

Tom R Gaunt

List of Publications by Year in descending order

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Version: 2024-02-01

261
papers

35,044
citations

10351

72
h-index

5101

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. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
2	The MR-Base platform supports systematic causal inference across the human phenome. <i>ELife</i> , 2018, 7, .	2.8	3,639
3	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011, 478, 103-109.	13.7	1,855
4	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	13.7	1,328
5	Predicting the Functional, Molecular, and Phenotypic Consequences of Amino Acid Substitutions using Hidden Markov Models. <i>Human Mutation</i> , 2013, 34, 57-65.	1.1	1,057
6	The UK10K project identifies rare variants in health and disease. <i>Nature</i> , 2015, 526, 82-90.	13.7	1,014
7	Hardy-Weinberg Equilibrium Testing of Biological Ascertainment for Mendelian Randomization Studies. <i>American Journal of Epidemiology</i> , 2009, 169, 505-514.	1.6	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. <i>Bioinformatics</i> , 2017, 33, 272-279.	1.8	822
9	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , 2017, 541, 81-86.	13.7	743
10	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. <i>American Journal of Human Genetics</i> , 2016, 98, 680-696.	2.6	717
11	Mendelian randomization of blood lipids for coronary heart disease. <i>European Heart Journal</i> , 2015, 36, 539-550.	1.0	567
12	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. <i>Lancet</i> , The, 2015, 385, 351-361.	6.3	562
13	Metabolite Profiling and Cardiovascular Event Risk. <i>Circulation</i> , 2015, 131, 774-785.	1.6	547
14	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. <i>BMJ</i> , The, 2014, 349, g4164-g4164.	3.0	528
15	An integrative approach to predicting the functional effects of non-coding and coding sequence variation. <i>Bioinformatics</i> , 2015, 31, 1536-1543.	1.8	524
16	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. <i>Nature Genetics</i> , 2011, 43, 1131-1138.	9.4	501
17	Systematic identification of genetic influences on methylation across the human life course. <i>Genome Biology</i> , 2016, 17, 61.	3.8	489
18	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016, 7, 10023.	5.8	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. <i>Lancet Diabetes and Endocrinology</i> , 2015, 3, 526-534.	5.5	396
20	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. <i>JAMA Oncology</i> , 2017, 3, 636.	3.4	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). <i>Human Molecular Genetics</i> , 2015, 24, 2201-2217.	1.4	345
22	Identification of new therapeutic targets for osteoarthritis through genome-wide analyses of UK Biobank data. <i>Nature Genetics</i> , 2019, 51, 230-236.	9.4	331
23	Causal Associations of Adiposity and Body Fat Distribution With Coronary Heart Disease, Stroke Subtypes, and Type 2 Diabetes Mellitus. <i>Circulation</i> , 2017, 135, 2373-2388.	1.6	304
24	C-reactive protein and its role in metabolic syndrome: mendelian randomisation study. <i>Lancet</i> , 2005, 366, 1954-1959.	6.3	300
25	Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. <i>Nature Communications</i> , 2015, 6, 8111.	5.8	300
26	Phenome-wide Mendelian randomization mapping the influence of the plasma proteome on complex diseases. <i>Nature Genetics</i> , 2020, 52, 1122-1131.	9.4	298
27	FATHMM-XF: accurate prediction of pathogenic point mutations via extended features. <i>Bioinformatics</i> , 2018, 34, 511-513.	1.8	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. <i>International Journal of Epidemiology</i> , 2015, 44, 1288-1304.	0.9	244
29	Cubic exact solutions for the estimation of pairwise haplotype frequencies: implications for linkage disequilibrium analyses and a web tool 'CubeX'. <i>BMC Bioinformatics</i> , 2007, 8, 428.	1.2	239
30	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. <i>American Journal of Human Genetics</i> , 2012, 90, 410-425.	2.6	239
31	Data Resource Profile: Accessible Resource for Integrated Epigenomic Studies (ARIES). <i>International Journal of Epidemiology</i> , 2015, 44, 1181-1190.	0.9	238
32	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. <i>American Journal of Human Genetics</i> , 2012, 91, 823-838.	2.6	227
33	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. <i>Nature Genetics</i> , 2021, 53, 1636-1648.	9.4	223
34	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	9.4	218
35	Predicting the functional consequences of cancer-associated amino acid substitutions. <i>Bioinformatics</i> , 2013, 29, 1504-1510.	1.8	208
36	Prenatal and early life influences on epigenetic age in children: a study of mother-offspring pairs from two cohort studies. <i>Human Molecular Genetics</i> , 2016, 25, 191-201.	1.4	205

