Tom R Gaunt

List of Publications by Year
in descending order

261 papers	35,044 citations	10389 72 h-index	5120 166 g-index
332 all docs	332 docs citations	332 times ranked	45420 citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
2	The MR-Base platform supports systematic causal inference across the human phenome. ELife, 2018, 7, .	6.0	3,639
3	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
4	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
5	Predicting the Functional, Molecular, and Phenotypic Consequences of Amino Acid Substitutions using Hidden Markov Models. Human Mutation, 2013, 34, 57-65.	2.5	1,057
6	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	27.8	1,014
7	Hardy-Weinberg Equilibrium Testing of Biological Ascertainment for Mendelian Randomization Studies. American Journal of Epidemiology, 2009, 169, 505-514.	3.4	886
8	LD Hub: a centralized database and web interface to perform LD score regression that maximizes the potential of summary level GWAS data for SNP heritability and genetic correlation analysis. Bioinformatics, 2017, 33, 272-279.	4.1	822
9	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. Nature, 2017, 541, 81-86.	27.8	743
10	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. American Journal of Human Genetics, 2016, 98, 680-696.	6.2	717
11	Mendelian randomization of blood lipids for coronary heart disease. European Heart Journal, 2015, 36, 539-550.	2.2	567
12	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. Lancet, The, 2015, 385, 351-361.	13.7	562
13	Metabolite Profiling and Cardiovascular Event Risk. Circulation, 2015, 131, 774-785.	1.6	547
14	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	6.0	528
15	An integrative approach to predicting the functional effects of non-coding and coding sequence variation. Bioinformatics, 2015, 31, 1536-1543.	4.1	524
16	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	21.4	501
17	Systematic identification of genetic influences on methylation across the human life course. Genome Biology, 2016, 17, 61.	8.8	489
18	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412

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19	Epigenome-wide association of DNA methylation markers in peripheral blood from Indian Asians and Europeans with incident type 2 diabetes: a nested case-control study. Lancet Diabetes and Endocrinology,the, 2015, 3, 526-534.	11.4	396
20	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	7.1	376
21	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.	2.9	345
22	Identification of new therapeutic targets for osteoarthritis through genome-wide analyses of UK Biobank data. Nature Genetics, 2019, 51, 230-236.	21.4	331
23	Causal Associations of Adiposity and Body Fat Distribution With Coronary Heart Disease, Stroke Subtypes, and Type 2 Diabetes Mellitus. Circulation, 2017, 135, 2373-2388.	1.6	304
24	C-reactive protein and its role in metabolic syndrome: mendelian randomisation study. Lancet, The, 2005, 366, 1954-1959.	13.7	300
25	Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. Nature Communications, 2015, 6, 8111.	12.8	300
26	Phenome-wide Mendelian randomization mapping the influence of the plasma proteome on complex diseases. Nature Genetics, 2020, 52, 1122-1131.	21.4	298
27	FATHMM-XF: accurate prediction of pathogenic point mutations via extended features. Bioinformatics, 2018, 34, 511-513.	4.1	296
28	Maternal pre-pregnancy BMI and gestational weight gain, offspring DNA methylation and later offspring adiposity: findings from the Avon Longitudinal Study of Parents and Children. International Journal of Epidemiology, 2015, 44, 1288-1304.	1.9	244
29	Cubic exact solutions for the estimation of pairwise haplotype frequencies: implications for linkage disequilibrium analyses and a web tool 'CubeX'. BMC Bioinformatics, 2007, 8, 428.	2.6	239
30	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. American Journal of Human Genetics, 2012, 90, 410-425.	6.2	239
31	Data Resource Profile: Accessible Resource for Integrated Epigenomic Studies (ARIES). International Journal of Epidemiology, 2015, 44, 1181-1190.	1.9	238
32	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838.	6.2	227
33	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. Nature Genetics, 2021, 53, 1636-1648.	21.4	223
34	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	21.4	218
35	Predicting the functional consequences of cancer-associated amino acid substitutions. Bioinformatics, 2013, 29, 1504-1510.	4.1	208
36	Prenatal and early life influences on epigenetic age in children: a study of motherâ€“offspring pairs from two cohort studies. Human Molecular Genetics, 2016, 25, 191-201.	2.9	205

