Tom R Gaunt

List of Publications by Year in Descending Order

281 papers	22,598 citations	65 h-index	147 g-index
332 ext. papers	29,677 ext. citations	8.7 avg, IF	6.21 L-index

#	Paper	IF	Citations
281	The Effect of Circulating Zinc, Selenium, Copper and Vitamin K on COVID-19 Outcomes: A Mendelian Randomization Study.. *Nutrients*, **2022**, 14,	6.7	5
280	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology.. *Nature Communications*, **2022**, 13, 634	17.4	3
279	Separating the direct effects of traits on atherosclerotic cardiovascular disease from those mediated by type 2 diabetes.. *Diabetologia*, **2022**, 1	10.3	1
278	The EWAS Catalog: a database of epigenome-wide association studies.. *Wellcome Open Research*, **2022**, 7, 41	4.8	3
277	Reply to Janssen et al. Comment on "Sobczyk, M.K.; Gaunt, T.R. The Effect of Circulating Zinc, Selenium, Copper and Vitamin K on COVID-19 Outcomes: A Mendelian Randomization Study. 2022, , 233".. *Nutrients*, **2022**, 14,	6.7	2
276	Using genetic variation to disentangle the complex relationship between food intake and health outcomes. *PLoS Genetics*, **2022**, 18, e1010162	6	0
275	Linking Physical Activity to Breast Cancer via Sex Hormones, Part 1: The Effect of Physical Activity on Sex Steroid Hormones. *Cancer Epidemiology Biomarkers and Prevention*, **2021**,	4	4
274	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	36.3	19
273	Linking Physical Activity to Breast Cancer: Text Mining Results and a Protocol for Systematically Reviewing Three Potential Mechanistic Pathways. *Cancer Epidemiology Biomarkers and Prevention*, **2021**,	4	4
272	Cholesteryl ester transfer protein (CETP) as a drug target for cardiovascular disease. *Nature Communications*, **2021**, 12, 5640	17.4	7
271	Validation of lipid-related therapeutic targets for coronary heart disease prevention using human genetics. *Nature Communications*, **2021**, 12, 6120	17.4	2
270	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*, **2021**,	4	2
269	An informatics consult approach for generating clinical evidence for treatment decisions. *BMC Medical Informatics and Decision Making*, **2021**, 21, 281	3.6	3
268	Prediction of driver variants in the cancer genome via machine learning methodologies. *Briefings in Bioinformatics*, **2021**, 22,	13.4	1
267	Triangulating Molecular Evidence to Prioritize Candidate Causal Genes at Established Atopic Dermatitis Loci. *Journal of Investigative Dermatology*, **2021**, 141, 2620-2629	4.3	3
266	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	7.8	4
265	Platelet Glycoprotein Ib Chain as a Putative Therapeutic Target for Juvenile Idiopathic Arthritis: A Mendelian Randomization Study. *Arthritis and Rheumatology*, **2021**, 73, 693-701	9.5	3

264	EpiGraphDB: a database and data mining platform for health data science. *Bioinformatics*, **2021**, 37, 1304-1311	7.2	5
263	Computational Tools for Causal Inference in Genetics. *Cold Spring Harbor Perspectives in Medicine*, **2021**, 11,	5.4	2
262	MELODI Presto: a fast and agile tool to explore semantic triples derived from biomedical literature. *Bioinformatics*, **2021**, 37, 583-585	7.2	5
261	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	2.2	0
260	Identifying drug targets for neurological and psychiatric disease via genetics and the brain transcriptome. *PLoS Genetics*, **2021**, 17, e1009224	6	10
259	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. *Human Molecular Genetics*, **2021**, 30, 393-409	5.6	6
258	The variant call format provides efficient and robust storage of GWAS summary statistics. *Genome Biology*, **2021**, 22, 32	18.3	8
257	A proteome-wide genetic investigation identifies several SARS-CoV-2-exploited host targets of clinical relevance. *ELife*, **2021**, 10,	8.9	2
256	Association of physical activity intensity and bout length with mortality: An observational study of 79,503 UK Biobank participants. *PLoS Medicine*, **2021**, 18, e1003757	11.6	3
255	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. *Nature Genetics*, **2021**, 53, 1311-1321	36.3	27
254	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. *Cell*, **2021**, 184, 4784-4818.e17	36.2	24
253	Epigenome-wide change and variation in DNA methylation in childhood: trajectories from birth to late adolescence. *Human Molecular Genetics*, **2021**, 30, 119-134	5.6	15
252	Trans-ethnic Mendelian-randomization study reveals causal relationships between cardiometabolic factors and chronic kidney disease. *International Journal of Epidemiology*, **2021**,	7.8	1
251	MendelVar: gene prioritization at GWAS loci using phenotypic enrichment of Mendelian disease genes. *Bioinformatics*, **2021**, 37, 1-8	7.2	4
250	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	11	15
249	Haptoglobin genotype and outcome after spontaneous intracerebral haemorrhage. *Journal of Neurology, Neurosurgery and Psychiatry*, **2020**, 91, 298-304	5.5	3
248	Circulating Fatty Acids and Risk of Coronary Heart Disease and Stroke: Individual Participant Data Meta-Analysis in Up to 16 126 Participants. *Journal of the American Heart Association*, **2020**, 9, e013131	6	13
247	Identifying epigenetic biomarkers of established prognostic factors and survival in a clinical cohort of individuals with oropharyngeal cancer. *Clinical Epigenetics*, **2020**, 12, 95	7.7	4