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37	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. <i>Cell</i> , 2021, 184, 4784-4818.e17.	13.5	188
38	Gene-centric Association Signals for Lipids and Apolipoproteins Identified via the HumanCVD BeadChip. <i>American Journal of Human Genetics</i> , 2009, 85, 628-642.	2.6	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. <i>Environmental Health Perspectives</i> , 2015, 123, 193-199.	2.8	178
40	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. <i>Human Molecular Genetics</i> , 2011, 20, 2273-2284.	1.4	168
41	Ranking non-synonymous single nucleotide polymorphisms based on disease concepts. <i>Human Genomics</i> , 2014, 8, 11.	1.4	163
42	Blood Pressure Loci Identified with a Gene-Centric Array. <i>American Journal of Human Genetics</i> , 2011, 89, 688-700.	2.6	159
43	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. <i>American Journal of Human Genetics</i> , 2014, 94, 349-360.	2.6	158
44	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , 2016, 7, 10494.	5.8	153
45	Software Application Profile: PHESANT: a tool for performing automated phenome scans in UK Biobank. <i>International Journal of Epidemiology</i> , 2018, 47, 29-35.	0.9	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. <i>International Journal of Epidemiology</i> , 2013, 42, 475-492.	0.9	145
47	Copy Number Variations and Cognitive Phenotypes in Unselected Populations. <i>JAMA - Journal of the American Medical Association</i> , 2015, 313, 2044.	3.8	143
48	Loci influencing blood pressure identified using a cardiovascular gene-centric array. <i>Human Molecular Genetics</i> , 2013, 22, 1663-1678.	1.4	141
49	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. <i>American Journal of Human Genetics</i> , 2017, 100, 865-884.	2.6	131
50	Age-related DNA methylation changes are tissue-specific with ELOVL2 promoter methylation as exception. <i>Epigenetics and Chromatin</i> , 2018, 11, 25.	1.8	130
51	Epigenetic profiling of ADHD symptoms trajectories: a prospective, methylome-wide study. <i>Molecular Psychiatry</i> , 2017, 22, 250-256.	4.1	124
52	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. <i>American Journal of Human Genetics</i> , 2011, 88, 6-18.	2.6	122
53	Plasma urate concentration and risk of coronary heart disease: a Mendelian randomisation analysis. <i>Lancet Diabetes and Endocrinology</i> , 2016, 4, 327-336.	5.5	122
54	Longitudinal analysis of DNA methylation associated with birth weight and gestational age. <i>Human Molecular Genetics</i> , 2015, 24, 3752-3763.	1.4	120

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55	Polymorphisms in the interleukin-4 and interleukin-4 receptor $\hat{\pm}$ chain genes confer susceptibility to asthma and atopy in a Caucasian population. <i>Clinical and Experimental Allergy</i> , 2003, 33, 1111-1117.	1.4	115
56	Secretory Phospholipase A2-IIA and Cardiovascular Disease. <i>Journal of the American College of Cardiology</i> , 2013, 62, 1966-1976.	1.2	115
57	MIDAS: software for analysis and visualisation of interallelic disequilibrium between multiallelic markers. <i>BMC Bioinformatics</i> , 2006, 7, 227.	1.2	110
58	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. <i>PLoS Genetics</i> , 2015, 11, e1005035.	1.5	107
59	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. <i>International Journal of Epidemiology</i> , 2018, 47, 22-23u.	0.9	105
60	Positive associations between single nucleotide polymorphisms in the IGF2 gene region and body mass index in adult males. <i>Human Molecular Genetics</i> , 2001, 10, 1491-1501.	1.4	102
61	Psychosocial adversity and socioeconomic position during childhood and epigenetic age: analysis of two prospective cohort studies. <i>Human Molecular Genetics</i> , 2018, 27, 1301-1308.	1.4	102
62	DNA Methylation and BMI: Investigating Identified Methylation Sites at <i>HIF3A</i> in a Causal Framework. <i>Diabetes</i> , 2016, 65, 1231-1244.	0.3	95
63	The EWAS Catalog: a database of epigenome-wide association studies. <i>Wellcome Open Research</i> , 0, 7, 41.	0.9	95
64	Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. <i>International Journal of Epidemiology</i> , 2016, 45, 1927-1937.	0.9	94
65	Sixty-Five Common Genetic Variants and Prediction of Type 2 Diabetes. <i>Diabetes</i> , 2015, 64, 1830-1840.	0.3	91
66	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. <i>Nature Genetics</i> , 2020, 52, 1314-1332.	9.4	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. <i>PLoS ONE</i> , 2008, 3, e3011.	1.1	90
68	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. <i>Journal of the American Heart Association</i> , 2017, 6, .	1.6	89
69	DNA methylation and substance-use risk: a prospective, genome-wide study spanning gestation to adolescence. <i>Translational Psychiatry</i> , 2016, 6, e976-e976.	2.4	86
70	The epigenetic clock and physical development during childhood and adolescence: longitudinal analysis from a UK birth cohort. <i>International Journal of Epidemiology</i> , 2017, 46, dyw307.	0.9	86
71	TAS2R38 (phenylthiocarbamide) haplotypes, coronary heart disease traits, and eating behavior in the British Women's Heart and Health Study. <i>American Journal of Clinical Nutrition</i> , 2005, 81, 1005-1011.	2.2	84
72	Gene-centric meta-analyses of 108 912 individuals confirm known body mass index loci and reveal three novel signals. <i>Human Molecular Genetics</i> , 2013, 22, 184-201.	1.4	82

