Andrew P Morris

List of Publications by Citations

191 papers	39,932 citations	76 h-index	199 g-index
221 ext. papers	49,648 ext. citations	16.4 avg, IF	5.89 L-index

#	Paper	IF	Citations
191	A second generation human haplotype map of over 3.1 million SNPs. *Nature*, **2007**, 449, 851-61	50.4	3647
190	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
189	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics*, **2010**, 42, 937-48	36.3	2267
188	Replication of genome-wide association signals in UK samples reveals risk loci for type 2 diabetes. *Science*, **2007**, 316, 1336-41	33.3	1823
187	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. *Nature Genetics*, **2010**, 42, 105-16	36.3	1673
186	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. *Nature Genetics*, **2012**, 44, 981-90	36.3	1482
185	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. *Nature Genetics*, **2010**, 42, 579-89	36.3	1449
184	Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86	36.3	1339
183	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. *Nature Genetics*, **2015**, 47, 1121-1130	36.3	1290
182	Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations. *Nature Genetics*, **2015**, 47, 979-986	36.3	1278
181	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
180	Conditional and joint multiple-SNP analysis of GWAS summary statistics identifies additional variants influencing complex traits. *Nature Genetics*, **2012**, 44, 369-75, S1-3	36.3	813
179	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. *Nature Genetics*, **2014**, 46, 234-44	36.3	784
178	The UK10K project identifies rare variants in health and disease. *Nature*, **2015**, 526, 82-90	50.4	776
177	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. *Nature Genetics*, **2010**, 42, 949-60	36.3	724
176	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
175	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. *Nature Genetics*, **2018**, 50, 1505-1513	36.3	675

174	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. *Nature Genetics*, **2012**, 44, 991-1005	36.3	621
173	Meta-analysis of genome-wide association studies identifies eight new loci for type 2 diabetes in east Asians. *Nature Genetics*, **2011**, 44, 67-72	36.3	475
172	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics*, **2013**, 45, 501-12	36.3	437
171	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. *Diabetes*, **2017**, 66, 2888-2902	8.9	414
170	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
169	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. *Nature Genetics*, **2011**, 43, 984-9	36.3	406
168	An evaluation of statistical approaches to rare variant analysis in genetic association studies. *Genetic Epidemiology*, **2010**, 34, 188-93	2.6	402
167	The metabochip, a custom genotyping array for genetic studies of metabolic, cardiovascular, and anthropometric traits. *PLoS Genetics*, **2012**, 8, e1002793	6	395
166	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. *Nature Genetics*, **2018**, 50, 1412-1425	36.3	386
165	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. *Nature Genetics*, **2014**, 46, 357-63	36.3	351
164	Bayesian refinement of association signals for 14 loci in 3 common diseases. *Nature Genetics*, **2012**, 44, 1294-301	36.3	347
163	GWAMA: software for genome-wide association meta-analysis. *BMC Bioinformatics*, **2010**, 11, 288	3.6	342
162	Novel loci for adiponectin levels and their influence on type 2 diabetes and metabolic traits: a multi-ethnic meta-analysis of 45,891 individuals. *PLoS Genetics*, **2012**, 8, e1002607	6	326
161	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
160	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. *Nature Genetics*, **2015**, 47, 1415-25	36.3	292
159	Multi-ethnic genome-wide association study for atrial fibrillation. *Nature Genetics*, **2018**, 50, 1225-1233	36.3	277
158	Genome-wide association analyses identifies a susceptibility locus for tuberculosis on chromosome 18q11.2. *Nature Genetics*, **2010**, 42, 739-741	36.3	276
157	Genome-wide associations for birth weight and correlations with adult disease. *Nature*, **2016**, 538, 248-252	50.4	266

