Andrew P Morris

List of Publications by Year
in descending order

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		3731	2448
197	56,374	89	197
papers	citations	h-index	g-index

221	221	221	53419
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	27.8	4,137
2	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
3	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	21.4	2,634
4	A comprehensive 1000 Genomesâ€“based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	21.4	2,054
5	Replication of Genome-Wide Association Signals in UK Samples Reveals Risk Loci for Type 2 Diabetes. Science, 2007, 316, 1336-1341.	12.6	2,040
6	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	21.4	1,982
7	Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations. Nature Genetics, 2015, 47, 979-986.	21.4	1,965
8	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
9	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	21.4	1,748
10	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	21.4	1,631
11	Conditional and joint multiple-SNP analysis of GWAS summary statistics identifies additional variants influencing complex traits. Nature Genetics, 2012, 44, 369-375.	21.4	1,338
12	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.	21.4	1,331
13	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
14	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	27.8	1,014
15	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	21.4	959
16	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
17	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
18	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, 949-960.	21.4	836

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19	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	21.4	746
20	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615
21	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	21.4	578
22	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	21.4	552
23	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
24	Meta-analysis of genome-wide association studies identifies eight new loci for type 2 diabetes in east Asians. Nature Genetics, 2012, 44, 67-72.	21.4	545
25	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
26	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. Nature Genetics, 2011, 43, 984-989.	21.4	481
27	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
28	Bayesian refinement of association signals for 14 loci in 3 common diseases. Nature Genetics, 2012, 44, 1294-1301.	21.4	469
29	GWAMA: software for genome-wide association meta-analysis. BMC Bioinformatics, 2010, 11, 288.	2.6	456
30	An evaluation of statistical approaches to rare variant analysis in genetic association studies. Genetic Epidemiology, 2010, 34, 188-193.	1.3	452
31	The Metabochip, a Custom Genotyping Array for Genetic Studies of Metabolic, Cardiovascular, and Anthropometric Traits. PLoS Genetics, 2012, 8, e1002793.	3.5	448
32	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. Nature Genetics, 2014, 46, 357-363.	21.4	428
33	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.	3.5	419
34	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	27.8	406
35	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	21.4	402
36	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	21.4	365

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37	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
38	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	21.4	356
39	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
40	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. Nature Genetics, 2019, 51, 481-493.	21.4	350
41	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, 769-781.	10.7	346
42	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.	8.4	341
43	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
44	Genome-wide association analyses identifies a susceptibility locus for tuberculosis on chromosome 18q11.2. Nature Genetics, 2010, 42, 739-741.	21.4	332
45	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.	3.5	331
46	Mosaic loss of chromosome Y in peripheral blood is associated with shorter survival and higher risk of cancer. Nature Genetics, 2014, 46, 624-628.	21.4	320
47	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	21.4	310
48	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
49	Transethnic metaâ€analysis of genomewide association studies. Genetic Epidemiology, 2011, 35, 809-822.	1.3	282
50	Identification of type 2 diabetes loci in 433,540 East Asian individuals. Nature, 2020, 582, 240-245.	27.8	282
51	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	21.4	279
52	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
53	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.	21.4	257
54	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250

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55	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	27.8	248
56	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	12.8	245
57	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	7.9	235
58	Genetic Evidence for Causal Relationships Between Maternal Obesity-Related Traits and Birth Weight. JAMA - Journal of the American Medical Association, 2016, 315, 1129.	7.4	220
59	Genome-Wide Association Study of Susceptibility to Idiopathic Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2020, 201, 564-574.	5.6	208
60	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	2.5	197
61	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.	3.5	190
62	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. Cell, 2021, 184, 4784-4818.e17.	28.9	188
63	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.	2.8	181
64	Gene-Lifestyle Interaction and Type 2 Diabetes: The EPIC InterAct Case-Cohort Study. PLoS Medicine, 2014, 11, e1001647.	8.4	180
65	Genetic variants underlying risk of endometriosis: insights from meta-analysis of eight genome-wide association and replication datasets. Human Reproduction Update, 2014, 20, 702-716.	10.8	171
66	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.	2.9	170
67	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
68	Genome-Wide Association Study Identifies a Novel Locus Contributing to Type 2 Diabetes Susceptibility in Sikhs of Punjabi Origin From India. Diabetes, 2013, 62, 1746-1755.	0.6	167
69	Smoking is associated with mosaic loss of chromosome Y. Science, 2015, 347, 81-83.	12.6	163
70	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	12.8	153
71	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. Cell, 2019, 179, 984-1002.e36.	28.9	152
72	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.	8.4	150

