

Ruth J F Loos

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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

#	Paper	IF	Citations
537	Population-Based Penetrance of Deleterious Clinical Variants.. <i>JAMA - Journal of the American Medical Association</i> , 2022 , 327, 350-359	27.4	3
536	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed.. <i>Cell Genomics</i> , 2022 , 2, 100084-100084		1
535	The energy balance model of obesity: beyond calories in, calories out.. <i>American Journal of Clinical Nutrition</i> , 2022 ,	7	13
534	Eating disorder symptoms and their associations with anthropometric and psychiatric polygenic scores.. <i>European Eating Disorders Review</i> , 2022 ,	5.3	1
533	Rare coding variants in RCN3 are associated with blood pressure.. <i>BMC Genomics</i> , 2022 , 23, 148	4.5	
532	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data.. <i>Nature Genetics</i> , 2022 ,	36.3	6
531	Ancestral diversity improves discovery and fine-mapping of genetic loci for anthropometric traits-The Hispanic/Latino Anthropometry Consortium.. <i>Human Genetics and Genomics Advances</i> , 2022 , 3, 100099	0.8	0
530	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
529	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential.. <i>Science Advances</i> , 2022 , 8, eabl6579	14.3	3
528	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
527	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. <i>Nature Genetics</i> , 2022 ,	36.3	7
526	The Value of Rare Genetic Variation in the Prediction of Common Obesity in European Ancestry Populations.. <i>Frontiers in Endocrinology</i> , 2022 , 13, 863893	5.7	
525	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022 , 5,	6.7	1
524	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
523	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021 ,	50.4	24
522	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
521	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

520	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. <i>Nature Genetics</i> , 2021 , 53, 1504-1516	36.3	7
519	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
518	Genome-wide polygenic risk score for retinopathy of type 2 diabetes. <i>Human Molecular Genetics</i> , 2021 , 30, 952-960	5.6	4
517	Strategies to Understand the Weight-Reduced State: Genetics and Brain Imaging. <i>Obesity</i> , 2021 , 29 Suppl 1, S39-S50	8	0
516	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. <i>Nature Communications</i> , 2021 , 12, 2182	17.4	5
515	Toward a fine-scale population health monitoring system. <i>Cell</i> , 2021 , 184, 2068-2083.e11	56.2	17
514	Genetic discovery and risk characterization in type 2 diabetes across diverse populations. <i>Human Genetics and Genomics Advances</i> , 2021 , 2, 100029-100029	0.8	7
513	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
512	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
511	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
510	Genetic pleiotropy of ERCC6 loss-of-function and deleterious missense variants links retinal dystrophy, arrhythmia, and immunodeficiency in diverse ancestries. <i>Human Mutation</i> , 2021 , 42, 969-977	4.7	0
509	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021 , 53, 840-860	36.3	44
508	Genome sequencing unveils a regulatory landscape of platelet reactivity. <i>Nature Communications</i> , 2021 , 12, 3626	17.4	6
507	Variant-specific inflation factors for assessing population stratification at the phenotypic variance level. <i>Nature Communications</i> , 2021 , 12, 3506	17.4	
506	Multi-ethnic genome-wide association analyses of white blood cell and platelet traits in the Population Architecture using Genomics and Epidemiology (PAGE) study. <i>BMC Genomics</i> , 2021 , 22, 432	4.5	0
505	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. <i>Nature Communications</i> , 2021 , 12, 3505	17.4	5
504	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
503	Childhood overeating is associated with adverse cardiometabolic and inflammatory profiles in adolescence. <i>Scientific Reports</i> , 2021 , 11, 12478	4.9	3