246	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	5.8	0
245	Smoking, DNA Methylation, and Lung Function: a Mendelian Randomization Analysis to Investigate Causal Pathways. *American Journal of Human Genetics*, **2020**, 106, 315-326	11	12
244	Exploiting horizontal pleiotropy to search for causal pathways within a Mendelian randomization framework. *Nature Communications*, **2020**, 11, 1010	17.4	23
243	Associations between high blood pressure and DNA methylation. *PLoS ONE*, **2020**, 15, e0227728	3.7	18
242	Haptoglobin genotype and outcome after aneurysmal subarachnoid haemorrhage. *Journal of Neurology, Neurosurgery and Psychiatry*, **2020**, 91, 305-313	5.5	5
241	CScape-somatic: distinguishing driver and passenger point mutations in the cancer genome. *Bioinformatics*, **2020**, 36, 3637-3644	7.2	4
240	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	3.9	9
239	A transcriptome-wide Mendelian randomization study to uncover tissue-dependent regulatory mechanisms across the human phenome. *Nature Communications*, **2020**, 11, 185	17.4	27
238	Machine learning improves mortality risk prediction after cardiac surgery: Systematic review and meta-analysis. *Journal of Thoracic and Cardiovascular Surgery*, **2020**,	1.5	12
237	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. *Nature Genetics*, **2020**, 52, 1314-1332	36.3	26
236	Phenome-wide Mendelian randomization mapping the influence of the plasma proteome on complex diseases. *Nature Genetics*, **2020**, 52, 1122-1131	36.3	75
235	Can machine learning improve mortality prediction following cardiac surgery?. *European Journal of Cardio-thoracic Surgery*, **2020**, 58, 1130-1136	3	11
234	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. *Frontiers in Endocrinology*, **2020**, 11, 630875	5.7	2
233	Associations between high blood pressure and DNA methylation **2020**, 15, e0227728		
232	Associations between high blood pressure and DNA methylation **2020**, 15, e0227728		
231	Associations between high blood pressure and DNA methylation **2020**, 15, e0227728		
230	Associations between high blood pressure and DNA methylation **2020**, 15, e0227728		
229	Associations between high blood pressure and DNA methylation **2020**, 15, e0227728		

228	Associations between high blood pressure and DNA methylation **2020**, 15, e0227728		
227	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	11.5	2
226	Appraising the causal relevance of DNA methylation for risk of lung cancer. *International Journal of Epidemiology*, **2019**, 48, 1493-1504	7.8	27
225	Estimating the Frequency of Single Point Driver Mutations across Common Solid Tumours. *Scientific Reports*, **2019**, 9, 13452	4.9	3
224	Low-frequency variation in TP53 has large effects on head circumference and intracranial volume. *Nature Communications*, **2019**, 10, 357	17.4	12
223	Identification of new therapeutic targets for osteoarthritis through genome-wide analyses of UK Biobank data. *Nature Genetics*, **2019**, 51, 230-236	36.3	143
222	Prioritizing putative influential genes in cardiovascular disease susceptibility by applying tissue-specific Mendelian randomization. *Genome Medicine*, **2019**, 11, 6	14.4	19
221	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	6	40
220	Hypertensive Disorders of Pregnancy and DNA Methylation in Newborns. *Hypertension*, **2019**, 74, 375-383	8.5	40
219	Liver Function and Risk of Type 2 Diabetes: Bidirectional Mendelian Randomization Study. *Diabetes*, **2019**, 68, 1681-1691	0.9	36
218	Genetic determinants of circulating haptoglobin concentration. *Clinica Chimica Acta*, **2019**, 494, 138-142	6.2	7
217	Leveraging brain cortex-derived molecular data to elucidate epigenetic and transcriptomic drivers of complex traits and disease. *Translational Psychiatry*, **2019**, 9, 105	8.6	8
216	A genome-wide association study of mitochondrial DNA copy number in two population-based cohorts. *Human Genomics*, **2019**, 13, 6	6.8	15
215	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	5.6	16
214	Using the MR-Base platform to investigate risk factors and drug targets for thousands of phenotypes. *Wellcome Open Research*, **2019**, 4, 113	4.8	18
213	Using the MR-Base platform to investigate risk factors and drug targets for thousands of phenotypes. *Wellcome Open Research*, **2019**, 4, 113	4.8	26
212	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	3.5	17
211	Longitudinal analysis strategies for modelling epigenetic trajectories. *International Journal of Epidemiology*, **2018**, 47, 516-525	7.8	8

