Nicholas J Timpson

List of Publications by Citations

394 papers	48,976 citations	99 h-index	217 g-index
459 ext. papers	60,974 ext. citations	11.9 avg, IF	6.57 L-index

#	Paper	IF	Citations
394	A common variant in the FTO gene is associated with body mass index and predisposes to childhood and adult obesity. *Science*, **2007**, 316, 889-94	33.3	3294
393	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics*, **2010**, 42, 937-48	36.3	2267
392	Replication of genome-wide association signals in UK samples reveals risk loci for type 2 diabetes. *Science*, **2007**, 316, 1336-41	33.3	1823
391	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. *Nature Genetics*, **2010**, 42, 105-16	36.3	1673
390	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. *Nature Genetics*, **2008**, 40, 638-45	36.3	1496
389	Mendelian randomization: using genes as instruments for making causal inferences in epidemiology. *Statistics in Medicine*, **2008**, 27, 1133-63	2.3	1496
388	A reference panel of 64,976 haplotypes for genotype imputation. *Nature Genetics*, **2016**, 48, 1279-83	36.3	1447
387	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. *Nature Genetics*, **2009**, 41, 25-34	36.3	1368
386	Newly identified loci that influence lipid concentrations and risk of coronary artery disease. *Nature Genetics*, **2008**, 40, 161-9	36.3	1304
385	The MR-Base platform supports systematic causal inference across the human phenome. *ELife*, **2018**, 7,	8.9	1190
384	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. *Nature Genetics*, **2007**, 39, 1329-37	36.3	1130
383	Common variants near MC4R are associated with fat mass, weight and risk of obesity. *Nature Genetics*, **2008**, 40, 768-75	36.3	1048
382	Genome-wide association study identifies 74 loci associated with educational attainment. *Nature*, **2016**, 533, 539-42	50.4	850
381	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. *Nature Genetics*, **2019**, 51, 63-75	36.3	826
380	The UK10K project identifies rare variants in health and disease. *Nature*, **2015**, 526, 82-90	50.4	776
379	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. *Nature Genetics*, **2010**, 42, 949-60	36.3	724
378	The interleukin-6 receptor as a target for prevention of coronary heart disease: a mendelian randomisation analysis. *Lancet, The*, **2012**, 379, 1214-24	40	658

377	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. *Nature Genetics*, **2012**, 44, 991-1005	36.3	621
376	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. *Nature Genetics*, **2016**, 48, 624-33	36.3	602
375	GWAS of 126,559 individuals identifies genetic variants associated with educational attainment. *Science*, **2013**, 340, 1467-71	33.3	563
374	Association between C reactive protein and coronary heart disease: mendelian randomisation analysis based on individual participant data. *BMJ, The*, **2011**, 342, d548	5.9	422
373	Using published data in Mendelian randomization: a blueprint for efficient identification of causal risk factors. *European Journal of Epidemiology*, **2015**, 30, 543-52	12.1	421
372	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. *Lancet, The*, **2015**, 385, 351-61	40	409
371	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. *Nature*, **2014**, 514, 92-97	50.4	401
370	Genome-wide association scan meta-analysis identifies three Loci influencing adiposity and fat distribution. *PLoS Genetics*, **2009**, 5, e1000508	6	393
369	Physical activity attenuates the influence of FTO variants on obesity risk: a meta-analysis of 218,166 adults and 19,268 children. *PLoS Medicine*, **2011**, 8, e1001116	11.6	379
368	A common variant of HMGA2 is associated with adult and childhood height in the general population. *Nature Genetics*, **2007**, 39, 1245-50	36.3	330
367	Novel loci for adiponectin levels and their influence on type 2 diabetes and metabolic traits: a multi-ethnic meta-analysis of 45,891 individuals. *PLoS Genetics*, **2012**, 8, e1002607	6	326
366	Common variants in the GDF5-UQCC region are associated with variation in human height. *Nature Genetics*, **2008**, 40, 198-203	36.3	315
365	Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. *Nature Genetics*, **2013**, 45, 314-8	36.3	314
364	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. *Nature*, **2015**, 526, 112-7	50.4	308
363	Clustered environments and randomized genes: a fundamental distinction between conventional and genetic epidemiology. *PLoS Medicine*, **2007**, 4, e352	11.6	297
362	A genome-wide association meta-analysis identifies new childhood obesity loci. *Nature Genetics*, **2012**, 44, 526-31	36.3	292
361	Using multiple genetic variants as instrumental variables for modifiable risk factors. *Statistical Methods in Medical Research*, **2012**, 21, 223-42	2.3	288
360	C-reactive protein and its role in metabolic syndrome: mendelian randomisation study. *Lancet, The*, **2005**, 366, 1954-9	40	266