502	Genome-wide association study identifies 48 common genetic variants associated with handedness. <i>Nature Human Behaviour</i> , 2021 , 5, 59-70	12.8	33
501	Host genetic effects in pneumonia. <i>American Journal of Human Genetics</i> , 2021 , 108, 194-201	11	5
500	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. <i>Kidney International</i> , 2021 , 99, 926-939	9.9	6
499	The genomics of childhood eating behaviours. <i>Nature Human Behaviour</i> , 2021 , 5, 625-630	12.8	0
498	Kidney disease genetic risk variants alter lysosomal beta-mannosidase () expression and disease severity. <i>Science Translational Medicine</i> , 2021 , 13,	17.5	7
497	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021 , 12, 24	17.4	30
496	Implementing genomic screening in diverse populations. <i>Genome Medicine</i> , 2021 , 13, 17	14.4	8
495	Genome-wide discovery of genetic loci that uncouple excess adiposity from its comorbidities. <i>Nature Metabolism</i> , 2021 , 3, 228-243	14.6	16
494	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
493	Copy Number Variant Analysis and Genome-wide Association Study Identify Loci with Large Effect for Vesicoureteral Reflux. <i>Journal of the American Society of Nephrology: JASN</i> , 2021 ,	12.7	5
492	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021 , 590, 290-299	50.4	268
491	Rare Coding Variants Associated With Electrocardiographic Intervals Identify Monogenic Arrhythmia Susceptibility Genes: A Multi-Ancestry Analysis. <i>Circulation Genomic and Precision Medicine</i> , 2021 , 14, e003300	5.2	0
490	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
489	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
488	The Genetic Architecture of Depression in Individuals of East Asian Ancestry: A Genome-Wide Association Study. <i>JAMA Psychiatry</i> , 2021 , 78, 1258-1269	14.5	7
487	Prognostic value of polygenic risk scores for adults with psychosis. <i>Nature Medicine</i> , 2021 , 27, 1576-1581	50.5	7
486	The genetics of obesity: from discovery to biology. <i>Nature Reviews Genetics</i> , 2021 ,	30.1	51
485	Clonal hematopoiesis in sickle cell disease. <i>Blood</i> , 2021 , 138, 2148-2152	2.2	7

484	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
483	Educational attainment of same-sex and opposite-sex dizygotic twins: An individual-level pooled study of 19 twin cohorts. <i>Hormones and Behavior</i> , 2021 , 136, 105054	3.7	
482	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. <i>PLoS ONE</i> , 2020 , 15, e0230815	3.5	4
481	Eating behavior trajectories in the first 10 years of life and their relationship with BMI. <i>International Journal of Obesity</i> , 2020 , 44, 1766-1775	5.5	13
480	Limitations of Contemporary Guidelines for Managing Patients at High Genetic Risk of Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2020 , 75, 2769-2780	15.1	33
479	Genetic and environmental influences on human height from infancy through adulthood at different levels of parental education. <i>Scientific Reports</i> , 2020 , 10, 7974	4.9	6
478	Evaluating drug targets through human loss-of-function genetic variation. <i>Nature</i> , 2020 , 581, 459-464	50.4	53
477	The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2020 , 581, 434-443	50.4	2278
476	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020 , 11, 2542	17.4	16
475	A structural variation reference for medical and population genetics. <i>Nature</i> , 2020 , 581, 444-451	50.4	223
474	Transcript expression-aware annotation improves rare variant interpretation. <i>Nature</i> , 2020 , 581, 452-458	50.4	55
473	The effect of LRRK2 loss-of-function variants in humans. <i>Nature Medicine</i> , 2020 , 26, 869-877	50.5	47
472	Ancestry-specific associations identified in genome-wide combined-phenotype study of red blood cell traits emphasize benefits of diversity in genomics. <i>BMC Genomics</i> , 2020 , 21, 228	4.5	8
471	A common variant in PNPLA3 is associated with age at diagnosis of NAFLD in patients from a multi-ethnic biobank. <i>Journal of Hepatology</i> , 2020 , 72, 1070-1081	13.4	14
470	The genetic architecture of membranous nephropathy and its potential to improve non-invasive diagnosis. <i>Nature Communications</i> , 2020 , 11, 1600	17.4	42
469	Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study. <i>PLoS Genetics</i> , 2020 , 16, e1008684	6	5
468	Polygenic Score for Body Mass Index Is Associated with Disordered Eating in a General Population Cohort. <i>Journal of Clinical Medicine</i> , 2020 , 9,	5.1	16
467	Acute Kidney Injury in Hospitalized Patients with COVID-19 2020 ,		24