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73	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	12.8	147
74	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.	21.4	143
75	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	12.8	133
76	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	21.4	131
77	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	6.2	131
78	Personalized risk prediction for type 2 diabetes: the potential of genetic risk scores. Genetics in Medicine, 2017, 19, 322-329.	2.4	127
79	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	2.7	123
80	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.	6.2	123
81	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. Nature Genetics, 2017, 49, 125-130.	21.4	116
82	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. Nature Communications, 2019, 10, 29.	12.8	113
83	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
84	Cystatin C and Cardiovascular Disease. Journal of the American College of Cardiology, 2016, 68, 934-945.	2.8	109
85	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	12.8	108
86	Pleiotropic genes for metabolic syndrome and inflammation. Molecular Genetics and Metabolism, 2014, 112, 317-338.	1.1	107
87	Genome Wide Association Identifies Common Variants at the SERPINA6/SERPINA1 Locus Influencing Plasma Cortisol and Corticosteroid Binding Globulin. PLoS Genetics, 2014, 10, e1004474.	3.5	105
88	Genome-wide association study of toxic metals and trace elements reveals novel associations. Human Molecular Genetics, 2015, 24, 4739-4745.	2.9	104
89	An integrated epigenomic analysis for type 2 diabetes susceptibility loci in monozygotic twins. Nature Communications, 2014, 5, 5719.	12.8	100
90	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. Science Translational Medicine, 2016, 8, 341ra76.	12.4	100

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91	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. Nature Communications, 2018, 9, 2252.	12.8	99
92	Metaâ€analysis of sexâ€specific genomeâ€wide association studies. Genetic Epidemiology, 2010, 34, 846-853.	1.3	96
93	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.	3.5	95
94	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	12.8	95
95	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	21.4	91
96	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
97	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
98	Genome-wide genetic analyses highlight mitogen-activated protein kinase (MAPK) signaling in the pathogenesis of endometriosis. Human Reproduction, 2017, 32, 780-793.	0.9	81
99	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. PLoS Genetics, 2015, 11, e1005230.	3.5	77
100	Trans-ethnic study design approaches for fine-mapping. European Journal of Human Genetics, 2016, 24, 1330-1336.	2.8	75
101	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
102	Genome-wide enrichment analysis between endometriosis and obesity-related traits reveals novel susceptibility loci. Human Molecular Genetics, 2015, 24, 1185-1199.	2.9	71
103	Discovery and Fine Mapping of Serum Protein Loci through Transethnic Meta-analysis. American Journal of Human Genetics, 2012, 91, 744-753.	6.2	69
104	Multi-ethnic genome-wide association study identifies novel locus for type 2 diabetes susceptibility. European Journal of Human Genetics, 2016, 24, 1175-1180.	2.8	69
105	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.	10.7	69
106	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	2.9	68
107	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. American Journal of Human Genetics, 2016, 99, 636-646.	6.2	67
108	Genome-Wide Association Study of the Modified Stumvoll Insulin Sensitivity Index Identifies BCL2 and FAM19A2 as Novel Insulin Sensitivity Loci. Diabetes, 2016, 65, 3200-3211.	0.6	67