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73	The variant call format provides efficient and robust storage of GWAS summary statistics. <i>Genome Biology</i> , 2021, 22, 32.	3.8	82
74	An epigenome-wide association meta-analysis of prenatal maternal stress in neonates: A model approach for replication. <i>Epigenetics</i> , 2016, 11, 140-149.	1.3	80
75	Liver Function and Risk of Type 2 Diabetes: Bidirectional Mendelian Randomization Study. <i>Diabetes</i> , 2019, 68, 1681-1691.	0.3	79
76	Mendelian Randomization Studies Do Not Support a Role for Raised Circulating Triglyceride Levels Influencing Type 2 Diabetes, Glucose Levels, or Insulin Resistance. <i>Diabetes</i> , 2011, 60, 1008-1018.	0.3	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. <i>Cancer Causes and Control</i> , 2015, 26, 1603-1616.	0.8	77
78	Whole-genome sequence-based analysis of thyroid function. <i>Nature Communications</i> , 2015, 6, 5681.	5.8	75
79	Hypertensive Disorders of Pregnancy and DNA Methylation in Newborns. <i>Hypertension</i> , 2019, 74, 375-383.	1.3	73
80	Prenatal unhealthy diet, insulin-like growth factor 2 gene (<i>IGF2</i>) methylation, and attention deficit hyperactivity disorder symptoms in youth with early-onset conduct problems. <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , 2017, 58, 19-27.	3.1	70
81	Searching for the causal effects of body mass index in over 300 000 participants in UK Biobank, using Mendelian randomization. <i>PLoS Genetics</i> , 2019, 15, e1007951.	1.5	70
82	A pathway-based data integration framework for prediction of disease progression. <i>Bioinformatics</i> , 2014, 30, 838-845.	1.8	67
83	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. <i>Nature Genetics</i> , 2016, 48, 1303-1312.	9.4	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. <i>Cancer Causes and Control</i> , 2017, 28, 497-528.	0.8	65
85	Mendelian Randomization Analysis Identifies CpG Sites as Putative Mediators for Genetic Influences on Cardiovascular Disease Risk. <i>American Journal of Human Genetics</i> , 2017, 101, 590-602.	2.6	65
86	Epigenome-wide change and variation in DNA methylation in childhood: trajectories from birth to late adolescence. <i>Human Molecular Genetics</i> , 2021, 30, 119-134.	1.4	65
87	The Relationship Between Plasma Angiopoietin-like Protein 4 Levels, Angiopoietin-like Protein 4 Genotype, and Coronary Heart Disease Risk. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2010, 30, 2277-2282.	1.1	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. <i>BMC Genetics</i> , 2004, 5, 17.	2.7	63
89	Molecular genetics of human growth hormone, insulin-like growth factors and their pathways in common disease. <i>Human Genetics</i> , 2007, 122, 1-21.	1.8	63
90	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. <i>Nature Communications</i> , 2014, 5, 4871.	5.8	62

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91	Epigenome-wide association study of asthma and wheeze in childhood and adolescence. <i>Clinical Epigenetics</i> , 2017, 9, 112.	1.8	60
92	Exploiting horizontal pleiotropy to search for causal pathways within a Mendelian randomization framework. <i>Nature Communications</i> , 2020, 11, 1010.	5.8	58
93	Haplotypic analyses of the IGF2-INS-TH gene cluster in relation to cardiovascular risk traits. <i>Human Molecular Genetics</i> , 2004, 13, 715-725.	1.4	57
94	Systematic Mendelian randomization framework elucidates hundreds of CpG sites which may mediate the influence of genetic variants on disease. <i>Human Molecular Genetics</i> , 2018, 27, 3293-3304.	1.4	57
95	Cholesteryl ester transfer protein (CETP) as a drug target for cardiovascular disease. <i>Nature Communications</i> , 2021, 12, 5640.	5.8	57
96	Variants in the Human Insulin Gene That Affect Pre-mRNA Splicing: Is -23HphI a Functional Single Nucleotide Polymorphism at IDDM2?. <i>Diabetes</i> , 2006, 55, 260-264.	0.3	56
97	The long-term impact of folic acid in pregnancy on offspring DNA methylation: follow-up of the Aberdeen Folic Acid Supplementation Trial (FAST). <i>International Journal of Epidemiology</i> , 2018, 47, 928-937.	0.9	56
98	Mosaic structural variation in children with developmental disorders. <i>Human Molecular Genetics</i> , 2015, 24, 2733-2745.	1.4	54
99	Appraising the causal relevance of DNA methylation for risk of lung cancer. <i>International Journal of Epidemiology</i> , 2019, 48, 1493-1504.	0.9	53
100	CScape: a tool for predicting oncogenic single-point mutations in the cancer genome. <i>Scientific Reports</i> , 2017, 7, 11597.	1.6	52
101	Using the MR-Base platform to investigate risk factors and drug targets for thousands of phenotypes. <i>Wellcome Open Research</i> , 2019, 4, 113.	0.9	52
102	TCTEX1D2 mutations underlie Jeune asphyxiating thoracic dystrophy with impaired retrograde intraflagellar transport. <i>Nature Communications</i> , 2015, 6, 7074.	5.8	51
103	Characterizing the Causal Pathway for Genetic Variants Associated with Neurological Phenotypes Using Human Brain-Derived Proteome Data. <i>American Journal of Human Genetics</i> , 2020, 106, 885-892.	2.6	51
104	Variation in DNA methylation of the oxytocin receptor gene predicts children's resilience to prenatal stress. <i>Development and Psychopathology</i> , 2017, 29, 1663-1674.	1.4	50
105	Rare Variant Analysis of Human and Rodent Obesity Genes in Individuals with Severe Childhood Obesity. <i>Scientific Reports</i> , 2017, 7, 4394.	1.6	50
106	Machine learning improves mortality risk prediction after cardiac surgery: Systematic review and meta-analysis. <i>Journal of Thoracic and Cardiovascular Surgery</i> , 2022, 163, 2075-2087.e9.	0.4	49
107	Using the MR-Base platform to investigate risk factors and drug targets for thousands of phenotypes. <i>Wellcome Open Research</i> , 2019, 4, 113.	0.9	47
108	PhenoSpD: an integrated toolkit for phenotypic correlation estimation and multiple testing correction using GWAS summary statistics. <i>GigaScience</i> , 2018, 7, .	3.3	46