156	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. *Nature Genetics*, **2016**, 48, 1171-1184	36.3	251
155	Novel insights into the genetics of smoking behaviour, lung function, and chronic obstructive pulmonary disease (UK BiLEVE): a genetic association study in UK Biobank. *Lancet Respiratory Medicine,the*, **2015**, 3, 769-81	35.1	245
154	The impact of low-frequency and rare variants on lipid levels. *Nature Genetics*, **2015**, 47, 589-97	36.3	229
153	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. *PLoS Medicine*, **2017**, 14, e1002383	11.6	223
152	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics*, **2018**, 50, 559-571	36.3	221
151	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. *PLoS Genetics*, **2015**, 11, e1005378	6	220
150	Transethnic meta-analysis of genomewide association studies. *Genetic Epidemiology*, **2011**, 35, 809-22	2.6	218
149	A catalog of genetic loci associated with kidney function from analyses of a million individuals. *Nature Genetics*, **2019**, 51, 957-972	36.3	217
148	Mosaic loss of chromosome Y in peripheral blood is associated with shorter survival and higher risk of cancer. *Nature Genetics*, **2014**, 46, 624-8	36.3	213
147	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
146	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. *Nature Genetics*, **2019**, 51, 804-814	36.3	181
145	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
144	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180
143	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. *Nature Genetics*, **2017**, 49, 946-952	36.3	176
142	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. *Nature Genetics*, **2017**, 49, 416-425	36.3	170
141	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. *Molecular Psychiatry*, **2015**, 20, 647-656	15.1	167
140	Stratifying type 2 diabetes cases by BMI identifies genetic risk variants in LAMA1 and enrichment for risk variants in lean compared to obese cases. *PLoS Genetics*, **2012**, 8, e1002741	6	162
139	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. *Nature Genetics*, **2019**, 51, 481-493	36.3	156

138	Genetic Evidence for Causal Relationships Between Maternal Obesity-Related Traits and Birth Weight. *JAMA - Journal of the American Medical Association*, **2016**, 315, 1129-40	27.4	149
137	Gene-lifestyle interaction and type 2 diabetes: the EPIC interact case-cohort study. *PLoS Medicine*, **2014**, 11, e1001647	11.6	149
136	A genome-wide association search for type 2 diabetes genes in African Americans. *PLoS ONE*, **2012**, 7, e29202	3.7	138
135	Genetic variants underlying risk of endometriosis: insights from meta-analysis of eight genome-wide association and replication datasets. *Human Reproduction Update*, **2014**, 20, 702-16	15.8	131
134	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. *Nature*, **2019**, 570, 71-76	50.4	129
133	Genome-wide association study identifies a novel locus contributing to type 2 diabetes susceptibility in Sikhs of Punjabi origin from India. *Diabetes*, **2013**, 62, 1746-55	0.9	129
132	Mutagenesis. Smoking is associated with mosaic loss of chromosome Y. *Science*, **2015**, 347, 81-3	33.3	108
131	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. *Nature Communications*, **2016**, 7, 10494	17.4	107
130	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. *Nature Communications*, **2017**, 8, 14977	17.4	105
129	Genome-wide association analysis identifies six new loci associated with forced vital capacity. *Nature Genetics*, **2014**, 46, 669-77	36.3	104
128	Investigating the Causal Relationship of C-Reactive Protein with 32 Complex Somatic and Psychiatric Outcomes: A Large-Scale Cross-Consortium Mendelian Randomization Study. *PLoS Medicine*, **2016**, 13, e1001976	11.6	100
127	Identification of type 2 diabetes loci in 433,540 East Asian individuals. *Nature*, **2020**, 582, 240-245	50.4	89
126	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. *Nature Communications*, **2017**, 8, 80	17.4	88
125	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. *Hypertension*, **2017**,	8.5	85
124	An integrated epigenomic analysis for type 2 diabetes susceptibility loci in monozygotic twins. *Nature Communications*, **2014**, 5, 5719	17.4	85
123	Improved imputation accuracy of rare and low-frequency variants using population-specific high-coverage WGS-based imputation reference panel. *European Journal of Human Genetics*, **2017**, 25, 869-876	5.3	82
122	Regulatory variants at KLF14 influence type 2 diabetes risk via a female-specific effect on adipocyte size and body composition. *Nature Genetics*, **2018**, 50, 572-580	36.3	82
121	Pleiotropic genes for metabolic syndrome and inflammation. *Molecular Genetics and Metabolism*, **2014**, 112, 317-38	3.7	81

