

Andrew P Morris

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Identification of genetic effects underlying type 2 diabetes in South Asian and European populations.. <i>Communications Biology</i> , 2022 , 5, 329	6.7	2
190	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. <i>Nature Genetics</i> , 2022 ,	36.3	7
189	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022 , 5,	6.7	1
188	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021 ,	50.4	24
187	Genome-Wide association between EYA1 and Aspirin-induced peptic ulceration. <i>EBioMedicine</i> , 2021 , 74, 103728	8.8	0
186	Genome-Wide Association Study of Peripheral Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2021 , 14, e002862	5.2	3
185	Discovery and fine-mapping of kidney function loci in first genome-wide association study in Africans. <i>Human Molecular Genetics</i> , 2021 , 30, 1559-1568	5.6	3
184	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. <i>Genome Medicine</i> , 2021 , 13, 74	14.4	3
183	Uncovering genetic mechanisms of hypertension through multi-omic analysis of the kidney. <i>Nature Genetics</i> , 2021 , 53, 630-637	36.3	5
182	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021 , 53, 840-860	36.3	44
181	Assessing the impact of alcohol consumption on the genetic contribution to mean corpuscular volume. <i>Human Molecular Genetics</i> , 2021 , 30, 2040-2051	5.6	
180	snpQT: flexible, reproducible, and comprehensive quality control and imputation of genomic data.. <i>F1000Research</i> , 2021 , 10, 567	3.6	
179	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021 , 12, 24	17.4	30
178	Neuropeptide S receptor 1 is a nonhormonal treatment target in endometriosis. <i>Science Translational Medicine</i> , 2021 , 13,	17.5	2
177	Functional genomics atlas of synovial fibroblasts defining rheumatoid arthritis heritability. <i>Genome Biology</i> , 2021 , 22, 247	18.3	6
176	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. <i>Cell</i> , 2021 , 184, 4784-4818.e17	56.1	17
175	Trans-ethnic Mendelian-randomization study reveals causal relationships between cardiometabolic factors and chronic kidney disease. <i>International Journal of Epidemiology</i> , 2021 ,	7.8	1

174	Identification of type 2 diabetes loci in 433,540 East Asian individuals. <i>Nature</i> , 2020 , 582, 240-245	50.4	89
173	Mapping DNA interaction landscapes in psoriasis susceptibility loci highlights KLF4 as a target gene in 9q31. <i>BMC Biology</i> , 2020 , 18, 47	7.3	8
172	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020 , 11, 2542	17.4	16
171	Functional analysis of epilepsy-associated variants in STXBP1/Munc18-1 using humanized <i>Caenorhabditis elegans</i> . <i>Epilepsia</i> , 2020 , 61, 810-821	6.4	13
170	Functional validity, role, and implications of heavy alcohol consumption genetic loci. <i>Science Advances</i> , 2020 , 6, eaay5034	14.3	19
169	Pharmacogenetics of TNF inhibitor response in rheumatoid arthritis utilizing the two-component disease activity score. <i>Pharmacogenomics</i> , 2020 , 21, 1151-1156	2.6	1
168	Genome-Wide Association Study of Susceptibility to Idiopathic Pulmonary Fibrosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020 , 201, 564-574	10.2	81
167	Fine-scale population structure in the UK Biobank: implications for genome-wide association studies. <i>Human Molecular Genetics</i> , 2020 , 29, 2803-2811	5.6	4
166	Hypertension and renin-angiotensin system blockers are not associated with expression of angiotensin-converting enzyme 2 (ACE2) in the kidney. <i>European Heart Journal</i> , 2020 , 41, 4580-4588	9.5	22
165	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. <i>Nature Genetics</i> , 2020 , 52, 1314-1332	36.3	26
164	The genetic architecture of sporadic and multiple consecutive miscarriage. <i>Nature Communications</i> , 2020 , 11, 5980	17.4	11
163	What Can Machine Learning Approaches in Genomics Tell Us about the Molecular Basis of Amyotrophic Lateral Sclerosis?. <i>Journal of Personalized Medicine</i> , 2020 , 10,	3.6	9
162	Chronic obstructive pulmonary disease and related phenotypes: polygenic risk scores in population-based and case-control cohorts. <i>Lancet Respiratory Medicine</i> , 2020 , 8, 696-708	35.1	29
161	Analysis of chromatin organization and gene expression in T cells identifies functional genes for rheumatoid arthritis. <i>Nature Communications</i> , 2020 , 11, 4402	17.4	12
160	Governing antimicrobial resistance: a narrative review of global governance mechanisms. <i>Journal of Public Health Policy</i> , 2020 , 41, 515-528	2.9	5
159	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. <i>Diabetes</i> , 2020 , 69, 2806-2818	0.9	10
158	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, e002769	5.2	1
157	Combined genetic analysis of juvenile idiopathic arthritis clinical subtypes identifies novel risk loci, target genes and key regulatory mechanisms. <i>Annals of the Rheumatic Diseases</i> , 2020 ,	2.4	10