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109	A transcriptome-wide Mendelian randomization study to uncover tissue-dependent regulatory mechanisms across the human phenome. <i>Nature Communications</i> , 2020, 11, 185.	5.8	45
110	The EWAS Catalog: a database of epigenome-wide association studies. <i>Wellcome Open Research</i> , 2022, 7, 41.	0.9	45
111	Gene-Centric Analysis Identifies Variants Associated With Interleukin-6 Levels and Shared Pathways With Other Inflammation Markers. <i>Circulation: Cardiovascular Genetics</i> , 2013, 6, 163-170.	5.1	44
112	Neonatal DNA methylation and early-onset conduct problems: A genome-wide, prospective study. <i>Development and Psychopathology</i> , 2018, 30, 383-397.	1.4	43
113	Identifying drug targets for neurological and psychiatric disease via genetics and the brain transcriptome. <i>PLoS Genetics</i> , 2021, 17, e1009224.	1.5	43
114	Importance of Genetic Studies in Consanguineous Populations for the Characterization of Novel Human Gene Functions. <i>Annals of Human Genetics</i> , 2016, 80, 187-196.	0.3	41
115	Inflammation-related epigenetic risk and child and adolescent mental health: A prospective study from pregnancy to middle adolescence. <i>Development and Psychopathology</i> , 2018, 30, 1145-1156.	1.4	39
116	Trans-ethnic Mendelian-randomization study reveals causal relationships between cardiometabolic factors and chronic kidney disease. <i>International Journal of Epidemiology</i> , 2022, 50, 1995-2010.	0.9	39
117	Population Genomics of Cardiometabolic Traits: Design of the University College London-London School of Hygiene and Tropical Medicine-Edinburgh-Bristol (UCL-EB) Consortium. <i>PLoS ONE</i> , 2013, 8, e71345.	1.1	39
118	Associations between high blood pressure and DNA methylation. <i>PLoS ONE</i> , 2020, 15, e0227728.	1.1	37
119	HiPred: an integrative approach to predicting haploinsufficient genes. <i>Bioinformatics</i> , 2017, 33, 1751-1757.	1.8	36
120	Circulating Fatty Acids and Risk of Coronary Heart Disease and Stroke: Individual Participant Data Meta-Analysis in Up to 16126 Participants. <i>Journal of the American Heart Association</i> , 2020, 9, e013131.	1.6	36
121	IGF2BP1, IGF2BP2 and IGF2BP3 genotype, haplotype and genetic model studies in metabolic syndrome traits and diabetes. <i>Growth Hormone and IGF Research</i> , 2010, 20, 310-318.	0.5	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. <i>Diabetologia</i> , 2011, 54, 1710-1719.	2.9	34
123	An integrative approach to predicting the functional effects of small indels in non-coding regions of the human genome. <i>BMC Bioinformatics</i> , 2017, 18, 442.	1.2	34
124	Influence of common genetic variation on blood lipid levels, cardiovascular risk, and coronary events in two British prospective cohort studies. <i>European Heart Journal</i> , 2013, 34, 972-981.	1.0	33
125	Nonsense Mutation in Coiled-Coil Domain Containing 151 Gene (<i>CCDC151</i>) Causes Primary Ciliary Dyskinesia. <i>Human Mutation</i> , 2014, 35, 1446-1448.	1.1	33
126	Role of DNA Methylation in Type 2 Diabetes Etiology: Using Genotype as a Causal Anchor. <i>Diabetes</i> , 2017, 66, 1713-1722.	0.3	32