359	Genome-wide associations for birth weight and correlations with adult disease. *Nature*, **2016**, 538, 248-252	36.4	266
358	Polygenic Prediction of Weight and Obesity Trajectories from Birth to Adulthood. *Cell*, **2019**, 177, 587-596.e9	36.2	265
357	Common variation in the FTO gene alters diabetes-related metabolic traits to the extent expected given its effect on BMI. *Diabetes*, **2008**, 57, 1419-26	0.9	260
356	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. *Nature Genetics*, **2019**, 51, 245-257	36.3	259
355	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. *Nature Genetics*, **2017**, 49, 834-841	36.3	257
354	Prenatal exposure to maternal smoking and offspring DNA methylation across the lifecourse: findings from the Avon Longitudinal Study of Parents and Children (ALSPAC). *Human Molecular Genetics*, **2015**, 24, 2201-17	5.6	256
353	Meta-analysis of genome-wide association studies identifies three new risk loci for atopic dermatitis. *Nature Genetics*, **2011**, 44, 187-92	36.3	244
352	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases: A Mendelian Randomization Study. *JAMA Oncology*, **2017**, 3, 636-651	13.4	236
351	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. *Nature Genetics*, **2013**, 45, 76-82	36.3	232
350	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. *JAMA Psychiatry*, **2015**, 72, 642-50	14.5	222
349	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics*, **2013**, 45, 621-31	36.3	219
348	Genetic architecture: the shape of the genetic contribution to human traits and disease. *Nature Reviews Genetics*, **2018**, 19, 110-124	30.1	219
347	The fat mass- and obesity-associated locus and dietary intake in children. *American Journal of Clinical Nutrition*, **2008**, 88, 971-8	7	213
346	The effect of elevated body mass index on ischemic heart disease risk: causal estimates from a Mendelian randomisation approach. *PLoS Medicine*, **2012**, 9, e1001212	11.6	204
345	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. *Human Molecular Genetics*, **2016**, 25, 389-403	5.6	202
344	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. *Nature Genetics*, **2016**, 48, 1462-1472	36.3	198
343	A road map for efficient and reliable human genome epidemiology. *Nature Genetics*, **2006**, 38, 3-5	36.3	198
342	WNT16 influences bone mineral density, cortical bone thickness, bone strength, and osteoporotic fracture risk. *PLoS Genetics*, **2012**, 8, e1002745	6	192