120	Genome-Wide Association Study of Susceptibility to Idiopathic Pulmonary Fibrosis. *American Journal of Respiratory and Critical Care Medicine*, **2020**, 201, 564-574	10.2	81
119	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. *Nature Genetics*, **2017**, 49, 125-130	36.3	80
118	Personalized risk prediction for type 2 diabetes: the potential of genetic risk scores. *Genetics in Medicine*, **2017**, 19, 322-329	8.1	79
117	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. *Nature Communications*, **2015**, 6, 8658	17.4	79
116	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. *Science Translational Medicine*, **2016**, 8, 341ra76	17.5	77
115	Identification and functional characterization of G6PC2 coding variants influencing glycemic traits define an effector transcript at the G6PC2-ABCB11 locus. *PLoS Genetics*, **2015**, 11, e1004876	6	76
114	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. *Cell*, **2019**, 179, 984-1002.e36	56.2	76
113	Genome-wide association study of toxic metals and trace elements reveals novel associations. *Human Molecular Genetics*, **2015**, 24, 4739-45	5.6	75
112	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. *American Journal of Human Genetics*, **2017**, 100, 865-884	11	74
111	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. *Nature Communications*, **2018**, 9, 2252	17.4	71
110	Genome wide association identifies common variants at the SERPINA6/SERPINA1 locus influencing plasma cortisol and corticosteroid binding globulin. *PLoS Genetics*, **2014**, 10, e1004474	6	71
109	Meta-analysis of sex-specific genome-wide association studies. *Genetic Epidemiology*, **2010**, 34, 846-53	2.6	69
108	Trans-ethnic meta-regression of genome-wide association studies accounting for ancestry increases power for discovery and improves fine-mapping resolution. *Human Molecular Genetics*, **2017**, 26, 3639-3650	5.6	67
107	Cystatin C and Cardiovascular Disease: A Mendelian Randomization Study. *Journal of the American College of Cardiology*, **2016**, 68, 934-45	15.1	65
106	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. *Nature Genetics*, **2019**, 51, 636-648	36.3	59
105	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. *American Journal of Human Genetics*, **2018**, 102, 375-400	11	59
104	Genome-wide genetic analyses highlight mitogen-activated protein kinase (MAPK) signaling in the pathogenesis of endometriosis. *Human Reproduction*, **2017**, 32, 780-793	5.7	59
103	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. *PLoS Genetics*, **2015**, 11, e1005230	6	59

102	Discovery and fine mapping of serum protein loci through transethnic meta-analysis. *American Journal of Human Genetics*, **2012**, 91, 744-53	11	58
101	Genome-wide enrichment analysis between endometriosis and obesity-related traits reveals novel susceptibility loci. *Human Molecular Genetics*, **2015**, 24, 1185-99	5.6	57
100	Multi-ethnic genome-wide association study identifies novel locus for type 2 diabetes susceptibility. *European Journal of Human Genetics*, **2016**, 24, 1175-80	5.3	54
99	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. *Nature Communications*, **2019**, 10, 29	17.4	51
98	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. *Nature Communications*, **2017**, 8, 15805	17.4	50
97	Beyond Endometriosis Genome-Wide Association Study: From Genomics to Phenomics to the Patient. *Seminars in Reproductive Medicine*, **2016**, 34, 242-54	1.4	50
96	Association between endometriosis and the interleukin 1A (IL1A) locus. *Human Reproduction*, **2015**, 30, 239-48	5.7	49
95	Evaluating the Performance of Fine-Mapping Strategies at Common Variant GWAS Loci. *PLoS Genetics*, **2015**, 11, e1005535	6	49
94	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. *Human Molecular Genetics*, **2015**, 24, 5955-64	5.6	48
93	Trans-ethnic study design approaches for fine-mapping. *European Journal of Human Genetics*, **2016**, 24, 1330-6	5.3	48
92	Genome-Wide Association Study of the Modified Stumvoll Insulin Sensitivity Index Identifies BCL2 and FAM19A2 as Novel Insulin Sensitivity Loci. *Diabetes*, **2016**, 65, 3200-11	0.9	47
91	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. *Nature Communications*, **2016**, 7, 13357	17.4	46
90	Genetic analysis of dyslexia candidate genes in the European cross-linguistic NeuroDys cohort. *European Journal of Human Genetics*, **2014**, 22, 675-80	5.3	46
89	Trans-ethnic meta-analysis of white blood cell phenotypes. *Human Molecular Genetics*, **2014**, 23, 6944-60	5.6	45
88	The trans-ancestral genomic architecture of glycemic traits. *Nature Genetics*, **2021**, 53, 840-860	36.3	44
87	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. *American Journal of Human Genetics*, **2016**, 99, 636-646	11	44
86	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
85	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. *Nature Communications*, **2019**, 10, 4130	17.4	43