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127	Smoking, DNA Methylation, and Lung Function: a Mendelian Randomization Analysis to Investigate Causal Pathways. <i>American Journal of Human Genetics</i> , 2020, 106, 315-326.	2.6	32
128	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. <i>Human Molecular Genetics</i> , 2021, 30, 393-409.	1.4	32
129	Angiotensin II type I receptor gene polymorphism: anthropometric and metabolic syndrome traits. <i>Journal of Medical Genetics</i> , 2005, 42, 396-401.	1.5	30
130	Molecular and Population Analysis of Natural Selection on the Human Haptoglobin Duplication. <i>Annals of Human Genetics</i> , 2012, 76, 352-362.	0.3	30
131	Texture classification using feature selection and kernel-based techniques. <i>Soft Computing</i> , 2015, 19, 2469-2480.	2.1	30
132	Low-frequency variation in TP53 has large effects on head circumference and intracranial volume. <i>Nature Communications</i> , 2019, 10, 357.	5.8	30
133	Prioritizing putative influential genes in cardiovascular disease susceptibility by applying tissue-specific Mendelian randomization. <i>Genome Medicine</i> , 2019, 11, 6.	3.6	30
134	EpiGraphDB: a database and data mining platform for health data science. <i>Bioinformatics</i> , 2021, 37, 1304-1311.	1.8	30
135	Late Life Metabolic Syndrome, Early Growth, and Common Polymorphism in the Growth Hormone and Placental Lactogen Gene Cluster. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2004, 89, 5569-5576.	1.8	29
136	Can machine learning improve mortality prediction following cardiac surgery?. <i>European Journal of Cardio-thoracic Surgery</i> , 2020, 58, 1130-1136.	0.6	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. <i>Paediatric and Perinatal Epidemiology</i> , 2006, 20, 244-250.	0.8	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. <i>Atherosclerosis</i> , 2008, 196, 871-878.	0.4	28
139	Homogeneous Assay of rs4343, anACEI/D Proxy, and an Analysis in the British Women's Heart and Health Study (BWHHS). <i>Disease Markers</i> , 2008, 24, 11-17.	0.6	28
140	Genetic Variants Associated with von Willebrand Factor Levels in Healthy Men and Women Identified Using the HumanCVD BeadChip. <i>Annals of Human Genetics</i> , 2011, 75, 456-467.	0.3	28
141	Four Genetic Loci Influencing Electrocardiographic Indices of Left Ventricular Hypertrophy. Circulation: <i>Cardiovascular Genetics</i> , 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. <i>Human Molecular Genetics</i> , 2014, 23, 2498-2510.	1.4	28
143	Metabolic Characterization of a Rare Genetic Variation Within <i>APOC3</i> and Its Lipoprotein Lipase-Independent Effects. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 231-239.	5.1	28
144	Manual 768 or 384 well microplate gel 'dry' electrophoresis for PCR checking and SNP genotyping. <i>Nucleic Acids Research</i> , 2003, 31, 48e-48.	6.5	27

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145	Canonical Correlation Analysis for Gene-Based Pleiotropy Discovery. PLoS Computational Biology, 2014, 10, e1003876.	1.5	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.	1.4	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.	1.4	26
148	Assessing the role of insulin-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.	2.3	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.	1.1	26
151	Developing the WCRF International/University of Bristol Methodology for Identifying and Carrying Out Systematic Reviews of Mechanisms of Exposure-Cancer Associations. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1667-1675.	1.1	25
152	A genome-wide association study of mitochondrial DNA copy number in two population-based cohorts. Human Genomics, 2019, 13, 6.	1.4	25
153	Linkage analysis of the 5q31-33 candidate region for asthma in 240 UK families. Genes and Immunity, 2001, 2, 20-24.	2.2	24
154	From a Single Whole Exome Read to Notions of Clinical Screening: Primary Ciliary Dyskinesia and <i>RSPH9</i> p.Lys268del in the Arabian Peninsula. Annals of Human Genetics, 2012, 76, 211-220.	0.3	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.	1.4	23
156	A proteome-wide genetic investigation identifies several SARS-CoV-2-exploited host targets of clinical relevance. ELife, 2021, 10, .	2.8	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.	1.4	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.	1.1	22
159	SNP Genotyping by Combination of 192-Well MADGE, ARMS and Computerized Gel Image Analysis. BioTechniques, 2000, 29, 500-506.	0.8	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.	0.6	21
161	The Effect of Circulating Zinc, Selenium, Copper and Vitamin K1 on COVID-19 Outcomes: A Mendelian Randomization Study. Nutrients, 2022, 14, 233.	1.7	21
162	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology. Nature Communications, 2022, 13, 634.	5.8	21

#	ARTICLE	IF	CITATIONS
163	Complexity of a complex trait locus: HP, HPR, haemoglobin and cholesterol. <i>Gene</i> , 2012, 499, 8-13.	1.0	20
164	Using multivariable Mendelian randomization to estimate the causal effect of bone mineral density on osteoarthritis risk, independently of body mass index. <i>International Journal of Epidemiology</i> , 2022, 51, 1254-1267.	0.9	20
165	Null mutation in human ciliary neurotrophic factor gene confers higher body mass index in males. <i>European Journal of Human Genetics</i> , 2002, 10, 749-752.	1.4	19
166	<i>C</i> Scape-somatic: distinguishing driver and passenger point mutations in the cancer genome. <i>Bioinformatics</i> , 2020, 36, 3637-3644.	1.8	19
167	Triglyceride-containing lipoprotein sub-fractions and risk of coronary heart disease and stroke: A prospective analysis in 11,560 adults. <i>European Journal of Preventive Cardiology</i> , 2020, 27, 1617-1626.	0.8	19
168	Linking Physical Activity to Breast Cancer via Sex Steroid Hormones, Part 2: The Effect of Sex Steroid Hormones on Breast Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, 31, 28-37.	1.1	19
169	Quantitated transcript haplotypes (QTH) of <i>AGTR1</i> , reduced abundance of mRNA haplotypes containing 1166C (rs5186:A>C), and relevance to metabolic syndrome traits. <i>Human Mutation</i> , 2007, 28, 365-373.	1.1	18
170	Identifying low density lipoprotein cholesterol associated variants in the Annexin A2 (<i>ANXA2</i>) gene. <i>Atherosclerosis</i> , 2017, 261, 60-68.	0.4	18
171	The causal effects of serum lipids and apolipoproteins on kidney function: multivariable and bidirectional Mendelian-randomization analyses. <i>International Journal of Epidemiology</i> , 2021, 50, 1569-1579.	0.9	18
172	Refined Association Mapping for a Quantitative Trait: Weight in the H19-IGF2-INS-TH Region. <i>Annals of Human Genetics</i> , 2006, 70, 848-856.	0.3	17
173	The association of the paraoxonase (PON1) Q192R polymorphism with depression in older women: findings from the British Women's Heart and Health Study. <i>Journal of Epidemiology and Community Health</i> , 2007, 61, 85-87.	2.0	17
174	Texture analysis in gel electrophoresis images using an integrative kernel-based approach. <i>Scientific Reports</i> , 2016, 6, 19256.	1.6	17
175	A Methylome-Wide Association Study of Trajectories of Oppositional Defiant Behaviors and Biological Overlap With Attention Deficit Hyperactivity Disorder. <i>Child Development</i> , 2018, 89, 1839-1855.	1.7	17
176	DNA methylation derived systemic inflammation indices are associated with head and neck cancer development and survival. <i>Oral Oncology</i> , 2018, 85, 87-94.	0.8	17
177	Association of physical activity intensity and bout length with mortality: An observational study of 79,503 UK Biobank participants. <i>PLoS Medicine</i> , 2021, 18, e1003757.	3.9	17
178	Combined analysis of <i>CHRNA5</i> , <i>CHRNA3</i> and <i>CYP2A6</i> in relation to adolescent smoking behaviour. <i>Journal of Psychopharmacology</i> , 2011, 25, 915-923.	2.0	16
179	A gene-centric analysis of activated partial thromboplastin time and activated protein C resistance using the HumanCVD focused genotyping array. <i>European Journal of Human Genetics</i> , 2013, 21, 779-783.	1.4	15
180	Maternal eating disorders affect offspring cord blood DNA methylation: a prospective study. <i>Clinical Epigenetics</i> , 2017, 9, 120.	1.8	15