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109	Evaluating the Performance of Fine-Mapping Strategies at Common Variant GWAS Loci. PLoS Genetics, 2015, 11, e1005535.	3.5	67
110	Beyond Endometriosis Genome-Wide Association Study: From Genomics to Phenomics to the Patient. Seminars in Reproductive Medicine, 2016, 34, 242-254.	1.1	62
111	Genetic overlap between endometriosis and endometrial cancer: evidence from crossâ€disease genetic correlation and GWAS metaâ€analyses. Cancer Medicine, 2018, 7, 1978-1987.	2.8	62
112	Trans-ethnic meta-analysis of white blood cell phenotypes. Human Molecular Genetics, 2014, 23, 6944-6960.	2.9	60
113	Genetic analysis of dyslexia candidate genes in the European cross-linguistic NeuroDys cohort. European Journal of Human Genetics, 2014, 22, 675-680.	2.8	59
114	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
115	Association between endometriosis and the interleukin 1A (IL1A) locus. Human Reproduction, 2015, 30, 239-248.	0.9	58
116	Genome-wide association study of type 2 diabetes in Africa. Diabetologia, 2019, 62, 1204-1211.	6.3	56
117	Trans-ethnic Meta-analysis and Functional Annotation Illuminates theÂGenetic Architecture of Fasting Glucose and Insulin. American Journal of Human Genetics, 2016, 99, 56-75.	6.2	55
118	Multiethnic Genome-Wide Association Study of Diabetic Retinopathy Using Liability Threshold Modeling of Duration of Diabetes and Glycemic Control. Diabetes, 2019, 68, 441-456.	0.6	54
119	A powerful approach to subâ€phenotype analysis in populationâ€based genetic association studies. Genetic Epidemiology, 2010, 34, 335-343.	1.3	52
120	Large-Scale Genome-Wide Association Studies and Meta-Analyses of Longitudinal Change in Adult Lung Function. PLoS ONE, 2014, 9, e100776.	2.5	52
121	Shared Genetic Risk Factors Across Carbamazepineâ€Induced Hypersensitivity Reactions. Clinical Pharmacology and Therapeutics, 2019, 106, 1028-1036.	4.7	52
122	The genetic architecture of sporadic and multiple consecutive miscarriage. Nature Communications, 2020, 11, 5980.	12.8	52
123	Functional validity, role, and implications of heavy alcohol consumption genetic loci. Science Advances, 2020, 6, eaay5034.	10.3	47
124	Multi-ancestry genome-wide association study of gestational diabetes mellitus highlights genetic links with type 2 diabetes. Human Molecular Genetics, 2022, 31, 3377-3391.	2.9	47
125	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.	6.2	45
126	Genome-wide association study of nevirapine hypersensitivity in a sub-Saharan African HIV-infected population. Journal of Antimicrobial Chemotherapy, 2017, 72, dkw545.	3.0	42

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127	Direct analysis of unphased SNP genotype data in population-based association studies via Bayesian partition modelling of haplotypes. Genetic Epidemiology, 2005, 29, 91-107.	1.3	41
128	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.	2.2	41
129	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.	2.8	40
130	Trans-ethnic Mendelian-randomization study reveals causal relationships between cardiometabolic factors and chronic kidney disease. International Journal of Epidemiology, 2022, 50, 1995-2010.	1.9	39
131	Disentangling the genetics of lean mass. American Journal of Clinical Nutrition, 2019, 109, 276-287.	4.7	38
132	Analysis of chromatin organization and gene expression in T cells identifies functional genes for rheumatoid arthritis. Nature Communications, 2020, 11, 4402.	12.8	37
133	Uncovering genetic mechanisms of hypertension through multi-omic analysis of the kidney. Nature Genetics, 2021, 53, 630-637.	21.4	37
134	Functional analysis of epilepsyâ€associated variants in STXBP1/Munc18â€1 using humanized Caenorhabditis elegans. Epilepsia, 2020, 61, 810-821.	5.1	34
135	Variability of genome-wide DNA methylation and mRNA expression profiles in reproductive and endocrine disease related tissues. Epigenetics, 2017, 12, 897-908.	2.7	33
136	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, 679-694.	6.2	32
137	Genome-wide DNA methylation study identifies genes associated with the cardiovascular biomarker GDF-15. Human Molecular Genetics, 2016, 25, 817-827.	2.9	32
138	GWAS-identified loci for coronary heart disease are associated with intima-media thickness and plaque presence at the carotid artery bulb. Atherosclerosis, 2015, 239, 304-310.	0.8	31
139	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
140	Combined genetic analysis of juvenile idiopathic arthritis clinical subtypes identifies novel risk loci, target genes and key regulatory mechanisms. Annals of the Rheumatic Diseases, 2021, 80, 321-328.	0.9	31
141	Genetic burden associated with varying degrees of disease severity in endometriosis. Molecular Human Reproduction, 2015, 21, 594-602.	2.8	30
142	Genetics of Chronic Kidney Disease Stages Across Ancestries: The PAGE Study. Frontiers in Genetics, 2019, 10, 494.	2.3	29
143	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, 13442-13446.	7.1	28
144	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.	7.1	28