341	Meta-analysis of genome-wide association studies identifies ten loci influencing allergic sensitization. *Nature Genetics*, **2013**, 45, 902-906	36.3	191
340	A genome-wide association meta-analysis of self-reported allergy identifies shared and allergy-specific susceptibility loci. *Nature Genetics*, **2013**, 45, 907-11	36.3	191
339	Association of plasma uric acid with ischaemic heart disease and blood pressure: mendelian randomisation analysis of two large cohorts. *BMJ, The*, **2013**, 347, f4262	5.9	188
338	Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. *Nature Communications*, **2015**, 6, 8111	17.4	186
337	Variants in ADCY5 and near CCNL1 are associated with fetal growth and birth weight. *Nature Genetics*, **2010**, 42, 430-5	36.3	184
336	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. *Nature Genetics*, **2019**, 51, 804-814	36.3	181
335	Common genetic variants associated with cognitive performance identified using the proxy-phenotype method. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 13790-4	11.5	181
334	C-reactive protein levels and body mass index: elucidating direction of causation through reciprocal Mendelian randomization. *International Journal of Obesity*, **2011**, 35, 300-8	5.5	180
333	Association between genetic variants on chromosome 15q25 locus and objective measures of tobacco exposure. *Journal of the National Cancer Institute*, **2012**, 104, 740-8	9.7	178
332	Childhood intelligence is heritable, highly polygenic and associated with FNBP1L. *Molecular Psychiatry*, **2014**, 19, 253-8	15.1	171
331	The Avon Longitudinal Study of Parents and Children (ALSPAC): an update on the enrolled sample of index children in 2019. *Wellcome Open Research*, **2019**, 4, 51	4.8	163
330	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. *Nature Genetics*, **2019**, 51, 51-62	36.3	152
329	Does greater adiposity increase blood pressure and hypertension risk?: Mendelian randomization using the FTO/MC4R genotype. *Hypertension*, **2009**, 54, 84-90	8.5	151
328	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. *American Journal of Human Genetics*, **2018**, 103, 691-706	11	151
327	Genome-wide association study of three-dimensional facial morphology identifies a variant in PAX3 associated with nasion position. *American Journal of Human Genetics*, **2012**, 90, 478-85	11	142
326	Genetic markers of adult obesity risk are associated with greater early infancy weight gain and growth. *PLoS Medicine*, **2010**, 7, e1000284	11.6	142
325	Association between common variation at the FTO locus and changes in body mass index from infancy to late childhood: the complex nature of genetic association through growth and development. *PLoS Genetics*, **2011**, 7, e1001307	6	141
324	Exploring the developmental overnutrition hypothesis using parental-offspring associations and FTO as an instrumental variable. *PLoS Medicine*, **2008**, 5, e33	11.6	139

323	Genome-wide association and longitudinal analyses reveal genetic loci linking pubertal height growth, pubertal timing and childhood adiposity. *Human Molecular Genetics*, **2013**, 22, 2735-47	5.6	138
322	A genome-wide association search for type 2 diabetes genes in African Americans. *PLoS ONE*, **2012**, 7, e29202	3.7	138
321	Apparent latent structure within the UK Biobank sample has implications for epidemiological analysis. *Nature Communications*, **2019**, 10, 333	17.4	131
320	Genome sequencing elucidates Sardinian genetic architecture and augments association analyses for lipid and blood inflammatory markers. *Nature Genetics*, **2015**, 47, 1272-1281	36.3	129
319	A genome-wide association study reveals variants in ARL15 that influence adiponectin levels. *PLoS Genetics*, **2009**, 5, e1000768	6	129
318	Clear detection of ADIPOQ locus as the major gene for plasma adiponectin: results of genome-wide association analyses including 4659 European individuals. *Atherosclerosis*, **2010**, 208, 412-20	3.1	128
317	Variations in the G6PC2/ABCB11 genomic region are associated with fasting glucose levels. *Journal of Clinical Investigation*, **2008**, 118, 2620-8	15.9	127
316	Mental health before and during the COVID-19 pandemic in two longitudinal UK population cohorts. *British Journal of Psychiatry*, **2020**, 1-10	5.4	123
315	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. *Behavior Genetics*, **2016**, 46, 170-82	3.2	122
314	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	30.4	119
313	Meta-analysis of genome-wide scans for total body BMD in children and adults reveals allelic heterogeneity and age-specific effects at the WNT16 locus. *PLoS Genetics*, **2012**, 8, e1002718	6	118
312	Type 2 diabetes risk alleles are associated with reduced size at birth. *Diabetes*, **2009**, 58, 1428-33	0.9	117
311	Nine loci for ocular axial length identified through genome-wide association studies, including shared loci with refractive error. *American Journal of Human Genetics*, **2013**, 93, 264-77	11	116
310	Early Cannabis Use, Polygenic Risk Score for Schizophrenia and Brain Maturation in Adolescence. *JAMA Psychiatry*, **2015**, 72, 1002-11	14.5	115
309	Obesity and Multiple Sclerosis: A Mendelian Randomization Study. *PLoS Medicine*, **2016**, 13, e1002053	11.6	115
308	Inflammation, insulin resistance, and diabetes--Mendelian randomization using CRP haplotypes points upstream. *PLoS Medicine*, **2008**, 5, e155	11.6	114
307	Genetic determinants of height growth assessed longitudinally from infancy to adulthood in the northern Finland birth cohort 1966. *PLoS Genetics*, **2009**, 5, e1000409	6	113
306	Assessing causality in the association between child adiposity and physical activity levels: a Mendelian randomization analysis. *PLoS Medicine*, **2014**, 11, e1001618	11.6	112