210	Psychosocial adversity and socioeconomic position during childhood and epigenetic age: analysis of two prospective cohort studies. *Human Molecular Genetics*, **2018**, 27, 1301-1308	5.6	75
209	MELODI: Mining Enriched Literature Objects to Derive Intermediates. *International Journal of Epidemiology*, **2018**,	7.8	10
208	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	7.8	32
207	Neonatal DNA methylation and early-onset conduct problems: A genome-wide, prospective study. *Development and Psychopathology*, **2018**, 30, 383-397	4.3	26
206	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. *International Journal of Epidemiology*, **2018**, 47, 22-23u	7.8	62
205	FATHMM-XF: accurate prediction of pathogenic point mutations via extended features. *Bioinformatics*, **2018**, 34, 511-513	7.2	147
204	Cardiometabolic phenotypes and mitochondrial DNA copy number in two cohorts of UK women. *Mitochondrion*, **2018**, 39, 9-19	4.9	11
203	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	4.3	19
202	Age-related DNA methylation changes are tissue-specific with ELOVL2 promoter methylation as exception. *Epigenetics and Chromatin*, **2018**, 11, 25	5.8	76
201	Genome-wide survey of parent-of-origin effects on DNA methylation identifies candidate imprinted loci in humans. *Human Molecular Genetics*, **2018**, 27, 2927-2939	5.6	15
200	Systematic Mendelian randomization framework elucidates hundreds of CpG sites which may mediate the influence of genetic variants on disease. *Human Molecular Genetics*, **2018**, 27, 3293-3304	5.6	40
199	Author response: The MR-Base platform supports systematic causal inference across the human phenome **2018**,		17
198	A Methylome-Wide Association Study of Trajectories of Oppositional Defiant Behaviors and Biological Overlap With Attention Deficit Hyperactivity Disorder. *Child Development*, **2018**, 89, 1839-1855	4.9	13
197	DNA methylation derived systemic inflammation indices are associated with head and neck cancer development and survival. *Oral Oncology*, **2018**, 85, 87-94	4.4	9
196	PhenoSpD: an integrated toolkit for phenotypic correlation estimation and multiple testing correction using GWAS summary statistics. *GigaScience*, **2018**, 7,	7.6	27
195	Software Application Profile: PHESANT: a tool for performing automated phenome scans in UK Biobank. *International Journal of Epidemiology*, **2018**, 47, 29-35	7.8	70
194	The MR-Base platform supports systematic causal inference across the human phenome. *ELife*, **2018**, 7,	8.9	1190
193	Epigenetic profiling of ADHD symptoms trajectories: a prospective, methylome-wide study. *Molecular Psychiatry*, **2017**, 22, 250-256	15.1	83

192	The epigenetic clock and physical development during childhood and adolescence: longitudinal analysis from a UK birth cohort. *International Journal of Epidemiology*, **2017**, 46, 549-558	7.8	60
191	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases: A Mendelian Randomization Study. *JAMA Oncology*, **2017**, 3, 636-651	13.4	236
190	Role of DNA Methylation in Type 2 Diabetes Etiology: Using Genotype as a Causal Anchor. *Diabetes*, **2017**, 66, 1713-1722	0.9	25
189	Causal Associations of Adiposity and Body Fat Distribution With Coronary Heart Disease, Stroke Subtypes, and Type 2 Diabetes Mellitus: A Mendelian Randomization Analysis. *Circulation*, **2017**, 135, 2373-2388	16.7	182
188	Identifying low density lipoprotein cholesterol associated variants in the Annexin A2 (ANXA2) gene. *Atherosclerosis*, **2017**, 261, 60-68	3.1	8
187	HIPred: an integrative approach to predicting haploinsufficient genes. *Bioinformatics*, **2017**, 33, 1751-1757	7.2	14
186	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. *Journal of the American Heart Association*, **2017**, 6,	6	65
185	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. *American Journal of Human Genetics*, **2017**, 100, 865-884	11	74
184	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	2.8	51
183	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. *Nature*, **2017**, 541, 81-86	50.4	511
182	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	4	13
181	Mendelian Randomization Analysis Identifies CpG Sites as Putative Mediators for Genetic Influences on Cardiovascular Disease Risk. *American Journal of Human Genetics*, **2017**, 101, 590-602	11	44
180	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. *BioData Mining*, **2017**, 10, 25	4.3	5
179	Maternal eating disorders affect offspring cord blood DNA methylation: a prospective study. *Clinical Epigenetics*, **2017**, 9, 120	7.7	11
178	Epigenome-wide association study of asthma and wheeze in childhood and adolescence. *Clinical Epigenetics*, **2017**, 9, 112	7.7	43
177	An integrative approach to predicting the functional effects of small indels in non-coding regions of the human genome. *BMC Bioinformatics*, **2017**, 18, 442	3.6	19
176	Physical activity phenotyping with activity bigrams, and their association with BMI. *International Journal of Epidemiology*, **2017**, 46, 1857-1870	7.8	6
175	CScape: a tool for predicting oncogenic single-point mutations in the cancer genome. *Scientific Reports*, **2017**, 7, 11597	4.9	22

