Nicholas J Timpson

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5813646/publications.pdf

Version: 2024-02-01

382 papers	71,667 citations	1294 109 h-index	906 241 g-index
459 all docs	459 docs citations	459 times ranked	60138 citing authors

#	Article	IF	Citations
1	A Common Variant in the FTO Gene Is Associated with Body Mass Index and Predisposes to Childhood and Adult Obesity. Science, 2007, 316, 889-894.	6.0	3,884
2	The MR-Base platform supports systematic causal inference across the human phenome. ELife, 2018, 7, .	2.8	3,639
3	Mendelian randomization: Using genes as instruments for making causal inferences in epidemiology. Statistics in Medicine, 2008, 27, 1133-1163.	0.8	2,716
4	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
5	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	9.4	2,421
6	Replication of Genome-Wide Association Signals in UK Samples Reveals Risk Loci for Type 2 Diabetes. Science, 2007, 316, 1336-1341.	6.0	2,040
7	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	9.4	1,982
8	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. Nature Genetics, 2008, 40, 638-645.	9.4	1,683
9	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nature Genetics, 2019, 51, 63-75.	9.4	1,594
10	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	9.4	1,572
11	Newly identified loci that influence lipid concentrations and risk of coronary artery disease. Nature Genetics, 2008, 40, 161-169.	9.4	1,488
12	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. Nature Genetics, 2007, 39, 1329-1337.	9.4	1,298
13	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
14	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	9.4	1,179
15	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
16	The interleukin-6 receptor as a target for prevention of coronary heart disease: a mendelian randomisation analysis. Lancet, The, 2012, 379, 1214-1224.	6.3	886
17	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. Nature Genetics, 2016, 48, 624-633.	9.4	870
18	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, 949-960.	9.4	836

#	Article	IF	Citations
19	Strengthening the Reporting of Observational Studies in Epidemiology Using Mendelian Randomization. JAMA - Journal of the American Medical Association, 2021, 326, 1614.	3.8	829
20	Using published data in Mendelian randomization: a blueprint for efficient identification of causal risk factors. European Journal of Epidemiology, 2015, 30, 543-552.	2.5	799
21	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	6.0	750
22	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	9.4	746
23	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	9.4	676
24	Using multiple genetic variants as instrumental variables for modifiable risk factors. Statistical Methods in Medical Research, 2012, 21, 223-242.	0.7	617
25	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. Lancet, The, 2015, 385, 351-361.	6.3	562
26	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	13.7	548
27	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.	9.4	536
28	Association between C reactive protein and coronary heart disease: mendelian randomisation analysis based on individual participant data. BMJ: British Medical Journal, 2011, 342, d548-d548.	2.4	530
29	Polygenic Prediction of Weight and Obesity Trajectories from Birth to Adulthood. Cell, 2019, 177, 587-596.e9.	13.5	516
30	Wholeâ€genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	13.7	483
31	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	1.5	453
32	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.	3.9	446
33	Clustered Environments and Randomized Genes: A Fundamental Distinction between Conventional and Genetic Epidemiology. PLoS Medicine, 2007, 4, e352.	3.9	428
34	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.	9.4	426
35	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.	1.5	419
36	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.	0.9	415

#	Article	IF	Citations
37	Strengthening the reporting of observational studies in epidemiology using mendelian randomisation (STROBE-MR): explanation and elaboration. BMJ, The, 2021, 375, n2233.	3.0	408
38	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	13.7	406
39	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	9.4	402
40	Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. Nature Genetics, 2013, 45, 314-318.	9.4	398
41	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	3.4	376
42	A common variant of HMGA2 is associated with adult and childhood height in the general population. Nature Genetics, 2007, 39, 1245-1250.	9.4	373
43	Common variants in the GDF5-UQCC region are associated with variation in human height. Nature Genetics, 2008, 40, 198-203.	9.4	369
44	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
45	A genome-wide association meta-analysis identifies new childhood obesity loci. Nature Genetics, 2012, 44, 526-531.	9.4	352
46	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, 2201-2217.	1.4	345
47	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
48	Genetic architecture: the shape of the genetic contribution to human traits and disease. Nature Reviews Genetics, 2018, 19, 110-124.	7.7	335
49	Mental health before and during the COVID-19 pandemic in two longitudinal UK population cohorts. British Journal of Psychiatry, 2021, 218, 334-343.	1.7	330
50	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	9.4	328
51	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.	2.6	326
52	Meta-analysis of genome-wide association studies identifies three new risk loci for atopic dermatitis. Nature Genetics, 2012, 44, 187-192.	9.4	311
53	C-reactive protein and its role in metabolic syndrome: mendelian randomisation study. Lancet, The, 2005, 366, 1954-1959.	6.3	300
54	Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. Nature Communications, 2015, 6, 8111.	5.8	300

#	Article	IF	Citations
55	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. Nature Genetics, 2013, 45, 76-82.	9.4	293
56	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. JAMA Psychiatry, 2015, 72, 642.	6.0	289
57	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	9.4	284
58	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
59	Common Variation in the FTO Gene Alters Diabetes-Related Metabolic Traits to the Extent Expected Given Its Effect on BMI. Diabetes, 2008, 57, 1419-1426.	0.3	277
60	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. Human Molecular Genetics, 2016, 25, 389-403.	1.4	275
61	C-reactive protein levels and body mass index: elucidating direction of causation through reciprocal Mendelian randomization. International Journal of Obesity, 2011, 35, 300-308.	1.6	267
62	The Effect of Elevated Body Mass Index on Ischemic Heart Disease Risk: Causal Estimates from a Mendelian Randomisation Approach. PLoS Medicine, 2012, 9, e1001212.	3.9	246
63	A road map for efficient and reliable human genome epidemiology. Nature Genetics, 2006, 38, 3-5.	9.4	244
64	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, 13790-13794.	3.3	244
65	Long COVID burden and risk factors in 10 UK longitudinal studies and electronic health records. Nature Communications, 2022, 13, .	5.8	243
66	Childhood intelligence is heritable, highly polygenic and associated with FNBP1L. Molecular Psychiatry, 2014, 19, 253-258.	4.1	241
67	WNT16 Influences Bone Mineral Density, Cortical Bone Thickness, Bone Strength, and Osteoporotic Fracture Risk. PLoS Genetics, 2012, 8, e1002745.	1.5	240
68	Apparent latent structure within the UK Biobank sample has implications for epidemiological analysis. Nature Communications, 2019, 10, 333.	5.8	240
69	The fat massâ€“and obesity-associated locus and dietary intake in children. American Journal of Clinical Nutrition, 2008, 88, 971-978.	2.2	239
70	A genome-wide association meta-analysis of self-reported allergy identifies shared and allergy-specific susceptibility loci. Nature Genetics, 2013, 45, 907-911.	9.4	232
71	Association of plasma uric acid with ischaemic heart disease and blood pressure: mendelian randomisation analysis of two large cohorts. BMJ, The, 2013, 347, f4262-f4262.	3.0	228
72	Variants in ADCY5 and near CCNL1 are associated with fetal growth and birth weight. Nature Genetics, 2010, 42, 430-435.	9.4	223