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37	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. Cell, 2021, 184, 4784-4818.e17.	28.9	188
38	Gene-centric Association Signals for Lipids and Apolipoproteins Identified via the HumanCVD BeadChip. American Journal of Human Genetics, 2009, 85, 628-642.	6.2	183
39	Prenatal Exposure to Maternal Cigarette Smoking and DNA Methylation: Epigenome-Wide Association in a Discovery Sample of Adolescents and Replication in an Independent Cohort at Birth through 17 Years of Age. Environmental Health Perspectives, 2015, 123, 193-199.	6.0	178
40	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Human Molecular Genetics, 2011, 20, 2273-2284.	2.9	168
41	Ranking non-synonymous single nucleotide polymorphisms based on disease concepts. Human Genomics, 2014, 8, 11.	2.9	163
42	Blood Pressure Loci Identified with a Gene-Centric Array. American Journal of Human Genetics, 2011, 89, 688-700.	6.2	159
43	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	6.2	158
44	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	12.8	153
45	Software Application Profile: PHESANT: a tool for performing automated phenome scans in UK Biobank. International Journal of Epidemiology, 2018, 47, 29-35.	1.9	151
46	Apolipoprotein E genotype, cardiovascular biomarkers and risk of stroke: Systematic review and meta-analysis of 14 015 stroke cases and pooled analysis of primary biomarker data from up to 60 883 individuals. International Journal of Epidemiology, 2013, 42, 475-492.	1.9	145
47	Copy Number Variations and Cognitive Phenotypes in Unselected Populations. JAMA - Journal of the American Medical Association, 2015, 313, 2044.	7.4	143
48	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	2.9	141
49	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	6.2	131
50	Age-related DNA methylation changes are tissue-specific with ELOVL2 promoter methylation as exception. Epigenetics and Chromatin, 2018, 11, 25.	3.9	130
51	Epigenetic profiling of ADHD symptoms trajectories: a prospective, methylome-wide study. Molecular Psychiatry, 2017, 22, 250-256.	7.9	124
52	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	6.2	122
53	Plasma urate concentration and risk of coronary heart disease: a Mendelian randomisation analysis. Lancet Diabetes and Endocrinology,the, 2016, 4, 327-336.	11.4	122
54	Longitudinal analysis of DNA methylation associated with birth weight and gestational age. Human Molecular Genetics, 2015, 24, 3752-3763.	2.9	120

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55	Polymorphisms in the interleukinâ€4 and interleukinâ€4 receptor Î± chain genes confer susceptibility to asthma and atopy in a Caucasian population. Clinical and Experimental Allergy, 2003, 33, 1111-1117.	2.9	115
56	Secretory Phospholipase A2-IIA and Cardiovascular Disease. Journal of the American College of Cardiology, 2013, 62, 1966-1976.	2.8	115
57	MIDAS: software for analysis and visualisation of interallelic disequilibrium between multiallelic markers. BMC Bioinformatics, 2006, 7, 227.	2.6	110
58	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. PLoS Genetics, 2015, 11, e1005035.	3.5	107
59	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. International Journal of Epidemiology, 2018, 47, 22-23u.	1.9	105
60	Positive associations between single nucleotide polymorphisms in the IGF2 gene region and body mass index in adult males. Human Molecular Genetics, 2001, 10, 1491-1501.	2.9	102
61	Psychosocial adversity and socioeconomic position during childhood and epigenetic age: analysis of two prospective cohort studies. Human Molecular Genetics, 2018, 27, 1301-1308.	2.9	102
62	DNA Methylation and BMI: Investigating Identified Methylation Sites at HIF3A in a Causal Framework. Diabetes, 2016, 65, 1231-1244.	0.6	95
63	The EWAS Catalog: a database of epigenome-wide association studies. Wellcome Open Research, 0, 7, 41.	1.8	95
64	Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. International Journal of Epidemiology, 2016, 45, 1927-1937.	1.9	94
65	Sixty-Five Common Genetic Variants and Prediction of Type 2 Diabetes. Diabetes, 2015, 64, 1830-1840.	0.6	91
66	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	21.4	91
67	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.	2.5	90
68	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	3.7	89
69	DNA methylation and substance-use risk: a prospective, genome-wide study spanning gestation to adolescence. Translational Psychiatry, 2016, 6, e976-e976.	4.8	86
70	The epigenetic clock and physical development during childhood and adolescence: longitudinal analysis from a UK birth cohort. International Journal of Epidemiology, 2017, 46, dyw307.	1.9	86
71	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.	4.7	84
72	Gene-centric meta-analyses of 108 912 individuals confirm known body mass index loci and reveal three novel signals. Human Molecular Genetics, 2013, 22, 184-201.	2.9	82