466	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
465	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020 , 182, 1214-1231.e11	56.2	96
464	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020 , 586, 763-768	50.4	127
463	The role of polygenic susceptibility to obesity among carriers of pathogenic mutations in MC4R in the UK Biobank population. <i>PLoS Medicine</i> , 2020 , 17, e1003196	11.6	17
462	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. <i>Nature Genetics</i> , 2020 , 52, 1314-1332	36.3	26
461	15 years of genome-wide association studies and no signs of slowing down. <i>Nature Communications</i> , 2020 , 11, 5900	17.4	26
460	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
459	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
458	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. <i>Diabetes</i> , 2020 , 69, 2806-2818	0.9	10
457	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. <i>Nature Genetics</i> , 2020 , 52, 969-983	36.3	33
456	Striatal Rgs4 regulates feeding and susceptibility to diet-induced obesity. <i>Molecular Psychiatry</i> , 2020 , 25, 2058-2069	15.1	10
455	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
454	A longitudinal study of eating behaviours in childhood and later eating disorder behaviours and diagnoses. <i>British Journal of Psychiatry</i> , 2020 , 216, 113-119	5.4	33
453	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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447	The role of polygenic susceptibility to obesity among carriers of pathogenic mutations in MC4R in the UK Biobank population 2020 , 17, e1003196		
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442	The role of polygenic susceptibility to obesity among carriers of pathogenic mutations in MC4R in the UK Biobank population 2020 , 17, e1003196		
441	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose 2020 , 15, e0230815		
440	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose 2020 , 15, e0230815		
439	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose 2020 , 15, e0230815		
438	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose 2020 , 15, e0230815		
437	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019 , 51, 1459-1474	36.3	122
436	Associations between Blood Metabolic Profile at 7 Years Old and Eating Disorders in Adolescence: Findings from the Avon Longitudinal Study of Parents and Children. <i>Metabolites</i> , 2019 , 9,	5.6	1
435	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019 , 10, 376	17.4	41
434	Genetic analyses of diverse populations improves discovery for complex traits. <i>Nature</i> , 2019 , 570, 514-518	50.4	291
433	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. <i>American Journal of Human Genetics</i> , 2019 , 105, 15-28	11	12
432	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
431	The role of country of birth, and genetic and self-identified ancestry, in obesity susceptibility among African and Hispanic Americans. <i>American Journal of Clinical Nutrition</i> , 2019 , 110, 16-23	7	2

430	Genetics of Chronic Kidney Disease Stages Across Ancestries: The PAGE Study. <i>Frontiers in Genetics</i> , 2019 , 10, 494	4.5	14
429	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019 , 570, 71-76	50.4	129
428	Dysregulation of a long noncoding RNA reduces leptin leading to a leptin-responsive form of obesity. <i>Nature Medicine</i> , 2019 , 25, 507-516	50.5	49
427	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. <i>Human Molecular Genetics</i> , 2019 , 28, 2615-2633	5.6	14
426	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
425	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
424	Parental Education and Genetics of BMI from Infancy to Old Age: A Pooled Analysis of 29 Twin Cohorts. <i>Obesity</i> , 2019 , 27, 855-865	8	11
423	A Genome-Wide Association Study Identifies Blood Disorder-Related Variants Influencing Hemoglobin A With Implications for Glycemic Status in U.S. Hispanics/Latinos. <i>Diabetes Care</i> , 2019 , 42, 1784-1791	14.6	6
422	The CODATwins Project: The Current Status and Recent Findings of Collaborative Project of Development of Anthropometrical Measures in Twins. <i>Twin Research and Human Genetics</i> , 2019 , 22, 800-808	3.2	14
421	Augmented intelligence with natural language processing applied to electronic health records for identifying patients with non-alcoholic fatty liver disease at risk for disease progression. <i>International Journal of Medical Informatics</i> , 2019 , 129, 334-341	5.3	15
420	Disentangling the genetics of lean mass. <i>American Journal of Clinical Nutrition</i> , 2019 , 109, 276-287	7	24
419	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019 , 10, 4957	17.4	40
418	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
417	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. <i>Nature Communications</i> , 2019 , 10, 5121	17.4	31
416	Exome sequencing reveals a high prevalence of BRCA1 and BRCA2 founder variants in a diverse population-based biobank. <i>Genome Medicine</i> , 2019 , 12, 2	14.4	25
415	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019 , 51, 452-469	36.3	44
414	F54POLYGENIC RISK SCORE FOR OBESITY IS ASSOCIATED WITH EATING BEHAVIORS OF TEENAGERS IN THE AVON LONGITUDINAL STUDY OF PARENTS AND CHILDREN (ALSPAC). <i>European Neuropsychopharmacology</i> , 2019 , 29, S1138-S1139	1.2	
413	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