#	Article	IF	Citations
73	Meta-analysis of genome-wide association studies identifies ten loci influencing allergic sensitization. Nature Genetics, 2013, 45, 902-906.	9.4	221
74	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, 478-485.	2.6	202
75	Association Between Genetic Variants on Chromosome 15q25 Locus and Objective Measures of Tobacco Exposure. Journal of the National Cancer Institute, 2012, 104, 740-748.	3.0	198
76	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
77	Genome sequencing elucidates Sardinian genetic architecture and augments association analyses for lipid and blood inflammatory markers. Nature Genetics, 2015, 47, 1272-1281.	9.4	193
78	Genome-wide association and longitudinal analyses reveal genetic loci linking pubertal height growth, pubertal timing and childhood adiposity. Human Molecular Genetics, 2013, 22, 2735-2747.	1.4	188
79	Genome-wide analysis of dental caries and periodontitis combining clinical and self-reported data. Nature Communications, 2019, 10, 2773.	5.8	183
80	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183
81	Does Greater Adiposity Increase Blood Pressure and Hypertension Risk?. Hypertension, 2009, 54, 84-90.	1.3	181
82	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. Behavior Genetics, 2016, 46, 170-182.	1.4	178
83	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
84	Obesity and Multiple Sclerosis: A Mendelian Randomization Study. PLoS Medicine, 2016, 13, e1002053.	3.9	171
85	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.	1.5	165
86	Exploring the Developmental Overnutrition Hypothesis Using Parentalâ€“Offspring Associations and FTO as an Instrumental Variable. PLoS Medicine, 2008, 5, e33.	3.9	162
87	Genetic Markers of Adult Obesity Risk Are Associated with Greater Early Infancy Weight Gain and Growth. PLoS Medicine, 2010, 7, e1000284.	3.9	158
88	Early Cannabis Use, Polygenic Risk Score for Schizophrenia and Brain Maturation in Adolescence. JAMA Psychiatry, 2015, 72, 1002.	6.0	156
89	Mendelian randomization: where are we now and where are we going?. International Journal of Epidemiology, 2015, 44, 379-388.	0.9	155
90	A genomeâ€wide approach to children's aggressive behavior: The EAGLE consortium. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2016, 171, 562-572.	1.1	153

#	Article	IF	Citations
91	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	5.8	153
92	A Genome-Wide Association Study Reveals Variants in ARL15 that Influence Adiponectin Levels. PLoS Genetics, 2009, 5, e1000768.	1.5	148
93	Assessing Causality in the Association between Child Adiposity and Physical Activity Levels: A Mendelian Randomization Analysis. PLoS Medicine, 2014, 11, e1001618.	3.9	147
94	AHRR(cg05575921) hypomethylation marks smoking behaviour, morbidity and mortality. Thorax, 2017, 72, 646-653.	2.7	147
95	GARFIELD classifies disease-relevant genomic features through integration of functional annotations with association signals. Nature Genetics, 2019, 51, 343-353.	9.4	147
96	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, 412-420.	0.4	146
97	Variations in the G6PC2/ABCB11 genomic region are associated with fasting glucose levels. Journal of Clinical Investigation, 2008, 118, 2620-8.	3.9	146
98	BMI as a Modifiable Risk Factor for Type 2 Diabetes: Refining and Understanding Causal Estimates Using Mendelian Randomization. Diabetes, 2016, 65, 3002-3007.	0.3	144
99	Genome-wide associations of human gut microbiome variation and implications for causal inference analyses. Nature Microbiology, 2020, 5, 1079-1087.	5.9	144
100	Genome-wide Association Study for Vitamin D Levels Reveals 69 Independent Loci. American Journal of Human Genetics, 2020, 106, 327-337.	2.6	144
101	Copy Number Variations and Cognitive Phenotypes in Unselected Populations. JAMA - Journal of the American Medical Association, 2015, 313, 2044.	3.8	143
102	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.	1.5	142
103	Genome-wide association study identifies loci affecting blood copper, selenium and zinc. Human Molecular Genetics, 2013, 22, 3998-4006.	1.4	140
104	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, 264-277.	2.6	139
105	Inflammation, Insulin Resistance, and Diabetesâ€"Mendelian Randomization Using CRP Haplotypes Points Upstream. PLoS Medicine, 2008, 5, e155.	3.9	136
106	Type 2 Diabetes Risk Alleles Are Associated With Reduced Size at Birth. Diabetes, 2009, 58, 1428-1433.	0.3	135
107	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.	1.5	134
108	Genetic Determinants of Height Growth Assessed Longitudinally from Infancy to Adulthood in the Northern Finland Birth Cohort 1966. PLoS Genetics, 2009, 5, e1000409.	1.5	131

#	Article	IF	Citations
109	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	2.6	131
110	Common variants at 12q15 and 12q24 are associated with infant head circumference. Nature Genetics, 2012, 44, 532-538.	9.4	130
111	Common Variants in Left/Right Asymmetry Genes and Pathways Are Associated with Relative Hand Skill. PLoS Genetics, 2013, 9, e1003751.	1.5	129
112	Remnant Cholesterol, Low-Density Lipoprotein Cholesterol, and Blood Pressure as Mediators From Obesity to Ischemic Heart Disease. Circulation Research, 2015, 116, 665-673.	2.0	129
113	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, 352-360.	4.1	126
114	Common variants at 6q22 and 17q21 are associated with intracranial volume. Nature Genetics, 2012, 44, 539-544.	9.4	126
115	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	2.6	122
116	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.	2.6	118
117	Common variants in the region around Osterix are associated with bone mineral density and growth in childhood. Human Molecular Genetics, 2009, 18, 1510-1517.	1.4	117
118	A genome-wide association study of body mass index across early life and childhood. International Journal of Epidemiology, 2015, 44, 700-712.	0.9	114
119	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.	0.3	112
120	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.	2.6	112
121	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	3.3	110
122	Adiposity-Related Heterogeneity in Patterns of Type 2 Diabetes Susceptibility Observed in Genome-Wide Association Data. Diabetes, 2009, 58, 505-510.	0.3	109
123	A novel common variant in DCST2 is associated with length in early life and height in adulthood. Human Molecular Genetics, 2015, 24, 1155-1168.	1.4	109
124	Functional Gene Group Analysis Reveals a Role of Synaptic Heterotrimeric G Proteins in Cognitive Ability. American Journal of Human Genetics, 2010, 86, 113-125.	2.6	106
125	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. American Journal of Human Genetics, 2019, 104, 112-138.	2.6	106
126	Genome-Wide Population-Based Association Study of Extremely Overweight Young Adults â€“ The GOYA Study. PLoS ONE, 2011, 6, e24303.	1.1	105