305	Common variants in left/right asymmetry genes and pathways are associated with relative hand skill. *PLoS Genetics*, **2013**, 9, e1003751	6	112
304	A genome-wide approach to children's aggressive behavior: The EAGLE consortium. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2016**, 171, 562-72	3.5	111
303	The thermolabile variant of MTHFR is associated with depression in the British Women's Heart and Health Study and a meta-analysis. *Molecular Psychiatry*, **2006**, 11, 352-60	15.1	110
302	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. *Nature Communications*, **2016**, 7, 10494	17.4	107
301	Phenotypic dissection of bone mineral density reveals skeletal site specificity and facilitates the identification of novel loci in the genetic regulation of bone mass attainment. *PLoS Genetics*, **2014**, 10, e1004423	6	107
300	Common variants in the region around Osterix are associated with bone mineral density and growth in childhood. *Human Molecular Genetics*, **2009**, 18, 1510-7	5.6	107
299	Common variants at 6q22 and 17q21 are associated with intracranial volume. *Nature Genetics*, **2012** , 44, 539-44	36.3	104
298	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2011**, 88, 6-18	11	103
297	A common haplotype of the glucokinase gene alters fasting glucose and birth weight: association in six studies and population-genetics analyses. *American Journal of Human Genetics*, **2006**, 79, 991-1001	11	103
296	Adiposity-related heterogeneity in patterns of type 2 diabetes susceptibility observed in genome-wide association data. *Diabetes*, **2009**, 58, 505-10	0.9	98
295	Copy number variations and cognitive phenotypes in unselected populations. *JAMA - Journal of the American Medical Association*, **2015**, 313, 2044-54	27.4	96
294	BMI as a Modifiable Risk Factor for Type 2 Diabetes: Refining and Understanding Causal Estimates Using Mendelian Randomization. *Diabetes*, **2016**, 65, 3002-7	0.9	95
293	Common variants at 12q15 and 12q24 are associated with infant head circumference. *Nature Genetics*, **2012**, 44, 532-538	36.3	94
292	A genome-wide association study of body mass index across early life and childhood. *International Journal of Epidemiology*, **2015**, 44, 700-12	7.8	92
291	Genetic variants linked to education predict longevity. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 13366-13371	11.5	90
290	Genome-wide population-based association study of extremely overweight young adults--the GOYA study. *PLoS ONE*, **2011**, 6, e24303	3.7	90
289	Functional gene group analysis reveals a role of synaptic heterotrimeric G proteins in cognitive ability. *American Journal of Human Genetics*, **2010**, 86, 113-25	11	89
288	Remnant cholesterol, low-density lipoprotein cholesterol, and blood pressure as mediators from obesity to ischemic heart disease. *Circulation Research*, **2015**, 116, 665-73	15.7	87