174	Variation in DNA methylation of the oxytocin receptor gene predicts children's resilience to prenatal stress. *Development and Psychopathology*, **2017**, 29, 1663-1674	4.3	42
173	GTB - an online genome tolerance browser. *BMC Bioinformatics*, **2017**, 18, 20	3.6	3
172	Rare Variant Analysis of Human and Rodent Obesity Genes in Individuals with Severe Childhood Obesity. *Scientific Reports*, **2017**, 7, 4394	4.9	31
171	Prenatal unhealthy diet, insulin-like growth factor 2 gene (IGF2) methylation, and attention deficit hyperactivity disorder symptoms in youth with early-onset conduct problems. *Journal of Child Psychology and Psychiatry and Allied Disciplines*, **2017**, 58, 19-27	7.9	51
170	Frequency of KLK3 gene deletions in the general population. *Annals of Clinical Biochemistry*, **2017**, 54, 472-480	2.2	
169	HAPRAP: a haplotype-based iterative method for statistical fine mapping using GWAS summary statistics. *Bioinformatics*, **2017**, 33, 79-86	7.2	4
168	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	7.2	541
167	Metabolic Profiling of Adiponectin Levels in Adults: Mendelian Randomization Analysis. *Circulation: Cardiovascular Genetics*, **2017**, 10,		16
166	Functional Analysis of the Coronary Heart Disease Risk Locus on Chromosome 21q22. *Disease Markers*, **2017**, 2017, 1096916	3.2	4
165	Early life adiposity and telomere length across the life course: a systematic review and meta-analysis. *Wellcome Open Research*, **2017**, 2, 118	4.8	1
164	Early life adiposity and telomere length across the life course: a systematic review and meta-analysis. *Wellcome Open Research*, **2017**, 2, 118	4.8	2
163	Predicting the Pathogenic Impact of Sequence Variation in the Human Genome. *Studies in Health Technology and Informatics*, **2017**, 235, 91-95	0.5	
162	A pathway-centric approach to rare variant association analysis. *European Journal of Human Genetics*, **2016**, 25, 123-129	5.3	11
161	Plasma urate concentration and risk of coronary heart disease: a Mendelian randomisation analysis. *Lancet Diabetes and Endocrinology,the*, **2016**, 4, 327-36	18.1	100
160	Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. *International Journal of Epidemiology*, **2016**, 45, 1927-1937	7.8	65
159	DNA Methylation and BMI: Investigating Identified Methylation Sites at HIF3A in a Causal Framework. *Diabetes*, **2016**, 65, 1231-44	0.9	76
158	An epigenome-wide association meta-analysis of prenatal maternal stress in neonates: A model approach for replication. *Epigenetics*, **2016**, 11, 140-9	5.7	62
157	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. *Nature Communications*, **2016**, 7, 10494	17.4	107