#	Article	IF	Citations
127	Genome Wide Association Identifies Common Variants at the SERPINA6/SERPINA1 Locus Influencing Plasma Cortisol and Corticosteroid Binding Globulin. PLoS Genetics, 2014, 10, e1004474.	1.5	105
128	Melanesian Blond Hair Is Caused by an Amino Acid Change in TYRP1. Science, 2012, 336, 554-554.	6.0	104
129	Meta-analysis of geneâ€“environment-wide association scans accounting for education level identifies additional loci for refractive error. Nature Communications, 2016, 7, 11008.	5.8	104
130	Association of Genetic Loci With Glucose Levels in Childhood and Adolescence. Diabetes, 2011, 60, 1805-1812.	0.3	103
131	Genetic and Environmental Risk Factors Associated With Trajectories of Depression Symptoms From Adolescence to Young Adulthood. JAMA Network Open, 2019, 2, e196587.	2.8	103
132	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, 375-382.	2.2	102
133	Identifying Critical Points of Trajectories of Depressive Symptoms from Childhood to Young Adulthood. Journal of Youth and Adolescence, 2019, 48, 815-827.	1.9	97
134	Obesity and cancer: Mendelian randomization approach utilizing the FTO genotype. International Journal of Epidemiology, 2009, 38, 971-975.	0.9	96
135	Height-reducing variants and selection for short stature in Sardinia. Nature Genetics, 2015, 47, 1352-1356.	9.4	96
136	Novel loci for childhood body mass index and shared heritability with adult cardiometabolic traits. PLoS Genetics, 2020, 16, e1008718.	1.5	95
137	Associations of Body Mass and FatÂIndexesÂWith Cardiometabolic Traits. Journal of the American College of Cardiology, 2018, 72, 3142-3154.	1.2	93
138	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	9.4	91
139	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.	1.1	90
140	Strengthening causal inference in cardiovascular epidemiology through Mendelian randomization. Annals of Medicine, 2008, 40, 524-541.	1.5	88
141	Severe Obesity in Young Women and Reproductive Health: The Danish National Birth Cohort. PLoS ONE, 2009, 4, e8444.	1.1	88
142	How Does Body Fat Influence Bone Mass in Childhood? A Mendelian Randomization Approach. Journal of Bone and Mineral Research, 2009, 24, 522-533.	3.1	88
143	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, 547-558.	3.1	87
144	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	5.8	87

#	Article	IF	Citations
145	Association of the DRD2 gene Taq1A polymorphism and smoking behavior: A meta-analysis and new data. Nicotine and Tobacco Research, 2009, 11, 64-76.	1.4	86
146	Genome-wide association study of height-adjusted BMI in childhood identifies functional variant inADCY3. Obesity, 2014, 22, 2252-2259.	1.5	86
147	GWAS on longitudinal growth traits reveals different genetic factors influencing infant, child, and adult BMI. Science Advances, 2019, 5, eaaw3095.	4.7	86
148	Genetic association study of BDNF in depression: Finding from two cohort studies and a metaâ€analysis. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 814-821.	1.1	85
149	TAS2R38 (phenylthiocarbamide) haplotypes, coronary heart disease traits, and eating behavior in the British Womenâ€™s Heart and Health Study. American Journal of Clinical Nutrition, 2005, 81, 1005-1011.	2.2	84
150	Mining the Human Phenome Using Allelic Scores That Index Biological Intermediates. PLoS Genetics, 2013, 9, e1003919.	1.5	84
151	Genome-wide association study of primary tooth eruption identifies pleiotropic loci associated with height and craniofacial distances. Human Molecular Genetics, 2013, 22, 3807-3817.	1.4	84
152	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
153	Common variation near ROBO2 is associated with expressive vocabulary in infancy. Nature Communications, 2014, 5, 4831.	5.8	82
154	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, 4452-4464.	1.4	82
155	Assessing the utility of intermediate phenotypes for genetic mapping of psychiatric disease. Trends in Neurosciences, 2014, 37, 733-741.	4.2	80
156	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.	1.6	80
157	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, 519-525.	2.6	79
158	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	6.2	79
159	Influence of puberty timing on adiposity and cardiometabolic traits: A Mendelian randomisation study. PLoS Medicine, 2018, 15, e1002641.	3.9	77
160	A trans-ancestral meta-analysis of genome-wide association studies reveals loci associated with childhood obesity. Human Molecular Genetics, 2019, 28, 3327-3338.	1.4	76
161	Adiposity, metabolites, and colorectal cancer risk: Mendelian randomization study. BMC Medicine, 2020, 18, 396.	2.3	76
162	Whole-genome sequence-based analysis of thyroid function. Nature Communications, 2015, 6, 5681.	5.8	75

#	Article	IF	Citations
163	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, 322-327.	0.3	75
164	A Population-Based Study of Genetic Variation and Psychotic Experiences in Adolescents. Schizophrenia Bulletin, 2014, 40, 1254-1262.	2.3	74
165	Dietary Intake, FTO Genetic Variants, and Adiposity: A Combined Analysis of Over 16,000 Children and Adolescents. Diabetes, 2015, 64, 2467-2476.	0.3	74
166	Prenatal alcohol exposure and offspring mental health: A systematic review. Drug and Alcohol Dependence, 2019, 197, 344-353.	1.6	72
167	Is population structure in the genetic biobank era irrelevant, a challenge, or an opportunity?. Human Genetics, 2020, 139, 23-41.	1.8	72
168	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, 1050-1055.	1.4	71
169	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.	3.9	71
170	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.	1.5	69
171	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, 808-811.	1.2	67
172	Examination of the relationship between variation at 17q21 and childhood wheeze phenotypes. Journal of Allergy and Clinical Immunology, 2013, 131, 685-694.	1.5	66
173	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	9.4	66
174	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.	2.6	65
175	BMI and Mortality in UK Biobank: Revised Estimates Using Mendelian Randomization. Obesity, 2018, 26, 1796-1806.	1.5	65
176	Lactase persistence-related genetic variant: population substructure and health outcomes. European Journal of Human Genetics, 2009, 17, 357-367.	1.4	64
177	Genome-Wide Association Study Reveals Multiple Loci Associated with Primary Tooth Development during Infancy. PLoS Genetics, 2010, 6, e1000856.	1.5	64
178	Evidence for three genetic loci involved in both anorexia nervosa risk and variation of body mass index. Molecular Psychiatry, 2017, 22, 192-201.	4.1	63
179	Shared genetic variants suggest common pathways in allergy and autoimmune diseases. Journal of Allergy and Clinical Immunology, 2017, 140, 771-781.	1.5	63
180	The Causal Effect of Vitamin D Binding Protein (DBP) Levels on Calcemic and Cardiometabolic Diseases: A Mendelian Randomization Study. PLoS Medicine, 2014, 11, e1001751.	3.9	62