287	Melanesian blond hair is caused by an amino acid change in TYRP1. *Science*, **2012**, 336, 554	33.3	85
286	Genetic variation at the SLC23A1 locus is associated with circulating concentrations of L-ascorbic acid (vitamin C): evidence from 5 independent studies with >15,000 participants. *American Journal of Clinical Nutrition*, **2010**, 92, 375-82	7	84
285	Association of genetic Loci with glucose levels in childhood and adolescence: a meta-analysis of over 6,000 children. *Diabetes*, **2011**, 60, 1805-12	0.9	83
284	(cg05575921) hypomethylation marks smoking behaviour, morbidity and mortality. *Thorax*, **2017**, 72, 646-653	7.3	82
283	Obesity and cancer: Mendelian randomization approach utilizing the FTO genotype. *International Journal of Epidemiology*, **2009**, 38, 971-5	7.8	82
282	A Genome-Wide Association Meta-Analysis of Attention-Deficit/Hyperactivity Disorder Symptoms in Population-Based Pediatric Cohorts. *Journal of the American Academy of Child and Adolescent Psychiatry*, **2016**, 55, 896-905.e6	7.2	80
281	Large-scale association analyses identify host factors influencing human gut microbiome composition. *Nature Genetics*, **2021**, 53, 156-165	36.3	80
280	Meta-analysis of gene-environment-wide association scans accounting for education level identifies additional loci for refractive error. *Nature Communications*, **2016**, 7, 11008	17.4	79
279	The association of C-reactive protein and CRP genotype with coronary heart disease: findings from five studies with 4,610 cases amongst 18,637 participants. *PLoS ONE*, **2008**, 3, e3011	3.7	79
278	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2012**, 90, 1116-1117	11	78
277	How does body fat influence bone mass in childhood? A Mendelian randomization approach. *Journal of Bone and Mineral Research*, **2009**, 24, 522-33	6.3	78
276	A novel common variant in DCST2 is associated with length in early life and height in adulthood. *Human Molecular Genetics*, **2015**, 24, 1155-68	5.6	77
275	MR-Base: a platform for systematic causal inference across the phenome using billions of genetic associations		77
274	Genome-wide association study identifies loci affecting blood copper, selenium and zinc. *Human Molecular Genetics*, **2013**, 22, 3998-4006	5.6	76
273	Low-Frequency Synonymous Coding Variation in CYP2R1 Has Large Effects on Vitamin D Levels and Risk of Multiple Sclerosis. *American Journal of Human Genetics*, **2017**, 101, 227-238	11	76
272	Strengthening causal inference in cardiovascular epidemiology through Mendelian randomization. *Annals of Medicine*, **2008**, 40, 524-41	1.5	75
271	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. *American Journal of Human Genetics*, **2017**, 100, 865-884	11	74
270	Meta-analysis of genome-wide studies identifies WNT16 and ESR1 SNPs associated with bone mineral density in premenopausal women. *Journal of Bone and Mineral Research*, **2013**, 28, 547-58	6.3	74