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145	Functional genomics atlas of synovial fibroblasts defining rheumatoid arthritis heritability. Genome Biology, 2021, 22, 247.	8.8	27
146	A Meta-Analysis of Genome-Wide Association Studies of Growth Differentiation Factor-15 Concentration in Blood. Frontiers in Genetics, 2018, 9, 97.	2.3	26
147	Governing antimicrobial resistance: a narrative review of global governance mechanisms. Journal of Public Health Policy, 2020, 41, 515-528.	2.0	26
148	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.6	26
149	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. Scientific Reports, 2016, 6, 35278.	3.3	25
150	SCOPA and META-SCOPA: software for the analysis and aggregation of genome-wide association studies of multiple correlated phenotypes. BMC Bioinformatics, 2017, 18, 25.	2.6	25
151	Progress in defining the genetic contribution to type 2 diabetes susceptibility. Current Opinion in Genetics and Development, 2018, 50, 41-51.	3.3	25
152	Ranking and characterization of established BMI and lipid associated loci as candidates for gene-environment interactions. PLoS Genetics, 2017, 13, e1006812.	3.5	24
153	Genome-Wide Association Study of Peripheral Artery Disease. Circulation Genomic and Precision Medicine, 2021, 14, e002862.	3.6	24
154	Neuropeptide S receptor 1 is a nonhormonal treatment target in endometriosis. Science Translational Medicine, 2021, 13, .	12.4	23
155	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. Human Molecular Genetics, 2016, 25, 2070-2081.	2.9	21
156	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	6.2	21
157	Identification of genetic effects underlying type 2 diabetes in South Asian and European populations. Communications Biology, 2022, 5, 329.	4.4	21
158	Fine-scale population structure in the UK Biobank: implications for genome-wide association studies. Human Molecular Genetics, 2020, 29, 2803-2811.	2.9	20
159	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. Genome Medicine, 2021, 13, 74.	8.2	20
160	Mapping DNA interaction landscapes in psoriasis susceptibility loci highlights KLF4 as a target gene in 9q31. BMC Biology, 2020, 18, 47.	3.8	19
161	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 2018, 3, 4.	1.8	19
162	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.	4.2	18

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163	Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. Kidney International, 2022, 102, 624-639.	5.2	18
164	MARV: a tool for genome-wide multi-phenotype analysis of rare variants. BMC Bioinformatics, 2017, 18, 110.	2.6	17
165	Contributions of obesity to kidney health and disease: insights from Mendelian randomization and the human kidney transcriptomics. Cardiovascular Research, 2022, 118, 3151-3161.	3.8	17
166	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	4.4	17
167	What Can Machine Learning Approaches in Genomics Tell Us about the Molecular Basis of Amyotrophic Lateral Sclerosis?. Journal of Personalized Medicine, 2020, 10, 247.	2.5	14
168	Discovery and fine-mapping of kidney function loci in first genome-wide association study in Africans. Human Molecular Genetics, 2021, 30, 1559-1568.	2.9	13
169	Blood copper and risk of cardiometabolic diseases: a Mendelian randomization study. Human Molecular Genetics, 2022, 31, 783-791.	2.9	12
170	Genetic variation in the CYP1A1 gene is related to circulating PCB118 levels in a population-based sample. Environmental Research, 2014, 133, 135-140.	7.5	11
171	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	1.8	11
172	Kidney omics in hypertension: from statistical associations to biological mechanisms and clinical applications. Kidney International, 2022, 102, 492-505.	5.2	11
173	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.	7.5	10
174	Linkage disequilibrium assessment via log-linear modeling of SNP haplotype frequencies. Genetic Epidemiology, 2003, 25, 106-114.	1.3	9
175	Influence of early identification and therapy on longâ€term outcomes in earlyâ€onset <scp>MTHFR</scp> deficiency. Journal of Inherited Metabolic Disease, 2022, 45, 848-861.	3.6	7
176	Identification of novel putative rheumatoid arthritis susceptibility genes via analysis of rare variants. BMC Proceedings, 2009, 3, S131.	1.6	6
177	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.	2.9	6
178	Genetics of kidney traits in worldwide populations: the Continental Origins and Genetic Epidemiology Network (COGENT) Kidney Consortium. Kidney International, 2020, 98, 35-41.	5.2	6
179	ADAMTS5 as a therapeutic target for osteoarthritis: Mendelian randomisation study. Annals of the Rheumatic Diseases, 2022, 81, 903-904.	0.9	6
180	Genetic and methylation variation in the CYP2B6 gene is related to circulating p,pâ€²-dde levels in a population-based sample. Environment International, 2017, 98, 212-218.	10.0	5

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181	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. Circulation Genomic and Precision Medicine, 2020, 13, e002769.	3.6	5
182	Genome-Wide association between EYA1 and Aspirin-induced peptic ulceration. EBioMedicine, 2021, 74, 103728.	6.1	5
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