#	Article	IF	Citations
181	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. Nature Communications, 2014, 5, 4871.	5.8	62
182	Identification of 371 genetic variants for age at first sex and birth linked to externalising behaviour. Nature Human Behaviour, 2021, 5, 1717-1730.	6.2	62
183	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, 2552-2560.	1.0	61
184	The CHRNA5â€“A3â€“B4 Gene Cluster and Smoking: From Discovery to Therapeutics. Trends in Neurosciences, 2016, 39, 851-861.	4.2	61
185	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25â€‰000 subjects. Molecular Psychiatry, 2015, 20, 735-743.	4.1	59
186	Evaluation of the causal effects between subjective wellbeing and cardiometabolic health: mendelian randomisation study. BMJ: British Medical Journal, 2018, 362, k3788.	2.4	59
187	The influence of obesity-related factors in the etiology of renal cell carcinomaâ€”A mendelian randomization study. PLoS Medicine, 2019, 16, e1002724.	3.9	59
188	MC3R links nutritional state to childhood growth and the timing of puberty. Nature, 2021, 599, 436-441.	13.7	59
189	Dietary Energy Density Affects Fat Mass in Early Adolescence and Is Not Modified by FTO Variants. PLoS ONE, 2009, 4, e4594.	1.1	58
190	European lactase persistence genotype shows evidence of association with increase in body mass index. Human Molecular Genetics, 2010, 19, 1129-1136.	1.4	58
191	Association Between C-Reactive Protein Genotype, Circulating Levels, and Aortic Pulse Wave Velocity. Hypertension, 2009, 53, 150-157.	1.3	57
192	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.	1.4	57
193	Assessing the Causal Role of Body Mass Index on Cardiovascular Health in Young Adults. Circulation, 2018, 138, 2187-2201.	1.6	55
194	Morning plasma cortisol as a cardiovascular risk factor: findings from prospective cohort and Mendelian randomization studies. European Journal of Endocrinology, 2019, 181, 429-438.	1.9	55
195	Using genetics to test the causal relationship of total adiposity and periodontitis: Mendelian randomization analyses in the Gene-Lifestyle Interactions and Dental Endpoints (GLIDE) Consortium. International Journal of Epidemiology, 2015, 44, 638-650.	0.9	54
196	Mosaic structural variation in children with developmental disorders. Human Molecular Genetics, 2015, 24, 2733-2745.	1.4	54
197	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. Nature Communications, 2018, 9, 711.	5.8	54
198	Using genetic loci to understand the relationship between adiposity and psychological distress: a Mendelian Randomization study in the Copenhagen General Population Study of 53â€ƒ221 adults. Journal of Internal Medicine, 2011, 269, 525-537.	2.7	53

#	Article	IF	Citations
199	Variability in the common genetic architecture of social-communication spectrum phenotypes during childhood and adolescence. Molecular Autism, 2014, 5, 18.	2.6	53
200	Comment on Papers by Evans et al . and Mekel-Bobrov et al . on Evidence for Positive Selection of MCPH1 and ASPM. Science, 2007, 317, 1036-1036.	6.0	52
201	A powerful approach to subâ€phenotype analysis in populationâ€based genetic association studies. Genetic Epidemiology, 2010, 34, 335-343.	0.6	52
202	Association of a Body Mass Index Genetic Risk Score with Growth throughout Childhood and Adolescence. PLoS ONE, 2013, 8, e79547.	1.1	51
203	Genome-wide prediction of childhood asthma and related phenotypes in a longitudinal birth cohort. Journal of Allergy and Clinical Immunology, 2012, 130, 503-509.e7.	1.5	50
204	Association between polygenic risk scores for attention-deficit hyperactivity disorder and educational and cognitive outcomes in the general population. International Journal of Epidemiology, 2017, 46, dyw216.	0.9	50
205	Genome wide analysis for mouth ulcers identifies associations at immune regulatory loci. Nature Communications, 2019, 10, 1052.	5.8	50
206	Cigarette smoke but not electronic cigarette aerosol activates a stress response in human coronary artery endothelial cells in culture. Drug and Alcohol Dependence, 2016, 163, 256-260.	1.6	49
207	Tooth loss is a complex measure of oral disease: Determinants and methodological considerations. Community Dentistry and Oral Epidemiology, 2018, 46, 555-562.	0.9	49
208	Loss-of-function mutations in the melanocortin 4 receptor in a UK birth cohort. Nature Medicine, 2021, 27, 1088-1096.	15.2	49
209	International Genome-Wide Association Study Consortium Identifies Novel Loci Associated With Blood Pressure in Children and Adolescents. Circulation: Cardiovascular Genetics, 2016, 9, 266-278.	5.1	48
210	Adult height variants affect birth length and growth rate in children. Human Molecular Genetics, 2011, 20, 4069-4075.	1.4	47
211	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.	2.7	46
212	Association between fat mass through adolescence and arterial stiffness: a population-based study from The Avon Longitudinal Study of Parents and Children. The Lancet Child and Adolescent Health, 2019, 3, 474-481.	2.7	45
213	The Dementias Platform UK (DPUK) Data Portal. European Journal of Epidemiology, 2020, 35, 601-611.	2.5	45
214	Association analysis of 31 common polymorphisms with type 2 diabetes and its related traits in Indian sib pairs. Diabetologia, 2012, 55, 349-357.	2.9	44
215	Cholesterol Auxotrophy as a Targetable Vulnerability in Clear Cell Renal Cell Carcinoma. Cancer Discovery, 2021, 11, 3106-3125.	7.7	44
216	Adiponectin and its association with bone mass accrual in childhood. Journal of Bone and Mineral Research, 2010, 25, 2212-2220.	3.1	43

#	Article	IF	Citations
217	Determinants of Intima-Media ThicknessÂin the Young. JACC: Cardiovascular Imaging, 2021, 14, 468-478.	2.3	43
218	Genome-Wide Association Study Identifies Four Loci Associated with Eruption of Permanent Teeth. PLoS Genetics, 2011, 7, e1002275.	1.5	42
219	Vitamin D levels and risk of type 1 diabetes: A Mendelian randomization study. PLoS Medicine, 2021, 18, e1003536.	3.9	42
220	Polygenic risk for depression, anxiety and neuroticism are associated with the severity and rate of change in depressive symptoms across adolescence. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2021, 62, 1462-1474.	3.1	41
221	Paradoxical Relationship Between Body Mass Index and Thyroid Hormone Levels: A Study Using Mendelian Randomization. Journal of Clinical Endocrinology and Metabolism, 2016, 101, 730-738.	1.8	40
222	Variation in the SERPINA6/SERPINA1 locus alters morning plasma cortisol, hepatic corticosteroid binding globulin expression, gene expression in peripheral tissues, and risk of cardiovascular disease. Journal of Human Genetics, 2021, 66, 625-636.	1.1	40
223	Does High C-reactive Protein Concentration Increase Atherosclerosis? The Whitehall II Study. PLoS ONE, 2008, 3, e3013.	1.1	39
224	C-Reactive Protein and Cardiovascular Disease Risk: Still an Unknown Quantity?. Annals of Internal Medicine, 2006, 145, 70.	2.0	38
225	Worldwide patterns of haplotype diversity at 9p21.3, a locus associated with type 2 diabetes and coronary heart disease. Genome Medicine, 2009, 1, 51.	3.6	38
226	Mendelian Randomization: Application to Cardiovascular Disease. Current Hypertension Reports, 2012, 14, 29-37.	1.5	38
227	Managing clinically significant findings in research: the UK10K example. European Journal of Human Genetics, 2014, 22, 1100-1104.	1.4	38
228	Re-Examining the Association between Vitamin D and Childhood Caries. PLoS ONE, 2015, 10, e0143769.	1.1	37
229	A meta-analysis of the associations between common variation in the PDE8B gene and thyroid hormone parameters, including assessment of longitudinal stability of associations over time and effect of thyroid hormone replacement. European Journal of Endocrinology, 2011, 164, 773-780.	1.9	36
230	Genomic analysis of male puberty timing highlights shared genetic basis with hair colour and lifespan. Nature Communications, 2020, 11, 1536.	5.8	36
231	Assumption-free estimation of the genetic contribution to refractive error across childhood. Molecular Vision, 2015, 21, 621-32.	1.1	36
232	KCTD8 Gene and Brain Growth in Adverse Intrauterine Environment: A Genome-wide Association Study. Cerebral Cortex, 2012, 22, 2634-2642.	1.6	35
233	A genome-wide association meta-analysis of diarrhoeal disease in young children identifiesFUT2locus and provides plausible biological pathways. Human Molecular Genetics, 2016, 25, 4127-4142.	1.4	35
234	Associations of device-measured physical activity across adolescence with metabolic traits: Prospective cohort study. PLoS Medicine, 2018, 15, e1002649.	3.9	35