#	ARTICLE	IF	CITATIONS
181	MELODI: Mining Enriched Literature Objects to Derive Intermediates. <i>International Journal of Epidemiology</i> , 2018, 47, 369-379.	0.9	15
182	Leveraging brain cortex-derived molecular data to elucidate epigenetic and transcriptomic drivers of complex traits and disease. <i>Translational Psychiatry</i> , 2019, 9, 105.	2.4	15
183	Genotype of galectin 2 (LGALS2) is associated with insulin-glucose profile in the British Women's Heart and Health Study. <i>Diabetologia</i> , 2006, 49, 673-677.	2.9	14
184	Mendelian Randomisation study of the influence of eGFR on coronary heart disease. <i>Scientific Reports</i> , 2016, 6, 28514.	1.6	14
185	Genetic determinants of circulating haptoglobin concentration. <i>Clinica Chimica Acta</i> , 2019, 494, 138-142.	0.5	14
186	MELODI Presto: a fast and agile tool to explore semantic triples derived from biomedical literature. <i>Bioinformatics</i> , 2021, 37, 583-585.	1.8	14
187	A pathway-centric approach to rare variant association analysis. <i>European Journal of Human Genetics</i> , 2017, 25, 123-129.	1.4	13
188	Cardiometabolic phenotypes and mitochondrial DNA copy number in two cohorts of UK women. <i>Mitochondrion</i> , 2018, 39, 9-19.	1.6	13
189	Prediction of driver variants in the cancer genome via machine learning methodologies. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	13
190	Validation of lipid-related therapeutic targets for coronary heart disease prevention using human genetics. <i>Nature Communications</i> , 2021, 12, 6120.	5.8	13
191	Integration of Genetics into a Systems Model of Electrocardiographic Traits Using HumanCVD BeadChip. <i>Circulation: Cardiovascular Genetics</i> , 2012, 5, 630-638.	5.1	12
192	Triangulating Molecular Evidence to Prioritize Candidate Causal Genes at Established Atopic Dermatitis Loci. <i>Journal of Investigative Dermatology</i> , 2021, 141, 2620-2629.	0.3	12
193	MendelVar: gene prioritization at GWAS loci using phenotypic enrichment of Mendelian disease genes. <i>Bioinformatics</i> , 2021, 37, 1-8.	1.8	12
194	Interaction between birthweight and polymorphism in the calcium-sensing receptor gene in determination of adult bone mass: the Hertfordshire cohort study. <i>Journal of Rheumatology</i> , 2007, 34, 769-75.	1.0	12
195	Linking Physical Activity to Breast Cancer via Sex Hormones, Part 1: The Effect of Physical Activity on Sex Steroid Hormones. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, 31, 16-27.	1.1	12
196	Using genetic variation to disentangle the complex relationship between food intake and health outcomes. <i>PLoS Genetics</i> , 2022, 18, e1010162.	1.5	12
197	A study of TH01 and IGF2-INS-TH haplotypes in relation to smoking initiation in three independent surveys. <i>Pharmacogenetics and Genomics</i> , 2006, 16, 15-23.	0.7	11
198	A Study of Relationships Between Single Nucleotide Polymorphisms from the Growth Hormone-Insulin-like Growth Factor Axis and Bone Mass: the Hertfordshire Cohort Study. <i>Journal of Rheumatology</i> , 2009, 36, 1520-1526.	1.0	11