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73	The variant call format provides efficient and robust storage of GWAS summary statistics. Genome Biology, 2021, 22, 32.	8.8	82
74	An epigenome-wide association meta-analysis of prenatal maternal stress in neonates: A model approach for replication. Epigenetics, 2016, 11, 140-149.	2.7	80
75	Liver Function and Risk of Type 2 Diabetes: Bidirectional Mendelian Randomization Study. Diabetes, 2019, 68, 1681-1691.	0.6	79
76	Mendelian Randomization Studies Do Not Support a Role for Raised Circulating Triglyceride Levels Influencing Type 2 Diabetes, Glucose Levels, or Insulin Resistance. Diabetes, 2011, 60, 1008-1018.	0.6	77
77	The effects of height and BMI on prostate cancer incidence and mortality: a Mendelian randomization study in 20,848 cases and 20,214 controls from the PRACTICAL consortium. Cancer Causes and Control, 2015, 26, 1603-1616.	1.8	77
78	Whole-genome sequence-based analysis of thyroid function. Nature Communications, 2015, 6, 5681.	12.8	75
79	Hypertensive Disorders of Pregnancy and DNA Methylation in Newborns. Hypertension, 2019, 74, 375-383.	2.7	73
80	Prenatal unhealthy diet, insulinâ€like growth factor 2 gene (<scp>IGF</scp>2) methylation, and attention deficit hyperactivity disorder symptoms in youth with earlyâ€onset conduct problems. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2017, 58, 19-27.	5.2	70
81	Searching for the causal effects of body mass index in over 300 000 participants in UK Biobank, using Mendelian randomization. PLoS Genetics, 2019, 15, e1007951.	3.5	70
82	A pathway-based data integration framework for prediction of disease progression. Bioinformatics, 2014, 30, 838-845.	4.1	67
83	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	21.4	66
84	Does milk intake promote prostate cancer initiation or progression via effects on insulin-like growth factors (IGFs)? A systematic review and meta-analysis. Cancer Causes and Control, 2017, 28, 497-528.	1.8	65
85	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.	6.2	65
86	Epigenome-wide change and variation in DNA methylation in childhood: trajectories from birth to late adolescence. Human Molecular Genetics, 2021, 30, 119-134.	2.9	65
87	The Relationship Between Plasma Angiopoietin-like Protein 4 Levels, Angiopoietin-like Protein 4 Genotype, and Coronary Heart Disease Risk. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 2277-2282.	2.4	64
88	The association of the PON1 Q192R polymorphism with coronary heart disease: findings from the British Women's Heart and Health cohort study and a meta-analysis. BMC Genetics, 2004, 5, 17.	2.7	63
89	Molecular genetics of human growth hormone, insulin-like growth factors and their pathways in common disease. Human Genetics, 2007, 122, 1-21.	3.8	63
90	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. Nature Communications, 2014, 5, 4871.	12.8	62