269	A variant in LIN28B is associated with 2D:4D finger-length ratio, a putative retrospective biomarker of prenatal testosterone exposure. *American Journal of Human Genetics*, **2010**, 86, 519-25	11	74
268	TAS2R38 (phenylthiocarbamide) haplotypes, coronary heart disease traits, and eating behavior in the British Women's Heart and Health Study. *American Journal of Clinical Nutrition*, **2005**, 81, 1005-11	7	73
267	Genome-wide analysis of dental caries and periodontitis combining clinical and self-reported data. *Nature Communications*, **2019**, 10, 2773	17.4	72
266	Genetic association study of BDNF in depression: finding from two cohort studies and a meta-analysis. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2008**, 147B, 814-21	3.5	72
265	GARFIELD classifies disease-relevant genomic features through integration of functional annotations with association signals. *Nature Genetics*, **2019**, 51, 343-353	36.3	71
264	Height-reducing variants and selection for short stature in Sardinia. *Nature Genetics*, **2015**, 47, 1352-1356	36.3	71
263	Genome wide association identifies common variants at the SERPINA6/SERPINA1 locus influencing plasma cortisol and corticosteroid binding globulin. *PLoS Genetics*, **2014**, 10, e1004474	6	71
262	Severe obesity in young women and reproductive health: the Danish National Birth Cohort. *PLoS ONE*, **2009**, 4, e8444	3.7	71
261	Association of the DRD2 gene Taq1A polymorphism and smoking behavior: a meta-analysis and new data. *Nicotine and Tobacco Research*, **2009**, 11, 64-76	4.9	71
260	Dietary Intake, FTO Genetic Variants, and Adiposity: A Combined Analysis of Over 16,000 Children and Adolescents. *Diabetes*, **2015**, 64, 2467-76	0.9	66
259	Genome-wide association study of sexual maturation in males and females highlights a role for body mass and menarche loci in male puberty. *Human Molecular Genetics*, **2014**, 23, 4452-64	5.6	66
258	Two British women studies replicated the association between the Val66Met polymorphism in the brain-derived neurotrophic factor (BDNF) and BMI. *European Journal of Human Genetics*, **2009**, 17, 1050-5	5.3	64
257	Assessing the utility of intermediate phenotypes for genetic mapping of psychiatric disease. *Trends in Neurosciences*, **2014**, 37, 733-41	13.3	60
256	A population-based study of genetic variation and psychotic experiences in adolescents. *Schizophrenia Bulletin*, **2014**, 40, 1254-62	1.3	59
255	Genome-wide association meta-analysis of cortical bone mineral density unravels allelic heterogeneity at the RANKL locus and potential pleiotropic effects on bone. *PLoS Genetics*, **2010**, 6, e1001217	6	59
254	Mining the human phenome using allelic scores that index biological intermediates. *PLoS Genetics*, **2013**, 9, e1003919	6	58
253	Childhood gene-environment interactions and age-dependent effects of genetic variants associated with refractive error and myopia: The CREAM Consortium. *Scientific Reports*, **2016**, 6, 25853	4.9	57
252	Genome-wide association study of primary tooth eruption identifies pleiotropic loci associated with height and craniofacial distances. *Human Molecular Genetics*, **2013**, 22, 3807-17	5.6	57

251	Avoiding milk is associated with a reduced risk of insulin resistance and the metabolic syndrome: findings from the British Women's Heart and Health Study. *Diabetic Medicine*, **2005**, 22, 808-11	3.5	57
250	Whole-genome sequence-based analysis of thyroid function. *Nature Communications*, **2015**, 6, 5681	17.4	56
249	Genome-wide associations of human gut microbiome variation and implications for causal inference analyses. *Nature Microbiology*, **2020**, 5, 1079-1087	26.6	55
248	Shared genetic influences between attention-deficit/hyperactivity disorder (ADHD) traits in children and clinical ADHD. *Journal of the American Academy of Child and Adolescent Psychiatry*, **2015**, 54, 322-7	7.2	54
247	Genome-wide Association Study for Vitamin D Levels Reveals 69 Independent Loci. *American Journal of Human Genetics*, **2020**, 106, 327-337	11	54
246	Common variation near ROBO2 is associated with expressive vocabulary in infancy. *Nature Communications*, **2014**, 5, 4831	17.4	54
245	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. *American Journal of Human Genetics*, **2019**, 104, 112-138	11	54
244	Genome-wide association study of height-adjusted BMI in childhood identifies functional variant in ADCY3. *Obesity*, **2014**, 22, 2252-9	8	53
243	Association between C-reactive protein genotype, circulating levels, and aortic pulse wave velocity. *Hypertension*, **2009**, 53, 150-7	8.5	53
242	The causal effect of vitamin D binding protein (DBP) levels on calcemic and cardiometabolic diseases: a Mendelian randomization study. *PLoS Medicine*, **2014**, 11, e1001751	11.6	52
241	Lactase persistence-related genetic variant: population substructure and health outcomes. *European Journal of Human Genetics*, **2009**, 17, 357-67	5.3	52
240	Lifetime body mass index and later atherosclerosis risk in young adults: examining causal links using Mendelian randomization in the Cardiovascular Risk in Young Finns study. *European Heart Journal*, **2008**, 29, 2552-60	9.5	52
239	Associations of Body Mass and Fat Indexes With Cardiometabolic Traits. *Journal of the American College of Cardiology*, **2018**, 72, 3142-3154	15.1	52
238	Examination of the relationship between variation at 17q21 and childhood wheeze phenotypes. *Journal of Allergy and Clinical Immunology*, **2013**, 131, 685-94	11.5	51
237	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. *Nature Genetics*, **2016**, 48, 1303-1312	36.3	51
236	European lactase persistence genotype shows evidence of association with increase in body mass index. *Human Molecular Genetics*, **2010**, 19, 1129-36	5.6	50
235	Genome-wide association study reveals multiple loci associated with primary tooth development during infancy. *PLoS Genetics*, **2010**, 6, e1000856	6	50
234	Dietary energy density affects fat mass in early adolescence and is not modified by FTO variants. *PLoS ONE*, **2009**, 4, e4594	3.7	50