#	ARTICLE	IF	CITATIONS
199	Collapsed methylation quantitative trait loci analysis for low frequency and rare variants. <i>Human Molecular Genetics</i> , 2016, 25, 4339-4349.	1.4	11
200	Haptoglobin genotype and outcome after aneurysmal subarachnoid haemorrhage. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2020, 91, 305-313.	0.9	11
201	Haplotype of growth hormone and angiotensin I-converting enzyme genes, serum angiotensin I-converting enzyme and ventricular growth: pathway inference in pharmacogenetics. <i>Pharmacogenetics and Genomics</i> , 2007, 17, 291-294.	0.7	10
202	Amplification ratio control system for copy number variation genotyping. <i>Nucleic Acids Research</i> , 2011, 39, e54-e54.	6.5	10
203	A Multi-Cohort Study of Polymorphisms in the GH/IGF Axis and Physical Capability: The HALCYon Programme. <i>PLoS ONE</i> , 2012, 7, e29883.	1.1	10
204	Diagnosis of Coronary Heart Diseases Using Gene Expression Profiling; Stable Coronary Artery Disease, Cardiac Ischemia with and without Myocardial Necrosis. <i>PLoS ONE</i> , 2016, 11, e0149475.	1.1	10
205	Longitudinal analysis strategies for modelling epigenetic trajectories. <i>International Journal of Epidemiology</i> , 2018, 47, 516-525.	0.9	10
206	Incorporating Non-Coding Annotations into Rare Variant Analysis. <i>PLoS ONE</i> , 2016, 11, e0154181.	1.1	10
207	eNOS and coronary artery disease: Publication bias and the eclipse of hypothesis-driven meta-analysis in genetic association studies. <i>Gene</i> , 2015, 556, 257-258.	1.0	9
208	Linking Physical Activity to Breast Cancer: Text Mining Results and a Protocol for Systematically Reviewing Three Potential Mechanistic Pathways. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, , .	1.1	9
209	Separating the direct effects of traits on atherosclerotic cardiovascular disease from those mediated by type 2 diabetes. <i>Diabetologia</i> , 2022, 65, 790-799.	2.9	9
210	An expectation-maximization program for determining allelic spectrum from CNV data (CoNVEM): insights into population allelic architecture and its mutational history. <i>Human Mutation</i> , 2010, 31, 414-420.	1.1	8
211	Gene-centric association signals for haemostasis and thrombosis traits identified with the HumanCVD BeadChip. <i>Thrombosis and Haemostasis</i> , 2013, 110, 995-1003.	1.8	8
212	Platelet Glycoprotein Ib Î±â€œChain as a Putative Therapeutic Target for Juvenile Idiopathic Arthritis: A Mendelian Randomization Study. <i>Arthritis and Rheumatology</i> , 2021, 73, 693-701.	2.9	8
213	An informatics consult approach for generating clinical evidence for treatment decisions. <i>BMC Medical Informatics and Decision Making</i> , 2021, 21, 281.	1.5	8
214	Questioning INS VNTR role in obesity and diabetes: subclasses tag IGF2-INS-TH haplotypes; and -23HphI as a STEP (splicing and translational efficiency polymorphism). <i>Physiological Genomics</i> , 2006, 28, 113-113.	1.0	7
215	Identifying Highly Penetrant Disease Causal Mutations Using Next Generation Sequencing: Guide to Whole Process. <i>BioMed Research International</i> , 2015, 2015, 1-16.	0.9	7
216	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. <i>BioData Mining</i> , 2017, 10, 25.	2.2	7

#	ARTICLE	IF	CITATIONS
217	Physical activity phenotyping with activity bigrams, and their association with BMI. <i>International Journal of Epidemiology</i> , 2017, 46, 1857-1870.	0.9	7
218	Multi-ancestry Mendelian randomization of omics traits revealing drug targets of COVID-19 severity. <i>EBioMedicine</i> , 2022, 81, 104112.	2.7	7
219	A Protein Domain and Family Based Approach to Rare Variant Association Analysis. <i>PLoS ONE</i> , 2016, 11, e0153803.	1.1	6
220	Functional Analysis of the Coronary Heart Disease Risk Locus on Chromosome 21q22. <i>Disease Markers</i> , 2017, 2017, 1-10.	0.6	6
221	Estimating the Frequency of Single Point Driver Mutations across Common Solid Tumours. <i>Scientific Reports</i> , 2019, 9, 13452.	1.6	6
222	Identifying epigenetic biomarkers of established prognostic factors and survival in a clinical cohort of individuals with oropharyngeal cancer. <i>Clinical Epigenetics</i> , 2020, 12, 95.	1.8	6
223	Sequential Sentinel SNP Regional Association Plots (SSSâ€RAP): An Approach for Testing Independence of SNP Association Signals Using Metaâ€Analysis Data. <i>Annals of Human Genetics</i> , 2013, 77, 67-79.	0.3	5
224	Haptoglobin Duplicon, Hemoglobin, and Vitamin C: Analyses in the British Womenâ€™s Heart and Health Study and Caerphilly Prospective Study. <i>Disease Markers</i> , 2014, 2014, 1-5.	0.6	5
225	Opportunities and Challenges in Functional Genomics Research in Osteoporosis: Report From a Workshop Held by the Causes Working Group of the Osteoporosis and Bone Research Academy of the Royal Osteoporosis Society on October 5th 2020. <i>Frontiers in Endocrinology</i> , 2020, 11, 630875.	1.5	5
226	Reply to Janssen et al. Comment on â€Sobczyk, M.K.; Gaunt, T.R. The Effect of Circulating Zinc, Selenium, Copper and Vitamin K1 on COVID-19 Outcomes: A Mendelian Randomization Study. <i>Nutrients</i> 2022, 14, 233â€ Nutrients, 2022, 14, 1113.	1.7	5
227	Phenotypic Causal Inference Using Genome-Wide Association Study Data: Mendelian Randomization and Beyond. <i>Annual Review of Biomedical Data Science</i> , 2022, 5, 1-17.	2.8	5
228	The impact of fatty acids biosynthesis on the risk of cardiovascular diseases in Europeans and East Asians: a Mendelian randomization study. <i>Human Molecular Genetics</i> , 2022, 31, 4034-4054.	1.4	5
229	Comment on: Marchand and Polychronakos (2007) Evaluation of Polymorphic Splicing in the Mechanism of the Association of the Insulin Gene with Diabetes: <i>Diabetes</i> 56:709 713. <i>Diabetes</i> , 2007, 56, e16-e16.	0.3	4
230	Genome-Wide Data-Mining of Candidate Human Splice Translational Efficiency Polymorphisms (STEPs) and an Online Database. <i>PLoS ONE</i> , 2010, 5, e13340.	1.1	4
231	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. <i>American Journal of Human Genetics</i> , 2012, 90, 753.	2.6	4
232	Proxy Molecular Diagnosis from Whole-Exome Sequencing Reveals Papillon-Lefevre Syndrome Caused by a Missense Mutation in CTSC. <i>PLoS ONE</i> , 2015, 10, e0121351.	1.1	4
233	HAPRAP: a haplotype-based iterative method for statistical fine mapping using GWAS summary statistics. <i>Bioinformatics</i> , 2017, 33, 79-86.	1.8	4
234	Haptoglobin genotype and outcome after spontaneous intracerebral haemorrhage. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2020, 91, 298-304.	0.9	4