156	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. *Nature Communications*, **2016**, 7, 10023	17.4	295
155	Prenatal and early life influences on epigenetic age in children: a study of mother-offspring pairs from two cohort studies. *Human Molecular Genetics*, **2016**, 25, 191-201	5.6	153
154	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, 106-12	5.3	20
153	Incorporating Non-Coding Annotations into Rare Variant Analysis. *PLoS ONE*, **2016**, 11, e0154181	3.7	7
152	Replication and Characterization of Association between ABO SNPs and Red Blood Cell Traits by Meta-Analysis in Europeans. *PLoS ONE*, **2016**, 11, e0156914	3.7	16
151	Collapsed methylation quantitative trait loci analysis for low frequency and rare variants. *Human Molecular Genetics*, **2016**, 25, 4339-4349	5.6	7
150	Diagnosis of Coronary Heart Diseases Using Gene Expression Profiling; Stable Coronary Artery Disease, Cardiac Ischemia with and without Myocardial Necrosis. *PLoS ONE*, **2016**, 11, e0149475	3.7	4
149	A Protein Domain and Family Based Approach to Rare Variant Association Analysis. *PLoS ONE*, **2016**, 11, e0153803	3.7	5
148	Texture analysis in gel electrophoresis images using an integrative kernel-based approach. *Scientific Reports*, **2016**, 6, 19256	4.9	15
147	DNA methylation and substance-use risk: a prospective, genome-wide study spanning gestation to adolescence. *Translational Psychiatry*, **2016**, 6, e976	8.6	73
146	Mendelian Randomisation study of the influence of eGFR on coronary heart disease. *Scientific Reports*, **2016**, 6, 28514	4.9	11
145	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. *American Journal of Human Genetics*, **2016**, 98, 680-96	11	489
144	Systematic identification of genetic influences on methylation across the human life course. *Genome Biology*, **2016**, 17, 61	18.3	331
143	Metabolic Characterization of a Rare Genetic Variation Within APOC3 and Its Lipoprotein Lipase-Independent Effects. *Circulation: Cardiovascular Genetics*, **2016**, 9, 231-9		20
142	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. *Nature Genetics*, **2016**, 48, 1303-1312	36.3	51
141	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, 1520-33	7.5	18
140	Importance of Genetic Studies in Consanguineous Populations for the Characterization of Novel Human Gene Functions. *Annals of Human Genetics*, **2016**, 80, 187-96	2.2	23
139	Metabolite profiling and cardiovascular event risk: a prospective study of 3 population-based cohorts. *Circulation*, **2015**, 131, 774-85	16.7	367

138	Prenatal exposure to maternal smoking and offspring DNA methylation across the lifecourse: findings from the Avon Longitudinal Study of Parents and Children (ALSPAC). *Human Molecular Genetics*, **2015**, 24, 2201-17	5.6	256
137	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	18.1	277
136	A meta-analysis of gene expression signatures of blood pressure and hypertension. *PLoS Genetics*, **2015**, 11, e1005035	6	83
135	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, 193-9	8.4	127
134	Data Resource Profile: Accessible Resource for Integrated Epigenomic Studies (ARIES). *International Journal of Epidemiology*, **2015**, 44, 1181-90	7.8	162
133	An integrative approach to predicting the functional effects of non-coding and coding sequence variation. *Bioinformatics*, **2015**, 31, 1536-43	7.2	340
132	Mendelian randomization of blood lipids for coronary heart disease. *European Heart Journal*, **2015**, 36, 539-50	9.5	417
131	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, 1603-16	2.8	56
130	TCTEX1D2 mutations underlie Jeune asphyxiating thoracic dystrophy with impaired retrograde intraflagellar transport. *Nature Communications*, **2015**, 6, 7074	17.4	41
129	The UK10K project identifies rare variants in health and disease. *Nature*, **2015**, 526, 82-90	50.4	776
128	Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. *Nature Communications*, **2015**, 6, 8111	17.4	186
127	Sixty-five common genetic variants and prediction of type 2 diabetes. *Diabetes*, **2015**, 64, 1830-40	0.9	76
126	eNOS and coronary artery disease: publication bias and the eclipse of hypothesis-driven meta-analysis in genetic association studies. *Gene*, **2015**, 556, 257-8	3.8	7
125	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. *Lancet, The*, **2015**, 385, 351-61	40	409
124	Proxy molecular diagnosis from whole-exome sequencing reveals Papillon-Lefevre syndrome caused by a missense mutation in CTSC. *PLoS ONE*, **2015**, 10, e0121351	3.7	4
123	Identifying Highly Penetrant Disease Causal Mutations Using Next Generation Sequencing: Guide to Whole Process. *BioMed Research International*, **2015**, 2015, 923491	3	6
122	Whole-genome sequence-based analysis of thyroid function. *Nature Communications*, **2015**, 6, 5681	17.4	56
121	Copy number variations and cognitive phenotypes in unselected populations. *JAMA - Journal of the American Medical Association*, **2015**, 313, 2044-54	27.4	96