84	Large-scale genome-wide association studies and meta-analyses of longitudinal change in adult lung function. *PLoS ONE*, **2014**, 9, e100776	3.7	42
83	Trans-ethnic Meta-analysis and Functional Annotation Illuminates the Genetic Architecture of Fasting Glucose and Insulin. *American Journal of Human Genetics*, **2016**, 99, 56-75	11	41
82	Genetic overlap between endometriosis and endometrial cancer: evidence from cross-disease genetic correlation and GWAS meta-analyses. *Cancer Medicine*, **2018**, 7, 1978-1987	4.8	40
81	A powerful approach to sub-phenotype analysis in population-based genetic association studies. *Genetic Epidemiology*, **2010**, 34, 335-43	2.6	39
80	Direct analysis of unphased SNP genotype data in population-based association studies via Bayesian partition modelling of haplotypes. *Genetic Epidemiology*, **2005**, 29, 91-107	2.6	38
79	Genome-wide association study of type 2 diabetes in Africa. *Diabetologia*, **2019**, 62, 1204-1211	10.3	36
78	Shared Genetic Risk Factors Across Carbamazepine-Induced Hypersensitivity Reactions. *Clinical Pharmacology and Therapeutics*, **2019**, 106, 1028-1036	6.1	34
77	Genome-wide association study of nevirapine hypersensitivity in a sub-Saharan African HIV-infected population. *Journal of Antimicrobial Chemotherapy*, **2017**, 72, 1152-1162	5.1	33
76	A flexible Bayesian framework for modeling haplotype association with disease, allowing for dominance effects of the underlying causative variants. *American Journal of Human Genetics*, **2006**, 79, 679-94	11	31
75	Multiethnic Genome-Wide Association Study of Diabetic Retinopathy Using Liability Threshold Modeling of Duration of Diabetes and Glycemic Control. *Diabetes*, **2019**, 68, 441-456	0.9	31
74	Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis. *American Journal of Human Genetics*, **2017**, 100, 51-63	11	30
73	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. *Nature Communications*, **2021**, 12, 24	17.4	30
72	Chronic obstructive pulmonary disease and related phenotypes: polygenic risk scores in population-based and case-control cohorts. *Lancet Respiratory Medicine,the*, **2020**, 8, 696-708	35.1	29
71	Guidance for the utility of linear models in meta-analysis of genetic association studies of binary phenotypes. *European Journal of Human Genetics*, **2017**, 25, 240-245	5.3	26
70	GWAS-identified loci for coronary heart disease are associated with intima-media thickness and plaque presence at the carotid artery bulb. *Atherosclerosis*, **2015**, 239, 304-10	3.1	26
69	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
68	Multipoint linkage-disequilibrium mapping narrows location interval and identifies mutation heterogeneity. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 13442-6	11.5	25
67	Disentangling the genetics of lean mass. *American Journal of Clinical Nutrition*, **2019**, 109, 276-287	7	24

