007 , 10, 6-7	2.2	1
54	Gestation and birthweight in dizygotic twins. <i>Lancet, The</i> , 2002 , 359, 172	40	1
53	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed <i>Cell Genomics</i> , 2022 , 2, 100084-100084		1

52	Multi-ethnic GWAS and fine-mapping of glycaemic traits identify novel loci in the PAGE Study <i>Diabetologia</i> , 2021 , 65, 477	10.3	1
51	APOL1 renal risk variants are associated with obesity and body composition in African ancestry adults: An observational genotype-phenotype association study. <i>Medicine (United States)</i> , 2021 , 100, e27785	1.8	1
50	Novel genetic determinants of telomere length from a trans-ethnic analysis of 109,122 whole genome sequences in TOPMed		1
49	Novel blood pressure locus and gene discovery using GWAS and expression datasets from blood and the kidney		1
48	One size does not fit all. Genomics differentiates among binge-eating disorder, bulimia nervosa, and anorexia nervosa		1
47	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes		1
46	Whole genome sequencing association analysis of quantitative red blood cell phenotypes: the NHLBI TOPMed program		1
45	Meta-analysis of genome-wide association studies for body fat distribution in 694,649 individuals of European ancestry		1
44	Multi-ancestry analysis of gene-sleep interactions in 126,926 individuals identifies multiple novel blood lipid loci that contribute to our understanding of sleep-associated adverse blood lipid profile		1
43	Association of Genetic Risk of Obesity with Postoperative Complications Using Mendelian Randomization. <i>World Journal of Surgery</i> , 2020 , 44, 84-94	3.3	1
42	Implementing genomic screening in diverse populations		1
41	The Promise of Selecting Individuals from the Extremes of Exposure in the Analysis of Gene-Physical Activity Interactions. <i>Human Heredity</i> , 2018 , 83, 315-332	1.1	1
40	Composite trait Mendelian randomization reveals distinct metabolic and lifestyle consequences of differences in body shape. <i>Communications Biology</i> , 2021 , 4, 1064	6.7	1
39	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2021 , 108, 1836-1851	11	1
38	Eating disorder symptoms and their associations with anthropometric and psychiatric polygenic scores European Eating Disorders Review, 2022,	5.3	1
37	Predicted gene expression in ancestrally diverse populations leads to discovery of susceptibility loci for lifestyle and cardiometabolic traits <i>American Journal of Human Genetics</i> , 2022 ,	11	1
36	Whole genome sequencing identifies common and rare structural variants contributing to hematologic traits in the NHLBI TOPMed program		1
35	Dysregulation of macrophage PEPD in obesity determines adipose tissue fibro-inflammation and insulin resistance <i>Nature Metabolism</i> , 2022 , 4, 476-494	14.6	1

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17	Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study 2020 , 16, e1008684		

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3	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose 2020 , 15, e0230815
2	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose 2020 , 15, e0230815
1	The Value of Rare Genetic Variation in the Prediction of Common Obesity in European Ancestry Populations <i>Frontiers in Endocrinology</i> , 2022 , 13, 863893