412	Association of the V122I Hereditary Transthyretin Amyloidosis Genetic Variant With Heart Failure Among Individuals of African or Hispanic/Latino Ancestry. <i>JAMA - Journal of the American Medical Association</i> , 2019 , 322, 2191-2202	27.4	45
411	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
410	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. <i>Nature Communications</i> , 2019 , 10, 29	17.4	51
409	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. <i>Journal of the American College of Cardiology</i> , 2019 , 73, 58-66	15.1	86
408	Patient Adipose Stem Cell-Derived Adipocytes Reveal Genetic Variation that Predicts Antidiabetic Drug Response. <i>Cell Stem Cell</i> , 2019 , 24, 299-308.e6	18	20
407	Whole genome sequence association with E-selectin levels reveals loss-of-function variant in African Americans. <i>Human Molecular Genetics</i> , 2019 , 28, 515-523	5.6	10
406	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
405	Combined linkage and association analysis identifies rare and low frequency variants for blood pressure at 1q31. <i>European Journal of Human Genetics</i> , 2019 , 27, 269-277	5.3	3
404	The genetics of adiposity. <i>Current Opinion in Genetics and Development</i> , 2018 , 50, 86-95	4.9	57
403	Birth size and gestational age in opposite-sex twins as compared to same-sex twins: An individual-based pooled analysis of 21 cohorts. <i>Scientific Reports</i> , 2018 , 8, 6300	4.9	16
402	Associations between birth size and later height from infancy through adulthood: An individual based pooled analysis of 28 twin cohorts participating in the CODATwins project. <i>Early Human Development</i> , 2018 , 120, 53-60	2.2	8
401	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
400	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
399	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
398	Trans-ethnic analysis of metabochip data identifies two new loci associated with BMI. <i>International Journal of Obesity</i> , 2018 , 42, 384-390	5.5	7
397	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
396	Genome-Wide Association Study of Heavy Smoking and Daily/Nondaily Smoking in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). <i>Nicotine and Tobacco Research</i> , 2018 , 20, 448-457	4.9	15
395	Evidence of genetic predisposition for metabolically healthy obesity and metabolically obese normal weight. <i>Physiological Genomics</i> , 2018 , 50, 169-178	3.6	20

394	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. <i>Nature Communications</i> , 2018 , 9, 2904	17.4	39
393	The genetic underpinnings of variation in ages at menarche and natural menopause among women from the multi-ethnic Population Architecture using Genomics and Epidemiology (PAGE) Study: A trans-ethnic meta-analysis. <i>PLoS ONE</i> , 2018 , 13, e0200486	3.7	14
392	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
391	GWAS for BMI: a treasure trove of fundamental insights into the genetic basis of obesity. <i>International Journal of Obesity</i> , 2018 , 42, 1524-1531	5.5	52
390	Generalization and fine mapping of red blood cell trait genetic associations to multi-ethnic populations: The PAGE Study. <i>American Journal of Hematology</i> , 2018 , 93, 1061	7.1	4
389	Addendum: A joint view on genetic variants for adiposity differentiates subtypes with distinct metabolic implications. <i>Nature Communications</i> , 2018 , 9, 2861	17.4	1
388	Genes that make you fat, but keep you healthy. <i>Journal of Internal Medicine</i> , 2018 , 284, 450-463	10.8	25
387	Association between birth weight and educational attainment: an individual-based pooled analysis of nine twin cohorts. <i>Journal of Epidemiology and Community Health</i> , 2018 , 72, 832-837	5.1	2
386	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018 , 50, 1225-1233	36.3	277
385	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
384	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
383	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
382	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
381	Complex patterns of direct and indirect association between the transcription Factor-7 like 2 gene, body mass index and type 2 diabetes diagnosis in adulthood in the Hispanic Community Health Study/Study of Latinos. <i>BMC Obesity</i> , 2018 , 5, 26	3.6	4
380	Genome-wide association study of primary open-angle glaucoma in continental and admixed African populations. <i>Human Genetics</i> , 2018 , 137, 847-862	6.3	25
379	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
378	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
377	A common loss-of-function variant is associated with lower vitamin B concentration in African Americans. <i>Blood</i> , 2018 , 131, 2859-2863	2.2	4