66	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
65	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. *Cell*, **2021**, 184, 4784-4818.e17	38.6	24
64	Genome-wide DNA methylation study identifies genes associated with the cardiovascular biomarker GDF-15. *Human Molecular Genetics*, **2016**, 25, 817-27	5.6	23
63	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
62	Genetic burden associated with varying degrees of disease severity in endometriosis. *Molecular Human Reproduction*, **2015**, 21, 594-602	4.4	22
61	Hypertension and renin-angiotensin system blockers are not associated with expression of angiotensin-converting enzyme 2 (ACE2) in the kidney. *European Heart Journal*, **2020**, 41, 4580-4588	9.5	22
60	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 379-384	11.5	21
59	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. *Human Molecular Genetics*, **2016**, 25, 2070-2081	5.6	20
58	Functional validity, role, and implications of heavy alcohol consumption genetic loci. *Science Advances*, **2020**, 6, eaay5034	14.3	19
57	A Meta-Analysis of Genome-Wide Association Studies of Growth Differentiation Factor-15 Concentration in Blood. *Frontiers in Genetics*, **2018**, 9, 97	4.5	19
56	Variability of genome-wide DNA methylation and mRNA expression profiles in reproductive and endocrine disease related tissues. *Epigenetics*, **2017**, 12, 897-908	5.7	19
55	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. *Scientific Reports*, **2016**, 6, 35278	4.9	18
54	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. *Nature Communications*, **2020**, 11, 2542	17.4	16
53	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*, **2018**, 3, 4	4.8	16
52	Progress in defining the genetic contribution to type 2 diabetes susceptibility. *Current Opinion in Genetics and Development*, **2018**, 50, 41-51	4.9	15
51	Genetics of Chronic Kidney Disease Stages Across Ancestries: The PAGE Study. *Frontiers in Genetics*, **2019**, 10, 494	4.5	14
50	Functional analysis of epilepsy-associated variants in STXBP1/Munc18-1 using humanized Caenorhabditis elegans. *Epilepsia*, **2020**, 61, 810-821	6.4	13
49	Ranking and characterization of established BMI and lipid associated loci as candidates for gene-environment interactions. *PLoS Genetics*, **2017**, 13, e1006812	6	13

48	SCOPA and META-SCOPA: software for the analysis and aggregation of genome-wide association studies of multiple correlated phenotypes. *BMC Bioinformatics*, **2017**, 18, 25	3.6	12
47	Discovery and fine-mapping of loci associated with MUFAs through trans-ethnic meta-analysis in Chinese and European populations. *Journal of Lipid Research*, **2017**, 58, 974-981	6.3	12
46	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. *American Journal of Human Genetics*, **2019**, 105, 15-28	11	12
45	MARV: a tool for genome-wide multi-phenotype analysis of rare variants. *BMC Bioinformatics*, **2017**, 18, 110	3.6	12
44	Analysis of chromatin organization and gene expression in T cells identifies functional genes for rheumatoid arthritis. *Nature Communications*, **2020**, 11, 4402	17.4	12
43	The genetic architecture of sporadic and multiple consecutive miscarriage. *Nature Communications*, **2020**, 11, 5980	17.4	11
42	Genome-wide association study of plasma levels of polychlorinated biphenyls disclose an association with the CYP2B6 gene in a population-based sample. *Environmental Research*, **2015**, 140, 95-101	7.9	10
41	Genetic variation in the CYP1A1 gene is related to circulating PCB118 levels in a population-based sample. *Environmental Research*, **2014**, 133, 135-40	7.9	10
40	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. *Diabetes*, **2020**, 69, 2806-2818	0.9	10
39	Combined genetic analysis of juvenile idiopathic arthritis clinical subtypes identifies novel risk loci, target genes and key regulatory mechanisms. *Annals of the Rheumatic Diseases*, **2020**,	2.4	10
38	Linkage disequilibrium assessment via log-linear modeling of SNP haplotype frequencies. *Genetic Epidemiology*, **2003**, 25, 106-14	2.6	9
37	What Can Machine Learning Approaches in Genomics Tell Us about the Molecular Basis of Amyotrophic Lateral Sclerosis?. *Journal of Personalized Medicine*, **2020**, 10,	3.6	9
36	Mapping DNA interaction landscapes in psoriasis susceptibility loci highlights KLF4 as a target gene in 9q31. *BMC Biology*, **2020**, 18, 47	7.3	8
35	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. *Nature Genetics*, **2022**,	36.3	7
34	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*,3, 4	4.8	6
33	Functional genomics atlas of synovial fibroblasts defining rheumatoid arthritis heritability. *Genome Biology*, **2021**, 22, 247	18.3	6
32	Identification of novel putative rheumatoid arthritis susceptibility genes via analysis of rare variants. *BMC Proceedings*, **2009**, 3 Suppl 7, S131	2.3	5
31	Governing antimicrobial resistance: a narrative review of global governance mechanisms. *Journal of Public Health Policy*, **2020**, 41, 515-528	2.9	5

