# Tom R Gaunt

List of Publications by Year
in descending order



| | | | |
|---|---|---|---|
| 261 papers | 35,044 citations | 10373 72 h-index | 5118 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. | 13.7 | 3,823 |
| 2 | The MR-Base platform supports systematic causal inference across the human phenome. ELife, 2018, 7, . | 2.8 | 3,639 |
| 3 | Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109. | 13.7 | 1,855 |
| 4 | New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196. | 13.7 | 1,328 |
| 5 | Predicting the Functional, Molecular, and Phenotypic Consequences of Amino Acid Substitutions using Hidden Markov Models. Human Mutation, 2013, 34, 57-65. | 1.1 | 1,057 |
| 6 | The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90. | 13.7 | 1,014 |
| 7 | Hardy-Weinberg Equilibrium Testing of Biological Ascertainment for Mendelian Randomization Studies. American Journal of Epidemiology, 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. Bioinformatics, 2017, 33, 272-279. | 1.8 | 822 |
| 9 | Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. Nature, 2017, 541, 81-86. | 13.7 | 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. | 2.6 | 717 |
| 11 | Mendelian randomization of blood lipids for coronary heart disease. European Heart Journal, 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. Lancet, The, 2015, 385, 351-361. | 6.3 | 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. | 3.0 | 528 |
| 15 | An integrative approach to predicting the functional effects of non-coding and coding sequence variation. Bioinformatics, 2015, 31, 1536-1543. | 1.8 | 524 |
| 16 | Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138. | 9.4 | 501 |
| 17 | Systematic identification of genetic influences on methylation across the human life course. Genome Biology, 2016, 17, 61. | 3.8 | 489 |
| 18 | Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 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. Lancet Diabetes and Endocrinology,the, 2015, 3, 526-534. | 5.5 | 396 |
| 20 | Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 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). Human Molecular Genetics, 2015, 24, 2201-2217. | 1.4 | 345 |
| 22 | Identification of new therapeutic targets for osteoarthritis through genome-wide analyses of UK Biobank data. Nature Genetics, 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. 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. | 6.3 | 300 |
| 25 | Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. Nature Communications, 2015, 6, 8111. | 5.8 | 300 |
| 26 | Phenome-wide Mendelian randomization mapping the influence of the plasma proteome on complex diseases. Nature Genetics, 2020, 52, 1122-1131. | 9.4 | 298 |
| 27 | FATHMM-XF: accurate prediction of pathogenic point mutations via extended features. Bioinformatics, 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. International Journal of Epidemiology, 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'. BMC Bioinformatics, 2007, 8, 428. | 1.2 | 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. | 2.6 | 239 |
| 31 | Data Resource Profile: Accessible Resource for Integrated Epigenomic Studies (ARIES). International Journal of Epidemiology, 2015, 44, 1181-1190. | 0.9 | 238 |
| 32 | Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838. | 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. Nature Genetics, 2021, 53, 1636-1648. | 9.4 | 223 |
| 34 | Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321. | 9.4 | 218 |
| 35 | Predicting the functional consequences of cancer-associated amino acid substitutions. Bioinformatics, 2013, 29, 1504-1510. | 1.8 | 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. | 1.4 | 205 |

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

| # | Article | IF | Citations |
|---|---|---|---|
| 55 | Polymorphisms in the interleukin-4 and interleukin-4 receptor Î± chain genes confer susceptibility to asthma and atopy in a Caucasian population. Clinical and Experimental Allergy, 2003, 33, 1111-1117. | 1.4 | 115 |
| 56 | Secretory Phospholipase A2-IIA and Cardiovascular Disease. Journal of the American College of Cardiology, 2013, 62, 1966-1976. | 1.2 | 115 |
| 57 | MIDAS: software for analysis and visualisation of interallelic disequilibrium between multiallelic markers. BMC Bioinformatics, 2006, 7, 227. | 1.2 | 110 |
| 58 | A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. PLoS Genetics, 2015, 11, e1005035. | 1.5 | 107 |
| 59 | Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. International Journal of Epidemiology, 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. Human Molecular Genetics, 2001, 10, 1491-1501. | 1.4 | 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. | 1.4 | 102 |
| 62 | DNA Methylation and BMI: Investigating Identified Methylation Sites at HIF3A in a Causal Framework. Diabetes, 2016, 65, 1231-1244. | 0.3 | 95 |
| 63 | The EWAS Catalog: a database of epigenome-wide association studies. Wellcome Open Research, 0, 7, 41. | 0.9 | 95 |
| 64 | Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. International Journal of Epidemiology, 2016, 45, 1927-1937. | 0.9 | 94 |
| 65 | Sixty-Five Common Genetic Variants and Prediction of Type 2 Diabetes. Diabetes, 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. Nature Genetics, 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. PLoS ONE, 2008, 3, e3011. | 1.1 | 90 |
| 68 | Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, . | 1.6 | 89 |
| 69 | DNA methylation and substance-use risk: a prospective, genome-wide study spanning gestation to adolescence. Translational Psychiatry, 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. International Journal of Epidemiology, 2017, 46, dyw307. | 0.9 | 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. | 2.2 | 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. | 1.4 | 82 |