233	Using Genetic Variation to Explore the Causal Effect of Maternal Pregnancy Adiposity on Future Offspring Adiposity: A Mendelian Randomisation Study. *PLoS Medicine*, **2017**, 14, e1002221	11.6	49
232	Variability in the common genetic architecture of social-communication spectrum phenotypes during childhood and adolescence. *Molecular Autism*, **2014**, 5, 18	6.5	48
231	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. *Nature Communications*, **2014**, 5, 4871	17.4	46
230	Identifying Critical Points of Trajectories of Depressive Symptoms from Childhood to Young Adulthood. *Journal of Youth and Adolescence*, **2019**, 48, 815-827	4.5	45
229	Using genetic loci to understand the relationship between adiposity and psychological distress: a Mendelian Randomization study in the Copenhagen General Population Study of 53,221 adults. *Journal of Internal Medicine*, **2011**, 269, 525-37	10.8	45
228	Comment on papers by Evans et al. and Mekel-Bobrov et al. on Evidence for Positive Selection of MCPH1 and ASPM. *Science*, **2007**, 317, 1036; author reply 1036	33.3	45
227	BMI and Mortality in UK Biobank: Revised Estimates Using Mendelian Randomization. *Obesity*, **2018** , 26, 1796-1806	8	45
226	Mendelian Randomization Analysis Identifies CpG Sites as Putative Mediators for Genetic Influences on Cardiovascular Disease Risk. *American Journal of Human Genetics*, **2017**, 101, 590-602	11	44
225	The trans-ancestral genomic architecture of glycemic traits. *Nature Genetics*, **2021**, 53, 840-860	36.3	44
224	Adult height variants affect birth length and growth rate in children. *Human Molecular Genetics*, **2011**, 20, 4069-75	5.6	43
223	Mental health during the COVID-19 pandemic in two longitudinal UK population cohorts		42
222	Association analysis of 31 common polymorphisms with type 2 diabetes and its related traits in Indian sib pairs. *Diabetologia*, **2012**, 55, 349-57	10.3	41
221	Genome-wide prediction of childhood asthma and related phenotypes in a longitudinal birth cohort. *Journal of Allergy and Clinical Immunology*, **2012**, 130, 503-9.e7	11.5	41
220	Refining associations between TAS2R38 diplotypes and the 6-n-propylthiouracil (PROP) taste test: findings from the Avon Longitudinal Study of Parents and Children. *BMC Genetics*, **2007**, 8, 51	2.6	41
219	Association of a body mass index genetic risk score with growth throughout childhood and adolescence. *PLoS ONE*, **2013**, 8, e79547	3.7	41
218	Influence of puberty timing on adiposity and cardiometabolic traits: A Mendelian randomisation study. *PLoS Medicine*, **2018**, 15, e1002641	11.6	41
217	Prenatal alcohol exposure and offspring mental health: A systematic review. *Drug and Alcohol Dependence*, **2019**, 197, 344-353	4.9	40
216	Systematic Mendelian randomization framework elucidates hundreds of CpG sites which may mediate the influence of genetic variants on disease. *Human Molecular Genetics*, **2018**, 27, 3293-3304	5.6	40

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