120	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, 1288-304	7.8	181
119	Sequential data selection for predicting the pathogenic effects of sequence variation **2015**,		1
118	Longitudinal analysis of DNA methylation associated with birth weight and gestational age. *Human Molecular Genetics*, **2015**, 24, 3752-63	5.6	91
117	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
116	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
115	Mosaic structural variation in children with developmental disorders. *Human Molecular Genetics*, **2015**, 24, 2733-45	5.6	39
114	Texture classification using feature selection and kernel-based techniques. *Soft Computing*, **2015**, 19, 2469-2480	3.5	23
113	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, 2498-510	5.6	22
112	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. *Nature Communications*, **2014**, 5, 4871	17.4	46
111	Ranking non-synonymous single nucleotide polymorphisms based on disease concepts. *Human Genomics*, **2014**, 8, 11	6.8	105
110	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. *BMJ, The*, **2014**, 349, g4164	5.9	406
109	Nonsense mutation in coiled-coil domain containing 151 gene (CCDC151) causes primary ciliary dyskinesia. *Human Mutation*, **2014**, 35, 1446-8	4.7	24
108	Influence of adiposity-related genetic markers in a population of saudi arabians where other variables influencing obesity may be reduced. *Disease Markers*, **2014**, 2014, 758232	3.2	19
107	Haptoglobin duplicon, hemoglobin, and vitamin C: analyses in the british women's heart and health study and Caerphilly prospective study. *Disease Markers*, **2014**, 2014, 529456	3.2	5
106	Canonical correlation analysis for gene-based pleiotropy discovery. *PLoS Computational Biology*, **2014**, 10, e1003876	5	19
105	A pathway-based data integration framework for prediction of disease progression. *Bioinformatics*, **2014**, 30, 838-45	7.2	52
104	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. *American Journal of Human Genetics*, **2014**, 94, 349-60	11	131
103	Secretory phospholipase A(2)-IIA and cardiovascular disease: a mendelian randomization study. *Journal of the American College of Cardiology*, **2013**, 62, 1966-1976	15.1	91

102	Loci influencing blood pressure identified using a cardiovascular gene-centric array. *Human Molecular Genetics*, **2013**, 22, 1663-78	5.6	119
101	Predicting the functional, molecular, and phenotypic consequences of amino acid substitutions using hidden Markov models. *Human Mutation*, **2013**, 34, 57-65	4.7	723
100	Sequential sentinel SNP Regional Association Plots (SSS-RAP): an approach for testing independence of SNP association signals using meta-analysis data. *Annals of Human Genetics*, **2013**, 77, 67-79	2.2	5
99	Predicting the functional consequences of cancer-associated amino acid substitutions. *Bioinformatics*, **2013**, 29, 1504-10	7.2	154
98	A gene-centric analysis of activated partial thromboplastin time and activated protein C resistance using the HumanCVD focused genotyping array. *European Journal of Human Genetics*, **2013**, 21, 779-83	5.3	14
97	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, 972-81	9.5	28
96	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	5.6	73
95	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, 475-92	7.8	113
94	Gene-centric analysis identifies variants associated with interleukin-6 levels and shared pathways with other inflammation markers. *Circulation: Cardiovascular Genetics*, **2013**, 6, 163-70		34
93	Gene-centric association signals for haemostasis and thrombosis traits identified with the HumanCVD BeadChip. *Thrombosis and Haemostasis*, **2013**, 110, 995-1003	7	7
92	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	3.7	33
91	Texture Classification Using Kernel-Based Techniques. *Lecture Notes in Computer Science*, **2013**, 427-434	0.9	3
90	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, 211-20	2.2	18
89	Molecular and population analysis of natural selection on the human haptoglobin duplication. *Annals of Human Genetics*, **2012**, 76, 352-62	2.2	15
88	Complexity of a complex trait locus: HP, HPR, haemoglobin and cholesterol. *Gene*, **2012**, 499, 8-13	3.8	15
87	Large-scale gene-centric meta-analysis across 32 studies identifies multiple lipid loci. *American Journal of Human Genetics*, **2012**, 91, 823-38	11	189
86	Large-scale gene-centric meta-analysis across 39 studies identifies type 2 diabetes loci. *American Journal of Human Genetics*, **2012**, 90, 410-25	11	214
85	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. *American Journal of Human Genetics*, **2012**, 90, 753	11	4