30	Uncovering genetic mechanisms of hypertension through multi-omic analysis of the kidney. *Nature Genetics*, **2021**, 53, 630-637	36.3	5
29	Genetic and methylation variation in the CYP2B6 gene is related to circulating p,pRdde levels in a population-based sample. *Environment International*, **2017**, 98, 212-218	12.9	4
28	Identification of type 2 diabetes loci in 433,540 East Asian individuals		4
27	Tissue-Specific Alteration of Metabolic Pathways Influences Glycemic Regulation		4
26	Fine-scale population structure in the UK Biobank: implications for genome-wide association studies. *Human Molecular Genetics*, **2020**, 29, 2803-2811	5.6	4
25	A genome-wide association study of IgM antibody against phosphorylcholine: shared genetics and phenotypic relationship to chronic lymphocytic leukemia. *Human Molecular Genetics*, **2018**, 27, 1809-1818	5.6	3
24	A Bayesian Approach to the Overlap Analysis of Epidemiologically Linked Traits. *Genetic Epidemiology*, **2015**, 39, 624-34	2.6	3
23	Genome-wide association analysis and replication of coronary artery disease in South Korea suggests a causal variant common to diverse populations. *Heart Asia*, **2010**, 2, 104-8	1.9	3
22	Genome-Wide Association Study of Peripheral Artery Disease. *Circulation Genomic and Precision Medicine*, **2021**, 14, e002862	5.2	3
21	Discovery and fine-mapping of kidney function loci in first genome-wide association study in Africans. *Human Molecular Genetics*, **2021**, 30, 1559-1568	5.6	3
20	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. *Genome Medicine*, **2021**, 13, 74	14.4	3
19	Genome-Wide Association Studies **2019**, 597-550		2
18	Identification of a novel proinsulin-associated SNP and demonstration that proinsulin is unlikely to be a causal factor in subclinical vascular remodelling using Mendelian randomisation. *Atherosclerosis*, **2017**, 266, 196-204	3.1	2
17	Neuropeptide S receptor 1 is a nonhormonal treatment target in endometriosis. *Science Translational Medicine*, **2021**, 13,	17.5	2
16	Identification of genetic effects underlying type 2 diabetes in South Asian and European populations.. *Communications Biology*, **2022**, 5, 329	6.7	2
15	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*,3, 4	4.8	1
14	Obesity as a cause of kidney disease Insights from Mendelian randomisation studies		1
13	Pharmacogenetics of TNF inhibitor response in rheumatoid arthritis utilizing the two-component disease activity score. *Pharmacogenomics*, **2020**, 21, 1151-1156	2.6	1

12	Coalescent methods for fine-scale disease-gene mapping. *Methods in Molecular Biology*, **2007**, 376, 123-40	1.4	1
11	Trans-ethnic Mendelian randomization study reveals causal relationships between cardio-metabolic factors and chronic kidney disease		1
10	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. *Circulation Genomic and Precision Medicine*, **2020**, 13, e002769	5.2	1
9	Trans-Ethnic Mendelian Randomization Study Reveals Causal Relationships Between Cardiometabolic Factors and Chronic Kidney Disease. *SSRN Electronic Journal*,	1	1
8	Trans-ethnic Mendelian-randomization study reveals causal relationships between cardiometabolic factors and chronic kidney disease. *International Journal of Epidemiology*, **2021**,	7.8	1
7	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. *Communications Biology*, **2022**, 5,	6.7	1
6	Genome-Wide association between EYA1 and Aspirin-induced peptic ulceration. *EBioMedicine*, **2021** , 74, 103728	8.8	0
5	Copy number variations in "classical" obesity candidate genes are not frequently associated with severe early-onset obesity in children. *Journal of Pediatric Endocrinology and Metabolism*, **2017**, 30, 507-515	1.6	
4	Structural analysis of cell-surface glycopeptides which bind to wheat germ agglutinin. *Biochemical Society Transactions*, **1984**, 12, 655-655	5.1	
3	Suppressor Alleles in Multiple Sclerosis: Inheritance and Interactions. *PLoS Genetics*, **2005**, preprint, e150	6	
2	Assessing the impact of alcohol consumption on the genetic contribution to mean corpuscular volume. *Human Molecular Genetics*, **2021**, 30, 2040-2051	5.6	
1	snpQT: flexible, reproducible, and comprehensive quality control and imputation of genomic data.. *F1000Research*, **2021**, 10, 567	3.6	