#	ARTICLE	IF	CITATIONS
235	GTB – an online genome tolerance browser. BMC Bioinformatics, 2017, 18, 20.	1.2	3
236	Mendelian Randomization Analysis Reveals a Causal Effect of Urinary Sodium/Urinary Creatinine Ratio on Kidney Function in Europeans. Frontiers in Bioengineering and Biotechnology, 2020, 8, 662.	2.0	3
237	Computational Tools for Causal Inference in Genetics. Cold Spring Harbor Perspectives in Medicine, 2021, 11, a039248.	2.9	3
238	Texture Classification Using Kernel-Based Techniques. Lecture Notes in Computer Science, 2013, , 427-434.	1.0	3
239	Early life adiposity and telomere length across the life course: a systematic review and meta-analysis. Wellcome Open Research, 2017, 2, 118.	0.9	3
240	Early life adiposity and telomere length across the life course: a systematic review and meta-analysis. Wellcome Open Research, 2017, 2, 118.	0.9	3
241	Analysis of Potential Genomic Confounding in Genetic Association Studies and an Online Genomic Confounding Browser (GCB). Annals of Human Genetics, 2011, 75, 723-731.	0.3	2
242	Copy Number Variations and Cognitive Phenotypes in Unselected Populations. Obstetrical and Gynecological Survey, 2015, 70, 559-560.	0.2	2
243	Availability of public databases for triangulation of findings. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15766-15767.	3.3	2
244	Establishing reference intervals for triglyceride-containing lipoprotein subfraction metabolites measured using nuclear magnetic resonance spectroscopy in a UK population. Annals of Clinical Biochemistry, 2021, 58, 47-53.	0.8	2
245	Microplate-array diagonal-gel electrophoresis (MADGE) systems for high-throughput electrophoresis. Technical Tips Online, 2000, 5, 12-18.	0.2	1
246	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 3394-3395.	1.4	1
247	Sequential data selection for predicting the pathogenic effects of sequence variation. , 2015, , .		1
248	Trans-Ethnic Mendelian Randomization Study Reveals Causal Relationships Between Cardiometabolic Factors and Chronic Kidney Disease. SSRN Electronic Journal, 0, , .	0.4	1
249	MeltMADGE for mutation scanning of specific genes in population studies. Nature Protocols, 2010, 5, 1800-1812.	5.5	0
250	Population Mutation Scanning of Human GHR by meltMADGE and Identification of a Paucimorphic Variant. Genetic Testing and Molecular Biomarkers, 2011, 15, 855-860.	0.3	0
251	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
252	Frequency of KLK3 gene deletions in the general population. Annals of Clinical Biochemistry, 2017, 54, 472-480.	0.8	0

#	ARTICLE	IF	CITATIONS
253	221 Association of physical activity bout length and changing intensity with mortality in UK Biobank. International Journal of Epidemiology, 2021, 50, .	0.9	0
254	Microplate Array Diagonal Gel Electrophoresis for SNP and Microsatellite Genotyping and for Mutation Scanning. , 2004, , 836-841.		0
255	Predicting the Pathogenic Impact of Sequence Variation in the Human Genome. Studies in Health Technology and Informatics, 2017, 235, 91-95.	0.2	0
256	Associations between high blood pressure and DNA methylation. , 2020, 15, e0227728.		0
257	Associations between high blood pressure and DNA methylation. , 2020, 15, e0227728.		0
258	Associations between high blood pressure and DNA methylation. , 2020, 15, e0227728.		0
259	Associations between high blood pressure and DNA methylation. , 2020, 15, e0227728.		0
260	Associations between high blood pressure and DNA methylation. , 2020, 15, e0227728.		0
261	Associations between high blood pressure and DNA methylation. , 2020, 15, e0227728.		0