84	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2012**, 90, 1116-1117	11	78
83	Integration of genetics into a systems model of electrocardiographic traits using HumanCVD BeadChip. *Circulation: Cardiovascular Genetics*, **2012**, 5, 630-8		12
82	A multi-cohort study of polymorphisms in the GH/IGF axis and physical capability: the HALCyon programme. *PLoS ONE*, **2012**, 7, e29883	3.7	10
81	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. *Nature* , **2011**, 478, 103-9	50.4	1564
80	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. *Nature Genetics*, **2011**, 43, 1131-8	36.3	415
79	Genetic variants associated with Von Willebrand factor levels in healthy men and women identified using the HumanCVD BeadChip. *Annals of Human Genetics*, **2011**, 75, 456-67	2.2	24
78	Analysis of potential genomic confounding in genetic association studies and an online genomic confounding browser (GCB). *Annals of Human Genetics*, **2011**, 75, 723-31	2.2	1
77	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2011**, 88, 6-18	11	103
76	Blood pressure loci identified with a gene-centric array. *American Journal of Human Genetics*, **2011**, 89, 688-700	11	137
75	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, 1710-9	10.3	27
74	Combined analysis of CHRNA5, CHRNA3 and CYP2A6 in relation to adolescent smoking behaviour. *Journal of Psychopharmacology*, **2011**, 25, 915-23	4.6	14
73	Population mutation scanning of human GHR by meltMADGE and identification of a paucimorphic variant. *Genetic Testing and Molecular Biomarkers*, **2011**, 15, 855-60	1.6	
72	Amplification ratio control system for copy number variation genotyping. *Nucleic Acids Research*, **2011**, 39, e54	20.1	8
71	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. *Human Molecular Genetics*, **2011**, 20, 2273-84	5.6	146
70	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, 1008-18	0.9	60
69	Four genetic loci influencing electrocardiographic indices of left ventricular hypertrophy. *Circulation: Cardiovascular Genetics*, **2011**, 4, 626-35		22
68	MeltMADGE for mutation scanning of specific genes in population studies. *Nature Protocols*, **2010**, 5, 1800-12	18.8	
67	Genome-wide data-mining of candidate human splice translational efficiency polymorphisms (STEPs) and an online database. *PLoS ONE*, **2010**, 5, e13340	3.7	4

66	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, 2277-82	9.4	53
65	IGF2BP1, IGF2BP2 and IGF2BP3 genotype, haplotype and genetic model studies in metabolic syndrome traits and diabetes. *Growth Hormone and IGF Research*, **2010**, 20, 310-8	2	27
64	An expectation-maximization program for determining allelic spectrum from CNV data (CoNVEM): insights into population allelic architecture and its mutational history. *Human Mutation*, **2010**, 31, 414-20	4.7	8
63	A study of relationships between single nucleotide polymorphisms from the growth hormone-insulin-like growth factor axis and bone mass: the Hertfordshire cohort study. *Journal of Rheumatology*, **2009**, 36, 1520-6	4.1	11
62	Gene-centric association signals for lipids and apolipoproteins identified via the HumanCVD BeadChip. *American Journal of Human Genetics*, **2009**, 85, 628-42	11	163
61	Hardy-Weinberg equilibrium testing of biological ascertainment for Mendelian randomization studies. *American Journal of Epidemiology*, **2009**, 169, 505-14	3.8	777
60	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, 871-8	3.1	25
59	The association of C-reactive protein and CRP genotype with coronary heart disease: findings from five studies with 4,610 cases amongst 18,637 participants. *PLoS ONE*, **2008**, 3, e3011	3.7	79
58	Homogeneous assay of rs4343, an ACE I/D proxy, and an analysis in the British Women's Heart and Health Study (BWHHS). *Disease Markers*, **2008**, 24, 11-7	3.2	19
57	Quantitated transcript haplotypes (QTH) of AGTR1, reduced abundance of mRNA haplotypes containing 1166C (rs5186:A>C), and relevance to metabolic syndrome traits. *Human Mutation*, **2007** , 28, 365-73	4.7	15
56	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	3.6	205
55	Molecular genetics of human growth hormone, insulin-like growth factors and their pathways in common disease. *Human Genetics*, **2007**, 122, 1-21	6.3	57
54	Comment on: Marchand and Polychronakos (2007) Evaluation of polymorphic splicing in the mechanism of the association of the insulin gene with diabetes: Diabetes 56:709-713. *Diabetes*, **2007**, 56, e16; author reply e17	0.9	3
53	The association of the paraoxonase (PON1) Q192R polymorphism with depression in older women: findings from the British Women's Heart and Health Study. *Journal of Epidemiology and Community Health*, **2007**, 61, 85-7	5.1	16
52	Haplotype of growth hormone and angiotensin I-converting enzyme genes, serum angiotensin I-converting enzyme and ventricular growth: pathway inference in pharmacogenetics. *Pharmacogenetics and Genomics*, **2007**, 17, 291-4	1.9	9
51	Interaction between birthweight and polymorphism in the calcium-sensing receptor gene in determination of adult bone mass: the Hertfordshire cohort study. *Journal of Rheumatology*, **2007**, 34, 769-75	4.1	11
50	Genotype of galectin 2 (LGALS2) is associated with insulin-glucose profile in the British Women's Heart and Health Study. *Diabetologia*, **2006**, 49, 673-7	10.3	12
49	MIDAS: software for analysis and visualisation of interallelic disequilibrium between multiallelic markers. *BMC Bioinformatics*, **2006**, 7, 227	3.6	84