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91	Epigenome-wide association study of asthma and wheeze in childhood and adolescence. Clinical Epigenetics, 2017, 9, 112.	4.1	60
92	Exploiting horizontal pleiotropy to search for causal pathways within a Mendelian randomization framework. Nature Communications, 2020, 11, 1010.	12.8	58
93	Haplotypic analyses of the IGF2-INS-TH gene cluster in relation to cardiovascular risk traits. Human Molecular Genetics, 2004, 13, 715-725.	2.9	57
94	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.	2.9	57
95	Cholesteryl ester transfer protein (CETP) as a drug target for cardiovascular disease. Nature Communications, 2021, 12, 5640.	12.8	57
96	Variants in the Human Insulin Gene That Affect Pre-mRNA Splicing: Is -23HphI a Functional Single Nucleotide Polymorphism at IDDM2?. Diabetes, 2006, 55, 260-264.	0.6	56
97	The long-term impact of folic acid in pregnancy on offspring DNA methylation: follow-up of the Aberdeen Folic Acid Supplementation Trial (AFAST). International Journal of Epidemiology, 2018, 47, 928-937.	1.9	56
98	Mosaic structural variation in children with developmental disorders. Human Molecular Genetics, 2015, 24, 2733-2745.	2.9	54
99	Appraising the causal relevance of DNA methylation for risk of lung cancer. International Journal of Epidemiology, 2019, 48, 1493-1504.	1.9	53
100	CScape: a tool for predicting oncogenic single-point mutations in the cancer genome. Scientific Reports, 2017, 7, 11597.	3.3	52
101	Using the MR-Base platform to investigate risk factors and drug targets for thousands of phenotypes. Wellcome Open Research, 2019, 4, 113.	1.8	52
102	TCTEX1D2 mutations underlie Jeune asphyxiating thoracic dystrophy with impaired retrograde intraflagellar transport. Nature Communications, 2015, 6, 7074.	12.8	51
103	Characterizing the Causal Pathway for Genetic Variants Associated with Neurological Phenotypes Using Human Brain-Derived Proteome Data. American Journal of Human Genetics, 2020, 106, 885-892.	6.2	51
104	Variation in DNA methylation of the oxytocin receptor gene predicts children's resilience to prenatal stress. Development and Psychopathology, 2017, 29, 1663-1674.	2.3	50
105	Rare Variant Analysis of Human and Rodent Obesity Genes in Individuals with Severe Childhood Obesity. Scientific Reports, 2017, 7, 4394.	3.3	50
106	Machine learning improves mortality risk prediction after cardiac surgery: Systematic review and meta-analysis. Journal of Thoracic and Cardiovascular Surgery, 2022, 163, 2075-2087.e9.	0.8	49
107	Using the MR-Base platform to investigate risk factors and drug targets for thousands of phenotypes. Wellcome Open Research, 2019, 4, 113.	1.8	47
108	PhenoSpD: an integrated toolkit for phenotypic correlation estimation and multiple testing correction using GWAS summary statistics. GigaScience, 2018, 7, .	6.4	46

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109	A transcriptome-wide Mendelian randomization study to uncover tissue-dependent regulatory mechanisms across the human phenome. Nature Communications, 2020, 11, 185.	12.8	45
110	The EWAS Catalog: a database of epigenome-wide association studies. Wellcome Open Research, 2022, 7, 41.	1.8	45
111	Gene-Centric Analysis Identifies Variants Associated With Interleukin-6 Levels and Shared Pathways With Other Inflammation Markers. Circulation: Cardiovascular Genetics, 2013, 6, 163-170.	5.1	44
112	Neonatal DNA methylation and early-onset conduct problems: A genome-wide, prospective study. Development and Psychopathology, 2018, 30, 383-397.	2.3	43
113	Identifying drug targets for neurological and psychiatric disease via genetics and the brain transcriptome. PLoS Genetics, 2021, 17, e1009224.	3.5	43
114	Importance of Genetic Studies in Consanguineous Populations for the Characterization of Novel Human Gene Functions. Annals of Human Genetics, 2016, 80, 187-196.	0.8	41
115	Inflammation-related epigenetic risk and child and adolescent mental health: A prospective study from pregnancy to middle adolescence. Development and Psychopathology, 2018, 30, 1145-1156.	2.3	39
116	Trans-ethnic Mendelian-randomization study reveals causal relationships between cardiometabolic factors and chronic kidney disease. International Journal of Epidemiology, 2022, 50, 1995-2010.	1.9	39
117	Population Genomics of Cardiometabolic Traits: Design of the University College London-London School of Hygiene and Tropical Medicine-Edinburgh-Bristol (UCLEB) Consortium. PLoS ONE, 2013, 8, e71345.	2.5	39
118	Associations between high blood pressure and DNA methylation. PLoS ONE, 2020, 15, e0227728.	2.5	37
119	HIPred: an integrative approach to predicting haploinsufficient genes. Bioinformatics, 2017, 33, 1751-1757.	4.1	36
120	Circulating Fatty Acids and Risk of Coronary Heart Disease and Stroke: Individual Participant Data Metaâ€Analysis in Up to 16Â126 Participants. Journal of the American Heart Association, 2020, 9, e013131.	3.7	36
121	IGF2BP1, IGF2BP2 and IGF2BP3 genotype, haplotype and genetic model studies in metabolic syndrome traits and diabetes. Growth Hormone and IGF Research, 2010, 20, 310-318.	1.1	35
122	Variants of ADRA2A are associated with fasting glucose, blood pressure, body mass index and type 2 diabetes risk: meta-analysis of four prospective studies. Diabetologia, 2011, 54, 1710-1719.	6.3	34
123	An integrative approach to predicting the functional effects of small indels in non-coding regions of the human genome. BMC Bioinformatics, 2017, 18, 442.	2.6	34
124	Influence of common genetic variation on blood lipid levels, cardiovascular risk, and coronary events in two British prospective cohort studies. European Heart Journal, 2013, 34, 972-981.	2.2	33
125	Nonsense Mutation in Coiled-Coil Domain Containing 151 Gene (CCDC151) Causes Primary Ciliary Dyskinesia. Human Mutation, 2014, 35, 1446-1448.	2.5	33
126	Role of DNA Methylation in Type 2 Diabetes Etiology: Using Genotype as a Causal Anchor. Diabetes, 2017, 66, 1713-1722.	0.6	32