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|---|---|---|---|
| 73 | The variant call format provides efficient and robust storage of GWAS summary statistics. Genome Biology, 2021, 22, 32. | 3.8 | 82 |
| 74 | An epigenome-wide association meta-analysis of prenatal maternal stress in neonates: A model approach for replication. Epigenetics, 2016, 11, 140-149. | 1.3 | 80 |
| 75 | Liver Function and Risk of Type 2 Diabetes: Bidirectional Mendelian Randomization Study. Diabetes, 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. Diabetes, 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. Cancer Causes and Control, 2015, 26, 1603-1616. | 0.8 | 77 |
| 78 | Whole-genome sequence-based analysis of thyroid function. Nature Communications, 2015, 6, 5681. | 5.8 | 75 |
| 79 | Hypertensive Disorders of Pregnancy and DNA Methylation in Newborns. Hypertension, 2019, 74, 375-383. | 1.3 | 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. | 3.1 | 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. | 1.5 | 70 |
| 82 | A pathway-based data integration framework for prediction of disease progression. Bioinformatics, 2014, 30, 838-845. | 1.8 | 67 |
| 83 | Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 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. Cancer Causes and Control, 2017, 28, 497-528. | 0.8 | 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. | 2.6 | 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. | 1.4 | 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. | 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. 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. | 1.8 | 63 |
| 90 | A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. Nature Communications, 2014, 5, 4871. | 5.8 | 62 |

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|---|---|---|---|
| 91 | Epigenome-wide association study of asthma and wheeze in childhood and adolescence. Clinical Epigenetics, 2017, 9, 112. | 1.8 | 60 |
| 92 | Exploiting horizontal pleiotropy to search for causal pathways within a Mendelian randomization framework. Nature Communications, 2020, 11, 1010. | 5.8 | 58 |
| 93 | Haplotypic analyses of the IGF2-INS-TH gene cluster in relation to cardiovascular risk traits. Human Molecular Genetics, 2004, 13, 715-725. | 1.4 | 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. | 1.4 | 57 |
| 95 | Cholesteryl ester transfer protein (CETP) as a drug target for cardiovascular disease. Nature Communications, 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?. Diabetes, 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 (AFAST). International Journal of Epidemiology, 2018, 47, 928-937. | 0.9 | 56 |
| 98 | Mosaic structural variation in children with developmental disorders. Human Molecular Genetics, 2015, 24, 2733-2745. | 1.4 | 54 |
| 99 | Appraising the causal relevance of DNA methylation for risk of lung cancer. International Journal of Epidemiology, 2019, 48, 1493-1504. | 0.9 | 53 |
| 100 | CScape: a tool for predicting oncogenic single-point mutations in the cancer genome. Scientific Reports, 2017, 7, 11597. | 1.6 | 52 |
| 101 | Using the MR-Base platform to investigate risk factors and drug targets for thousands of phenotypes. Wellcome Open Research, 2019, 4, 113. | 0.9 | 52 |
| 102 | TCTEX1D2 mutations underlie Jeune asphyxiating thoracic dystrophy with impaired retrograde intraflagellar transport. Nature Communications, 2015, 6, 7074. | 5.8 | 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. | 2.6 | 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. | 1.4 | 50 |
| 105 | Rare Variant Analysis of Human and Rodent Obesity Genes in Individuals with Severe Childhood Obesity. Scientific Reports, 2017, 7, 4394. | 1.6 | 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. | 0.4 | 49 |
| 107 | Using the MR-Base platform to investigate risk factors and drug targets for thousands of phenotypes. Wellcome Open Research, 2019, 4, 113. | 0.9 | 47 |
| 108 | PhenoSpD: an integrated toolkit for phenotypic correlation estimation and multiple testing correction using GWAS summary statistics. GigaScience, 2018, 7, . | 3.3 | 46 |