48	Variants in the human insulin gene that affect pre-mRNA splicing: is -23HphI a functional single nucleotide polymorphism at IDDM2?. *Diabetes*, **2006**, 55, 260-4	0.9	45
47	Questioning INS VNTR role in obesity and diabetes: subclasses tag IGF2-INS-TH haplotypes; and -23HphI as a STEP (splicing and translational efficiency polymorphism). *Physiological Genomics*, **2006** , 28, 113	3.6	6
46	A study of TH01 and IGF2-INS-TH haplotypes in relation to smoking initiation in three independent surveys. *Pharmacogenetics and Genomics*, **2006**, 16, 15-23	1.9	11
45	Refined association mapping for a quantitative trait: weight in the H19-IGF2-INS-TH region. *Annals of Human Genetics*, **2006**, 70, 848-56	2.2	17
44	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, 244-50	2.7	23
43	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, 109-16	5.3	21
42	C-reactive protein and its role in metabolic syndrome: mendelian randomisation study. *Lancet, The*, **2005**, 366, 1954-9	40	266
41	TAS2R38 (phenylthiocarbamide) haplotypes, coronary heart disease traits, and eating behavior in the British Women's Heart and Health Study. *American Journal of Clinical Nutrition*, **2005**, 81, 1005-11	7	73
40	Angiotensin II type I receptor gene polymorphism: anthropometric and metabolic syndrome traits. *Journal of Medical Genetics*, **2005**, 42, 396-401	5.8	23
39	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, 5569-76	5.6	24
38	Haplotypic analyses of the IGF2-INS-TH gene cluster in relation to cardiovascular risk traits. *Human Molecular Genetics*, **2004**, 13, 715-25	5.6	49
37	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	2.6	57
36	Microplate Array Diagonal Gel Electrophoresis for SNP and Microsatellite Genotyping and for Mutation Scanning **2004**, 836-841		
35	Polymorphisms in the interleukin-4 and interleukin-4 receptor alpha chain genes confer susceptibility to asthma and atopy in a Caucasian population. *Clinical and Experimental Allergy*, **2003** , 33, 1111-7	4.1	98
34	Manual 768 or 384 well microplate gel 'dry' electrophoresis for PCR checking and SNP genotyping. *Nucleic Acids Research*, **2003**, 31, e48	20.1	22
33	Null mutation in human ciliary neurotrophic factor gene confers higher body mass index in males. *European Journal of Human Genetics*, **2002**, 10, 749-52	5.3	19
32	Linkage analysis of the 5q31-33 candidate region for asthma in 240 UK families. *Genes and Immunity* , **2001**, 2, 20-4	4.4	20
31	Positive associations between single nucleotide polymorphisms in the IGF2 gene region and body mass index in adult males. *Human Molecular Genetics*, **2001**, 10, 1491-501	5.6	93

30	Microplate-array diagonal-gel electrophoresis (MADGE) systems for high-throughput electrophoresis. *Technical Tips Online*, **2000**, 5, 12-18		
29	SNP genotyping by combination of 192-well MADGE, ARMS and computerized gel image analysis. *BioTechniques*, **2000**, 29, 500-4, 505-6	2.5	19
28	Evaluating and implementing block jackknife resampling Mendelian randomization to mitigate bias induced by overlapping samples		1
27	Validation of lipid-related therapeutic targets for coronary heart disease prevention using human genetics		1
26	Global Biobank Meta-analysis Initiative: powering genetic discovery across human diseases		6
25	MR-TRYX: A Mendelian randomization framework that exploits horizontal pleiotropy to infer novel causal pathways		5
24	Identifying epigenetic biomarkers of established prognostic factors and survival in a clinical cohort of individuals with oropharyngeal cancer		1
23	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		2
22	MR-Base: a platform for systematic causal inference across the phenome using billions of genetic associations		77
21	Sex-associated autosomal DNA methylation differences are wide-spread and stable throughout childhood		14
20	PhenoSpD: an integrated toolkit for phenotypic correlation estimation and multiple testing correction using GWAS summary statistics		3
19	Imprinted loci may be more widespread in humans than previously appreciated and enable limited assignment of parental allelic transmissions in unrelated individuals		4
18	Automating Mendelian randomization through machine learning to construct a putative causal map of the human phenome		34
17	Systematic Mendelian randomization framework elucidates hundreds of genetic loci which may influence disease through changes in DNA methylation levels		3
16	Multi-omics study revealing putative drug targets of COVID-19 severity and other viral infection diseases		7
15	The variant call format provides efficient and robust storage of GWAS summary statistics		4
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