#	Article	IF	Citations
235	Glycoprotein Acetyls: A Novel Inflammatory Biomarker of Early Cardiovascular Risk in the Young. Journal of the American Heart Association, 2022, 11, e024380.	1.6	35
236	Genome-Wide Association Scan Allowing for Epistasis in Type 2 Diabetes. Annals of Human Genetics, 2011, 75, 10-19.	0.3	34
237	Common variation contributes to the genetic architecture of social communication traits. Molecular Autism, 2013, 4, 34.	2.6	34
238	Heritability and Genome-Wide Association Analyses of Sleep Duration in Children: The EAGLE Consortium. Sleep, 2016, 39, 1859-1869.	0.6	34
239	A genome-wide association study for corneal curvature identifies the platelet-derived growth factor receptor Î± gene as a quantitative trait locus for eye size in white Europeans. Molecular Vision, 2013, 19, 243-53.	1.1	34
240	Fraction of exhaled nitric oxide values in childhood are associated with 17q11.2-q12 and 17q12-q21 variants. Journal of Allergy and Clinical Immunology, 2014, 134, 46-55.	1.5	33
241	Longitudinal evidence for persistent anxiety in young adults through COVID-19 restrictions. Wellcome Open Research, 0, 5, 195.	0.9	33
242	Common Variation in the WNK1 Gene and Blood Pressure in Childhood. Hypertension, 2008, 52, 974-979.	1.3	32
243	Genetic Influences on Trajectories of Systolic Blood Pressure Across Childhood and Adolescence. Circulation: Cardiovascular Genetics, 2013, 6, 608-614.	5.1	32
244	Consortium-based genome-wide meta-analysis for childhood dental caries traits. Human Molecular Genetics, 2018, 27, 3113-3127.	1.4	32
245	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. Human Molecular Genetics, 2021, 30, 393-409.	1.4	32
246	Effects of adiposity on the human plasma proteome: observational and Mendelian randomisation estimates. International Journal of Obesity, 2021, 45, 2221-2229.	1.6	31
247	The Avon Longitudinal Study of Parents and Children - A resource for COVID-19 research: Questionnaire data capture May-July 2020. Wellcome Open Research, 2020, 5, 210.	0.9	31
248	Genetic Variation Associated with Differential Educational Attainment in Adults Has Anticipated Associations with School Performance in Children. PLoS ONE, 2014, 9, e100248.	1.1	31
249	Association of Common Genetic Variants with Lipid Traits in the Indian Population. PLoS ONE, 2014, 9, e101688.	1.1	31
250	The association of oestrogen receptor Î±-haplotypes with cardiovascular risk factors in the British Women's Heart and Health Study. European Heart Journal, 2006, 27, 1597-1604.	1.0	30
251	Low-frequency variation in TP53 has large effects on head circumference and intracranial volume. Nature Communications, 2019, 10, 357.	5.8	30
252	Vitamin B-12 Status during Pregnancy and Childâ€™s IQ at Age 8: A Mendelian Randomization Study in the Avon Longitudinal Study of Parents and Children. PLoS ONE, 2012, 7, e51084.	1.1	30

#	Article	IF	Citations
253	Validation of Dual Energy X-Ray Absorptiometry Measures of Abdominal Fat by Comparison with Magnetic Resonance Imaging in an Indian Population. PLoS ONE, 2012, 7, e51042.	1.1	29
254	Lack of association between DRD2 and OPRM1 genotypes and adiposity. International Journal of Obesity, 2014, 38, 730-736.	1.6	29
255	Early Metabolic Features of Genetic Liability to Type 2 Diabetes: Cohort Study With Repeated Metabolomics Across Early Life. Diabetes Care, 2020, 43, 1537-1545.	4.3	29
256	The Avon Longitudinal Study of Parents and Children - A resource for COVID-19 research: Questionnaire data capture April-May 2020. Wellcome Open Research, 2020, 5, 127.	0.9	29
257	The association of the PON1 Q192R polymorphism with complications and outcomes of pregnancy: findings from the British Women's Heart and Health cohort study. Paediatric and Perinatal Epidemiology, 2006, 20, 244-250.	0.8	28
258	Alcohol dehydrogenase type 1C (ADH1C) variants, alcohol consumption traits, HDL-cholesterol and risk of coronary heart disease in women and men: British Women's Heart and Health Study and Caerphilly cohorts. Atherosclerosis, 2008, 196, 871-878.	0.4	28
259	Age- and puberty-dependent association between IQ score in early childhood and depressive symptoms in adolescence. Psychological Medicine, 2011, 41, 333-343.	2.7	28
260	Genome-wide association study of blood lead shows multiple associations near ALAD. Human Molecular Genetics, 2015, 24, 3871-3879.	1.4	28
261	Metabolic Characterization of a Rare Genetic Variation Within APOC3 and Its Lipoprotein Lipaseâ€“Independent Effects. Circulation: Cardiovascular Genetics, 2016, 9, 231-239.	5.1	28
262	Coordinated Genetic Scaling of the Human Eye: Shared Determination of Axial Eye Length and Corneal Curvature. , 2013, 54, 1715.		27
263	Assessment of reproducibility and biological variability of fasting and postprandial plasma metabolite concentrations using 1H NMR spectroscopy. PLoS ONE, 2019, 14, e0218549.	1.1	27
264	The Role of Inflammatory Cytokines as Intermediates in the Pathway from Increased Adiposity to Disease. Obesity, 2021, 29, 428-437.	1.5	27
265	The CRP genotype, serum levels and lung function in men: the Caerphilly Prospective Study. Clinical Science, 2011, 120, 347-355.	1.8	26
266	The Early Growth Genetics (EGG) and EArly Genetics and Lifecourse Epidemiology (EAGLE) consortia: design, results and future prospects. European Journal of Epidemiology, 2019, 34, 279-300.	2.5	26
267	Data Resource Profile: The ALSPAC birth cohort as a platform to study the relationship of environment and health and social factors. International Journal of Epidemiology, 2019, 48, 1038-1039k.	0.9	25
268	FUT2 secretor genotype and susceptibility to infections and chronic conditions in the ALSPAC cohort. Wellcome Open Research, 2018, 3, 65.	0.9	25
269	Does Bone Resorption Stimulate Periosteal Expansion? A Cross-Sectional Analysis of Î²-C-telopeptides of Type I Collagen (CTX), Genetic Markers of the RANKL Pathway, and Periosteal Circumference as Measured by pQCT. Journal of Bone and Mineral Research, 2014, 29, 1015-1024.	3.1	24
270	Genome-wide association study for refractive astigmatism reveals genetic co-determination with spherical equivalent refractive error: the CREAM consortium. Human Genetics, 2015, 134, 131-146.	1.8	24