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127	Smoking, DNA Methylation, and Lung Function: a Mendelian Randomization Analysis to Investigate Causal Pathways. American Journal of Human Genetics, 2020, 106, 315-326.	6.2	32
128	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. Human Molecular Genetics, 2021, 30, 393-409.	2.9	32
129	Angiotensin II type I receptor gene polymorphism: anthropometric and metabolic syndrome traits. Journal of Medical Genetics, 2005, 42, 396-401.	3.2	30
130	Molecular and Population Analysis of Natural Selection on the Human Haptoglobin Duplication. Annals of Human Genetics, 2012, 76, 352-362.	0.8	30
131	Texture classification using feature selection and kernel-based techniques. Soft Computing, 2015, 19, 2469-2480.	3.6	30
132	Low-frequency variation in TP53 has large effects on head circumference and intracranial volume. Nature Communications, 2019, 10, 357.	12.8	30
133	Prioritizing putative influential genes in cardiovascular disease susceptibility by applying tissue-specific Mendelian randomization. Genome Medicine, 2019, 11, 6.	8.2	30
134	EpiGraphDB: a database and data mining platform for health data science. Bioinformatics, 2021, 37, 1304-1311.	4.1	30
135	Late Life Metabolic Syndrome, Early Growth, and Common Polymorphism in the Growth Hormone and Placental Lactogen Gene Cluster. Journal of Clinical Endocrinology and Metabolism, 2004, 89, 5569-5576.	3.6	29
136	Can machine learning improve mortality prediction following cardiac surgery?. European Journal of Cardio-thoracic Surgery, 2020, 58, 1130-1136.	1.4	29
137	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.	1.7	28
138	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.	0.8	28
139	Homogeneous Assay of rs4343, anACEI/D Proxy, and an Analysis in the British Womenâ€™s Heart and Health Study (BWHHS). Disease Markers, 2008, 24, 11-17.	1.3	28
140	Genetic Variants Associated with von Willebrand Factor Levels in Healthy Men and Women Identified Using the HumanCVD BeadChip. Annals of Human Genetics, 2011, 75, 456-467.	0.8	28
141	Four Genetic Loci Influencing Electrocardiographic Indices of Left Ventricular Hypertrophy. Circulation: Cardiovascular Genetics, 2011, 4, 626-635.	5.1	28
142	Gene-centric meta-analyses for central adiposity traits in up to 57 412 individuals of European descent confirm known loci and reveal several novel associations. Human Molecular Genetics, 2014, 23, 2498-2510.	2.9	28
143	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
144	Manual 768 or 384 well microplate gel 'dry' electrophoresis for PCR checking and SNP genotyping. Nucleic Acids Research, 2003, 31, 48e-48.	14.5	27