376	Genetic and environmental factors affecting birth size variation: a pooled individual-based analysis of secular trends and global geographical differences using 26 twin cohorts. <i>International Journal of Epidemiology</i> , 2018 , 47, 1195-1206	7.8	12
375	A joint view on genetic variants for adiposity differentiates subtypes with distinct metabolic implications. <i>Nature Communications</i> , 2018 , 9, 1946	17.4	20
374	Adiposity-Mortality Relationships in Type 2 Diabetes, Coronary Heart Disease, and Cancer Subgroups in the UK Biobank, and Their Modification by Smoking. <i>Diabetes Care</i> , 2018 , 41, 1878-1886	14.6	20
373	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
372	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017 , 542, 186-190	50.4	412
371	Predicting Polygenic Obesity Using Genetic Information. <i>Cell Metabolism</i> , 2017 , 25, 535-543	24.6	57
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38	Length of gestation and birthweight in dizygotic twins. <i>Lancet, The</i> , 2001 , 358, 560-1	40	68
37	The Influence of Zygosity and Chorion Type on Fat Distribution in Young Adult Twins Consequences for Twin Studies. <i>Twin Research and Human Genetics</i> , 2001 , 4, 356-364		16
36	The influence of zygosity and chorion type on fat distribution in young adult twins consequences for twin studies. <i>Twin Research and Human Genetics</i> , 2001 , 4, 356-64		18
35	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

34	A quantitative study of unpaid caregiving in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2000 , 6, 274-9	5	54
33	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
32	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
31	A genetic study of anteroposterior and vertical facial proportions using model-fitting. <i>Angle Orthodontist</i> , 1998 , 68, 467-70	2.6	38
30	The genetic contribution to dental maturation. <i>Journal of Dental Research</i> , 1997 , 76, 1337-40	8.1	107
29	Gender-specific regional changes in genetic structure of muscularity in early adolescence. <i>Journal of Applied Physiology</i> , 1997 , 82, 1802-10	3.7	40
28	Retrospective Determination of Chorion Type in Twins Using a Simple Questionnaire		2
27	Global Biobank Meta-analysis Initiative: powering genetic discovery across human diseases		6
26	Novel genetic determinants of telomere length from a trans-ethnic analysis of 109,122 whole genome sequences in TOPMed		1
25	Composite trait Mendelian Randomization reveals distinct metabolic and lifestyle consequences of differences in body shape		2
24	Genome-wide association study of susceptibility to hospitalised respiratory infections. <i>Wellcome Open Research</i> , 6 , 290	4.8	0
23	Novel blood pressure locus and gene discovery using GWAS and expression datasets from blood and the kidney		1
22	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes		4
21	The PAGE Study: How Genetic Diversity Improves Our Understanding of the Architecture of Complex Traits		14
20	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4
19	The Polygenic and Monogenic Basis of Blood Traits and Diseases		3
18	One size does not fit all. Genomics differentiates among binge-eating disorder, bulimia nervosa, and anorexia nervosa		1
17	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes		1

16	Whole genome sequencing association analysis of quantitative red blood cell phenotypes: the NHLBI TOPMed program	1
15	Rare coding variants in 35 genes associate with circulating lipid levels in a multi-ancestry analysis of 170,000 exomes	2
14	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
13	Genomic risk prediction of coronary artery disease in nearly 500,000 adults: implications for early screening and primary prevention	17
12	Meta-analysis of genome-wide association studies for body fat distribution in 694,649 individuals of European ancestry	1
11	Characterising the loss-of-function impact of 5' untranslated region variants in whole genome sequence data from 15,708 individuals	5
10	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
9	Human loss-of-function variants suggest that partial LRRK2 inhibition is a safe therapeutic strategy for Parkinson's disease	7
8	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program	68
7	Recovery of trait heritability from whole genome sequence data	83
6	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
5	Towards a fine-scale population health monitoring system	10
4	Inherited Causes of Clonal Hematopoiesis of Indeterminate Potential in TOPMed Whole Genomes	11
3	Tissue-Specific Alteration of Metabolic Pathways Influences Glycemic Regulation	4
2	Implementing genomic screening in diverse populations	1
1	Whole genome sequencing identifies common and rare structural variants contributing to hematologic traits in the NHLBI TOPMed program	1