#	Article	IF	Citations
271	Exploring possible epigenetic mediation of early-life environmental exposures on adiposity and obesity development: Figure 1.. International Journal of Epidemiology, 2015, 44, 1191-1198.	0.9	24
272	Assessing the causal association between 25â€hydroxyvitamin D and the risk of oral and oropharyngeal cancer using Mendelian randomization. International Journal of Cancer, 2018, 143, 1029-1036.	2.3	24
273	Maturation in Serum Thyroid Function Parameters Over Childhood and Puberty: Results of a Longitudinal Study. Journal of Clinical Endocrinology and Metabolism, 2017, 102, 2508-2515.	1.8	23
274	Assessment and visualization of phenome-wide causal relationships using genetic data: an application to dental caries and periodontitis. European Journal of Human Genetics, 2021, 29, 300-308.	1.4	23
275	Bayesian methods for metaâ€analysis of causal relationships estimated using genetic instrumental variables. Statistics in Medicine, 2010, 29, 1298-1311.	0.8	22
276	Using Genetic Proxies for Lifecourse Sun Exposure to Assess the Causal Relationship of Sun Exposure with Circulating Vitamin D and Prostate Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 597-606.	1.1	22
277	Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits. Nature Communications, 2022, 13, 2743.	5.8	22
278	Carcinogenicity of radon/radon decay product inhalation in rats â€“ effect of dose, dose rate and unattached fraction. International Journal of Radiation Biology, 2005, 81, 631-647.	1.0	21
279	The ATXN1 and TRIM31 genes are related to intelligence in an ADHD background: Evidence from a large collaborative study totaling 4,963 Subjects. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2011, 156, 145-157.	1.1	21
280	Screening for familial hypercholesterolaemia in childhood: Avon Longitudinal Study of Parents and Children (ALSPAC). Atherosclerosis, 2017, 260, 47-55.	0.4	21
281	Does a short breastfeeding period protect fromFTO-induced adiposity in children?. Pediatric Obesity, 2011, 6, e326-e335.	3.2	20
282	The Avon Longitudinal Study of Parents and Children - A resource for COVID-19 research: Questionnaire data capture May-July 2020. Wellcome Open Research, 2020, 5, 210.	0.9	20
283	Can Lactase Persistence Genotype Be Used to Reassess the Relationship between Renal Cell Carcinoma and Milk Drinking? Potentials and Problems in the Application of Mendelian Randomization. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 1341-1348.	1.1	19
284	Association Study of 25 Type 2 Diabetes Related Loci with Measures of Obesity in Indian Sib Pairs. PLoS ONE, 2013, 8, e53944.	1.1	19
285	Body mass index: Has epidemiology started to break down causal contributions to health and disease?. Obesity, 2016, 24, 1630-1638.	1.5	19
286	Common Genetic Variants Influence Whorls inÂFingerprint Patterns. Journal of Investigative Dermatology, 2016, 136, 859-862.	0.3	19
287	Association of Prenatal Alcohol Exposure and Offspring Depression: A Negative Control Analysis of Maternal and Partner Consumption. Alcoholism: Clinical and Experimental Research, 2020, 44, 1132-1140.	1.4	19
288	A Polygenic Risk Score to Predict Future Adult Short Stature Among Children. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 1918-1928.	1.8	19

#	Article	IF	Citations
289	Investigating the impact of cigarette smoking behaviours on DNA methylation patterns in adolescence. Human Molecular Genetics, 2019, 28, 155-165.	1.4	18
290	Bias from questionnaire invitation and response in COVID-19 research: an example using ALSPAC. Wellcome Open Research, 0, 6, 184.	0.9	18
291	The association of the paraoxonase (PON1) Q192R polymorphism with depression in older women: findings from the British Women's Heart and Health Study. Journal of Epidemiology and Community Health, 2007, 61, 85-87.	2.0	17
292	Coronary artery disease, genetic risk and the metabolome in young individuals. Wellcome Open Research, 2018, 3, 114.	0.9	17
293	Genetic Studies of Metabolomics Change After a Liquid Meal Illuminate Novel Pathways for Glucose and Lipid Metabolism. Diabetes, 2021, 70, 2932-2946.	0.3	17
294	Prospective associations between problematic eating attitudes in midchildhood and the future onset of adolescent obesity and high blood pressure. American Journal of Clinical Nutrition, 2017, 105, 306-312.	2.2	16
295	The blood metabolome of incident kidney cancer: A caseâ€“control study nested within the MetKid consortium. PLoS Medicine, 2021, 18, e1003786.	3.9	16
296	GWAS of stool frequency provides insights into gastrointestinal motility and irritable bowel syndrome. Cell Genomics, 2021, 1, 100069.	3.0	15
297	Association of Maternal Smoking With Child Cotinine Levels. Nicotine and Tobacco Research, 2013, 15, 2029-2036.	1.4	14
298	A recall-by-genotype study of CHRNA5-A3-B4genotype, cotinine and smoking topography: study protocol. BMC Medical Genetics, 2014, 15, 13.	2.1	13
299	Heritability and genome-wide analyses of problematic peer relationships during childhood and adolescence. Human Genetics, 2015, 134, 539-551.	1.8	13
300	Variation in the SLC23A1 gene does not influence cardiometabolic outcomes to the extent expected given its association with l-ascorbic acid. American Journal of Clinical Nutrition, 2015, 101, 202-209.	2.2	13
301	A pathway-centric approach to rare variant association analysis. European Journal of Human Genetics, 2017, 25, 123-129.	1.4	13
302	Genome-Wide Association Study Identifies Genetic Associations with Perceived Age. Journal of Investigative Dermatology, 2020, 140, 2380-2385.	0.3	13
303	Common maternal and fetal genetic variants show expected polygenic effects on risk of small- or large-for-gestational-age (SGA or LGA), except in the smallest 3% of babies. PLoS Genetics, 2020, 16, e1009191.	1.5	13
304	An interactive genome browser of association results from the UK10K cohorts project. Bioinformatics, 2015, 31, 4029-4031.	1.8	12
305	FUT2 secretor genotype and susceptibility to infections and chronic conditions in the ALSPAC cohort. Wellcome Open Research, 2018, 3, 65.	0.9	12
306	Coronary artery disease, genetic risk and the metabolome in young individuals. Wellcome Open Research, 2018, 3, 114.	0.9	12