| # | Article | IF | Citations |
|---|---|---|---|
| 109 | A transcriptome-wide Mendelian randomization study to uncover tissue-dependent regulatory mechanisms across the human phenome. Nature Communications, 2020, 11, 185. | 5.8 | 45 |
| 110 | The EWAS Catalog: a database of epigenome-wide association studies. Wellcome Open Research, 2022, 7, 41. | 0.9 | 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. | 1.4 | 43 |
| 113 | Identifying drug targets for neurological and psychiatric disease via genetics and the brain transcriptome. PLoS Genetics, 2021, 17, e1009224. | 1.5 | 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. | 0.3 | 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. | 1.4 | 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. | 0.9 | 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. | 1.1 | 39 |
| 118 | Associations between high blood pressure and DNA methylation. PLoS ONE, 2020, 15, e0227728. | 1.1 | 37 |
| 119 | HIPred: an integrative approach to predicting haploinsufficient genes. Bioinformatics, 2017, 33, 1751-1757. | 1.8 | 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. | 1.6 | 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. | 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. Diabetologia, 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. BMC Bioinformatics, 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. European Heart Journal, 2013, 34, 972-981. | 1.0 | 33 |
| 125 | Nonsense Mutation in Coiled-Coil Domain Containing 151 Gene (CCDC151) Causes Primary Ciliary Dyskinesia. Human Mutation, 2014, 35, 1446-1448. | 1.1 | 33 |
| 126 | Role of DNA Methylation in Type 2 Diabetes Etiology: Using Genotype as a Causal Anchor. Diabetes, 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. American Journal of Human Genetics, 2020, 106, 315-326. | 2.6 | 32 |
| 128 | Genome-wide association study of circulating interleukin 6 levels identifies novel loci. Human Molecular Genetics, 2021, 30, 393-409. | 1.4 | 32 |
| 129 | Angiotensin II type I receptor gene polymorphism: anthropometric and metabolic syndrome traits. Journal of Medical Genetics, 2005, 42, 396-401. | 1.5 | 30 |
| 130 | Molecular and Population Analysis of Natural Selection on the Human Haptoglobin Duplication. Annals of Human Genetics, 2012, 76, 352-362. | 0.3 | 30 |
| 131 | Texture classification using feature selection and kernel-based techniques. Soft Computing, 2015, 19, 2469-2480. | 2.1 | 30 |
| 132 | Low-frequency variation in TP53 has large effects on head circumference and intracranial volume. Nature Communications, 2019, 10, 357. | 5.8 | 30 |
| 133 | Prioritizing putative influential genes in cardiovascular disease susceptibility by applying tissue-specific Mendelian randomization. Genome Medicine, 2019, 11, 6. | 3.6 | 30 |
| 134 | EpiGraphDB: a database and data mining platform for health data science. Bioinformatics, 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. Journal of Clinical Endocrinology and Metabolism, 2004, 89, 5569-5576. | 1.8 | 29 |
| 136 | Can machine learning improve mortality prediction following cardiac surgery?. European Journal of Cardio-thoracic Surgery, 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. Paediatric and Perinatal Epidemiology, 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. Atherosclerosis, 2008, 196, 871-878. | 0.4 | 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. | 0.6 | 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. | 0.3 | 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. | 1.4 | 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. | 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 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. | 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 Exposureâ€“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 5q31â€“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 RSPH9 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 |

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|---|---|---|---|
| 163 | Complexity of a complex trait locus: HP, HPR, haemoglobin and cholesterol. Gene, 2012, 499, 8-13. | 1.0 | 20 |
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