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145	Canonical Correlation Analysis for Gene-Based Pleiotropy Discovery. PLoS Computational Biology, 2014, 10, e1003876.	3.2	27
146	Integrating Mendelian randomization and multiple-trait colocalization to uncover cell-specific inflammatory drivers of autoimmune and atopic disease. Human Molecular Genetics, 2019, 28, 3293-3300.	2.9	27
147	Replication of IGF2-INS-TH*5 haplotype effect on obesity in older men and study of related phenotypes. European Journal of Human Genetics, 2006, 14, 109-116.	2.8	26
148	Assessing the role of insulinâ€like growth factors and binding proteins in prostate cancer using Mendelian randomization: Genetic variants as instruments for circulating levels. International Journal of Cancer, 2016, 139, 1520-1533.	5.1	26
149	Metabolic Profiling of Adiponectin Levels in Adults. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	26
150	Association of copy number variation across the genome with neuropsychiatric traits in the general population. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2018, 177, 489-502.	1.7	26
151	Developing the WCRF International/University of Bristol Methodology for Identifying and Carrying Out Systematic Reviews of Mechanisms of Exposureâ€“Cancer Associations. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1667-1675.	2.5	25
152	A genome-wide association study of mitochondrial DNA copy number in two population-based cohorts. Human Genomics, 2019, 13, 6.	2.9	25
153	Linkage analysis of the 5q31â€“33 candidate region for asthma in 240 UK families. Genes and Immunity, 2001, 2, 20-24.	4.1	24
154	From a Single Whole Exome Read to Notions of Clinical Screening: Primary Ciliary Dyskinesia and RSPH9 p.Lys268del in the Arabian Peninsula. Annals of Human Genetics, 2012, 76, 211-220.	0.8	24
155	Lipids, obesity and gallbladder disease in women: insights from genetic studies using the cardiovascular gene-centric 50K SNP array. European Journal of Human Genetics, 2016, 24, 106-112.	2.8	23
156	A proteome-wide genetic investigation identifies several SARS-CoV-2-exploited host targets of clinical relevance. ELife, 2021, 10, .	6.0	23
157	Genome-wide survey of parent-of-origin effects on DNA methylation identifies candidate imprinted loci in humans. Human Molecular Genetics, 2018, 27, 2927-2939.	2.9	22
158	Replication and Characterization of Association between ABO SNPs and Red Blood Cell Traits by Meta-Analysis in Europeans. PLoS ONE, 2016, 11, e0156914.	2.5	22
159	SNP Genotyping by Combination of 192-Well MADGE, ARMS and Computerized Gel Image Analysis. BioTechniques, 2000, 29, 500-506.	1.8	21
160	Influence of Adiposity-Related Genetic Markers in a Population of Saudi Arabians Where Other Variables Influencing Obesity May Be Reduced. Disease Markers, 2014, 2014, 1-6.	1.3	21
161	The Effect of Circulating Zinc, Selenium, Copper and Vitamin K1 on COVID-19 Outcomes: A Mendelian Randomization Study. Nutrients, 2022, 14, 233.	4.1	21
162	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology. Nature Communications, 2022, 13, 634.	12.8	21

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163	Complexity of a complex trait locus: HP, HPR, haemoglobin and cholesterol. Gene, 2012, 499, 8-13.	2.2	20
164	Using multivariable Mendelian randomization to estimate the causal effect of bone mineral density on osteoarthritis risk, independently of body mass index. International Journal of Epidemiology, 2022, 51, 1254-1267.	1.9	20
165	Null mutation in human ciliary neurotrophic factor gene confers higher body mass index in males. European Journal of Human Genetics, 2002, 10, 749-752.	2.8	19
166	CScape-somatic: distinguishing driver and passenger point mutations in the cancer genome. Bioinformatics, 2020, 36, 3637-3644.	4.1	19
167	Triglyceride-containing lipoprotein sub-fractions and risk of coronary heart disease and stroke: A prospective analysis in 11,560 adults. European Journal of Preventive Cardiology, 2020, 27, 1617-1626.	1.8	19
168	Linking Physical Activity to Breast Cancer via Sex Steroid Hormones, Part 2: The Effect of Sex Steroid Hormones on Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 28-37.	2.5	19
169	Quantitated transcript haplotypes (QTH) ofAGTR1, reduced abundance of mRNA haplotypes containing 1166C (rs5186:A>C), and relevance to metabolic syndrome traits. Human Mutation, 2007, 28, 365-373.	2.5	18
170	Identifying low density lipoprotein cholesterol associated variants in the Annexin A2 (ANXA2) gene. Atherosclerosis, 2017, 261, 60-68.	0.8	18
171	The causal effects of serum lipids and apolipoproteins on kidney function: multivariable and bidirectional Mendelian-randomization analyses. International Journal of Epidemiology, 2021, 50, 1569-1579.	1.9	18
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