#	Article	IF	Citations
307	The Avon Longitudinal Study of Parents and Children - A resource for COVID-19 research: Questionnaire data capture April-May 2020. Wellcome Open Research, 2020, 5, 127.	0.9	12
308	Collapsed methylation quantitative trait loci analysis for low frequency and rare variants. Human Molecular Genetics, 2016, 25, 4339-4349.	1.4	11
309	The Avon Longitudinal Study of Parents and Children - A resource for COVID-19 research: Home-based antibody testing results, October 2020. Wellcome Open Research, 2021, 6, 34.	0.9	11
310	Characterization of alcohol polygenic risk scores in the context of mental health outcomes: Within-individual and intergenerational analyses in the Avon Longitudinal Study of Parents and Children. Drug and Alcohol Dependence, 2021, 221, 108654.	1.6	11
311	The Avon Longitudinal Study of Parents and Children - A resource for COVID-19 research: Questionnaire data capture November 2020 â€“ March 2021. Wellcome Open Research, 2021, 6, 155.	0.9	11
312	A framework for research into continental ancestry groups of the UK Biobank. Human Genomics, 2022, 16, 3.	1.4	11
313	The UK Biobank: A Shining Example of Genome-Wide Association Study Science with the Power to Detect the Murky Complications of Real-World Epidemiology. Annual Review of Genomics and Human Genetics, 2022, 23, 569-589.	2.5	11
314	Genetics, sleep and memory: a recall-by-genotype study of ZNF804A variants and sleep neurophysiology. BMC Medical Genetics, 2015, 16, 96.	2.1	10
315	The ethics conundrum in Recall by Genotype (RbG) research: Perspectives from birth cohort participants. PLoS ONE, 2018, 13, e0202502.	1.1	10
316	Pleiotropic associations of heterozygosity for the SERPINA1 Z allele in the UK Biobank. ERJ Open Research, 2021, 7, 00049-2021.	1.1	10
317	Incorporating Non-Coding Annotations into Rare Variant Analysis. PLoS ONE, 2016, 11, e0154181.	1.1	10
318	metaboprep: an R package for preanalysis data description and processing. Bioinformatics, 2022, 38, 1980-1987.	1.8	10
319	Epigenetic Regulation of F2RL3 Associates With Myocardial Infarction and Platelet Function. Circulation Research, 2022, 130, 384-400.	2.0	10
320	Evaluation of seven common lipid associated loci in a large Indian sib pair study. Lipids in Health and Disease, 2012, 11, 155.	1.2	9
321	Genome-wide association study identifies SNPs in the MHC class II loci that are associated with self-reported history of whooping cough. Human Molecular Genetics, 2015, 24, 5930-5939.	1.4	9
322	Estimating the causal effect of BMI on mortality risk in people with heart disease, diabetes and cancer using Mendelian randomization. International Journal of Cardiology, 2021, 330, 214-220.	0.8	9
323	Investigation of the interplay between circulating lipids and IGF-I and relevance to breast cancer risk: an observational and Mendelian randomization study. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, cebp.0315.2021.	1.1	9
324	Enhanced Protection Against Diarrhea Among Breastfed Infants of Nonsecretor Mothers. Pediatric Infectious Disease Journal, 2021, 40, 260-263.	1.1	9

#	Article	IF	Citations
325	Higher body mass index raises immature platelet count: potential contribution to obesity-related thrombosis. Platelets, 2022, 33, 869-878.	1.1	9
326	Bias from questionnaire invitation and response in COVID-19 research: an example using ALSPAC. Wellcome Open Research, 0, 6, 184.	0.9	9
327	Blood pressure and mortality: using offspring blood pressure as an instrument for own blood pressure in the HUNT study. Scientific Reports, 2015, 5, 12399.	1.6	8
328	Is the adiposityâ€associated <scp>FTO</scp> gene variant related to allâ€cause mortality independent of adiposity? Metaâ€analysis of data from 169,551 <scp>C</scp>aucasian adults. Obesity Reviews, 2015, 16, 327-340.	3.1	8
329	Genotype-Based Recall Studies in Complex Cardiometabolic Traits. Circulation Genomic and Precision Medicine, 2018, 11, e001947.	1.6	8
330	Reassessing the Association between Circulating Vitamin D and IGFBP-3: Observational and Mendelian Randomization Estimates from Independent Sources. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 1462-1471.	1.1	8
331	The Avon Longitudinal Study of Parents and Children - a resource for COVID-19 research: approaches to the identification of cases November 2020. Wellcome Open Research, 0, 6, 122.	0.9	8
332	Intelligence in offspring born to women exposed to intimate partner violence: a population-based cohort study. Wellcome Open Research, 2019, 4, 107.	0.9	8
333	The Avon Longitudinal Study of Parents and Children - A resource for COVID-19 research: Questionnaire data capture November 2020 â€“ March 2021. Wellcome Open Research, 0, 6, 155.	0.9	7
334	Effect of low thyroid hormone bioavailability on childhood cognitive development: data from the Avon Longitudinal Study of Parents and Children birth cohort. Lancet, The, 2014, 383, S100.	6.3	6
335	A Protein Domain and Family Based Approach to Rare Variant Association Analysis. PLoS ONE, 2016, 11, e0153803.	1.1	6
336	Letter regarding article, â€œAssociations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysisâ€. International Journal of Epidemiology, 2019, 48, 1014-1015.	0.9	6
337	The Avon Longitudinal Study of Parents and Children - A resource for COVID-19 research: Generation 2 questionnaire data capture May-July 2020. Wellcome Open Research, 2020, 5, 278.	0.9	6
338	LongITools: Dynamic longitudinal exposome trajectories in cardiovascular and metabolic noncommunicable diseases. Environmental Epidemiology, 2022, 6, e184.	1.4	6
339	Body muscle gain and markers of cardiovascular disease susceptibility in young adulthood: A cohort study. PLoS Medicine, 2021, 18, e1003751.	3.9	5
340	A multivariant recallâ€byâ€genotype study of the metabolomic signature of BMI. Obesity, 2022, 30, 1298-1310.	1.5	5
341	Letter by Timpson et al Regarding Article, â€œContribution of Clinical Correlates and 13 C-Reactive Protein Gene Polymorphisms to Interindividual Variability in Serum C-Reactive Protein Levelâ€. Circulation, 2006, 114, e256.	1.6	4
342	Commentary: One size fits all: are there standard rules for the use of genetic instruments in Mendelian randomization?. International Journal of Epidemiology, 2016, 45, 1617-1618.	0.9	4

#	Article	IF	Citations
343	Longitudinal serological measures of common infection in the Avon Longitudinal Study of Parents and Children cohort. Wellcome Open Research, 2018, 3, 49.	0.9	4
344	Using Y-Chromosomal Haplogroups in Genetic Association Studies and Suggested Implications. Genes, 2018, 9, 45.	1.0	4
345	Examining the causal association between 25-hydroxyvitamin D and caries in children and adults: a two-sample Mendelian randomization approach. Wellcome Open Research, 2020, 5, 281.	0.9	4
346	The Avon Longitudinal Study of Parents and Children - A resource for COVID-19 research: Antibody testing results, April â€“ June 2021. Wellcome Open Research, 2021, 6, 283.	0.9	4
347	HMOX1 genetic polymorphisms and outcomes in infectious disease: A systematic review. PLoS ONE, 2022, 17, e0267399.	1.1	4
348	Recent Findings on the Genetics of Obesity: Is there Public Health Relevance?. Current Nutrition Reports, 2012, 1, 239-248.	2.1	3
349	Metabolic characterisation of disturbances in the APOC3/triglyceride-rich lipoprotein pathway through sample-based recall by genotype. Metabolomics, 2020, 16, 69.	1.4	3
350	Common variation at 16p11.2 is associated with glycosuria in pregnancy: findings from a genome-wide association study in European women. Human Molecular Genetics, 2020, 29, 2098-2106.	1.4	3
351	Genome-Wide Association Study to Identify Common Variants Associated with Brachial Circumference: A Meta-Analysis of 14 Cohorts. PLoS ONE, 2012, 7, e31369.	1.1	3
352	Is vitamin D a modifiable risk factor for dental caries?. Wellcome Open Research, 2020, 5, 281.	0.9	3
353	The Avon Longitudinal Study of Parents and Children - A resource for COVID-19 research: Antibody testing results, April â€“ June 2021. Wellcome Open Research, 0, 6, 283.	0.9	3
354	Copy Number Variations and Cognitive Phenotypes in Unselected Populations. Obstetrical and Gynecological Survey, 2015, 70, 559-560.	0.2	2
355	Using inactivating mutations to provide insight into drug action. Genome Medicine, 2015, 7, 7.	3.6	2
356	The range of peripapillary retinal nerve fibre layer and optic disc parameters, in children aged up to but not including 18Âyears of age who were born prematurely: protocol for a systematic review. Systematic Reviews, 2016, 5, 144.	2.5	2
357	Gene discovery for oral ulceration: a UK Biobank Study. Lancet, The, 2017, 389, S46.	6.3	2
358	Limits of lockdown: characterising essential contacts during strict physical distancing. Wellcome Open Research, 0, 6, 116.	0.9	2
359	Longitudinal serological measures of common infection in the Avon Longitudinal Study of Parents and Children cohort. Wellcome Open Research, 2018, 3, 49.	0.9	2
360	The â€˜ALSPAC in Londonâ€™ dataset: adiposity, cardiometabolic risk profiles, and the emerging arterial phenotype in young adulthood. Wellcome Open Research, 0, 3, 162.	0.9	2

#	Article	IF	Citations
361	Chlamydia trachomatis in the Age of the Genome: Application of Molecular Genotyping to Improve Our Understanding of the Immunopathogenesis of Chlamydia Genital Tract Disease. Sexually Transmitted Diseases, 2011, 38, 495-498.	0.8	2
362	The Avon Longitudinal Study of Parents and Children - A resource for COVID-19 research: Generation 2 questionnaire data capture May-July 2020. Wellcome Open Research, 2020, 5, 278.	0.9	2
363	Evaluating the association of TRPA1 gene polymorphisms with pain sensitivity: a protocol for an adaptive recall by genotype study. BMC Medical Genomics, 2022, 15, 9.	0.7	2
364	The Avon Longitudinal Study of Parents and Children - A resource for COVID-19 research: Home-based antibody testing results, October 2020. An emphasis on self-screening at a population level. Wellcome Open Research, 0, 6, 34.	0.9	2
365	Participant acceptability of digital footprint data collection strategies: an exemplar approach to participant engagement and involvement in the ALSPAC birth cohort study.. International Journal of Population Data Science, 2020, 5, 1728.	0.1	2
366	Genetics of early-life head circumference and genetic correlations with neurological, psychiatric and cognitive outcomes. BMC Medical Genomics, 2022, 15, .	0.7	2
367	The range of peripapillary retinal nerve fibre layer and optic disc parameters in children aged up to but not including 18Âyears of age, as measured by optical coherence tomography: protocol for a systematic review. Systematic Reviews, 2016, 5, 71.	2.5	1
368	Heritable contributions versus genetic architecture. Nature Reviews Genetics, 2018, 19, 185-185.	7.7	1
369	Schizophrenia-associated variation at ZNF804A correlates with altered experience-dependent dynamics of sleep slow waves and spindles in healthy young adults. Sleep, 2021, 44, .	0.6	1
370	Collection of genetic data at scale for a nationally representative population: the UK Millennium Cohort Study. Longitudinal and Life Course Studies, 2022, 13, 169-187.	0.3	1
371	Piloting the objective measurement of eating behaviour at a population scale: a nested study within the Avon Longitudinal Study of Parents and Children. Wellcome Open Research, 2020, 5, 185.	0.9	1
372	P2-303 Development of predictive equations for DXA measures of adiposity in an Indian population. Journal of Epidemiology and Community Health, 2011, 65, A306-A306.	2.0	0
373	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2012, 90, 1116-1117.	2.6	0
374	Ethnicity, heart failure, atrial fibrillation and diabetes: collider bias. Heart, 2019, 105, 814-816.	1.2	0
375	Diving deepâ€"multipronged investigations into RIPK1 as a risk factor for obesity. Nature Metabolism, 2020, 2, 997-998.	5.1	0
376	204Effects of adiposity on the human proteome: Mendelian randomization study using individual-level data. International Journal of Epidemiology, 2021, 50, .	0.9	0
377	Assessing Causality in the Association between Child Adiposity and Physical Activity Levels: A Mendelian Randomization Analysis. , 2015, , 83-108.		0
378	Age 23 years + oral health questionnaire in Avon Longitudinal Study of Parents and Children.. Wellcome Open Research, 0, 3, 34.	0.9	0

#	Article	IF	Citations
379	Age 23 years + oral health questionnaire in Avon Longitudinal Study of Parents and Children.. Wellcome Open Research, 2018, 3, 34.	0.9	0
380	The Genetic Sphygmomanometer: an argument for routine genome-wide genotyping in the population and a new view on its use to inform clinical practice. Wellcome Open Research, 2018, 3, 138.	0.9	0
381	Mapping complex disease genes using linkage disequilibrium and genome-wide association scans. , 0, , 91-130.		0
382	Characterising the index mothers in the Avon Longitudinal Study of Parents and Children (ALSPAC) who are also UKBioBank participants. Wellcome Open Research, 0, 7, 190.	0.9	0