156	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019 , 10, 4130	17.4	43
155	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. <i>American Journal of Human Genetics</i> , 2019 , 105, 15-28	11	12
154	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019 , 51, 957-972	36.3	217
153	Genetics of Chronic Kidney Disease Stages Across Ancestries: The PAGE Study. <i>Frontiers in Genetics</i> , 2019 , 10, 494	4.5	14
152	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019 , 570, 71-76	50.4	129
151	Shared Genetic Risk Factors Across Carbamazepine-Induced Hypersensitivity Reactions. <i>Clinical Pharmacology and Therapeutics</i> , 2019 , 106, 1028-1036	6.1	34
150	Genome-wide association study of type 2 diabetes in Africa. <i>Diabetologia</i> , 2019 , 62, 1204-1211	10.3	36
149	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. <i>Nature Genetics</i> , 2019 , 51, 804-814	36.3	181
148	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019 , 51, 636-648	36.3	59
147	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. <i>Nature Genetics</i> , 2019 , 51, 481-493	36.3	156
146	Genome-Wide Association Studies 2019 , 597-550		2
145	Disentangling the genetics of lean mass. <i>American Journal of Clinical Nutrition</i> , 2019 , 109, 276-287	7	24
144	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. <i>Cell</i> , 2019 , 179, 984-1002.e36	56.2	76
143	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019 , 51, 452-469	36.3	44
142	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. <i>Nature Communications</i> , 2019 , 10, 29	17.4	51
141	Multiethnic Genome-Wide Association Study of Diabetic Retinopathy Using Liability Threshold Modeling of Duration of Diabetes and Glycemic Control. <i>Diabetes</i> , 2019 , 68, 441-456	0.9	31
140	Progress in defining the genetic contribution to type 2 diabetes susceptibility. <i>Current Opinion in Genetics and Development</i> , 2018 , 50, 41-51	4.9	15
139	Genetic overlap between endometriosis and endometrial cancer: evidence from cross-disease genetic correlation and GWAS meta-analyses. <i>Cancer Medicine</i> , 2018 , 7, 1978-1987	4.8	40

138	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018 , 50, 559-571	36.3	221
137	Regulatory variants at KLF14 influence type 2 diabetes risk via a female-specific effect on adipocyte size and body composition. <i>Nature Genetics</i> , 2018 , 50, 572-580	36.3	82
136	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018 , 102, 375-400	11	59
135	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 379-384	11.5	21
134	A genome-wide association study of IgM antibody against phosphorylcholine: shared genetics and phenotypic relationship to chronic lymphocytic leukemia. <i>Human Molecular Genetics</i> , 2018 , 27, 1809-1818	5.6	3
133	A Meta-Analysis of Genome-Wide Association Studies of Growth Differentiation Factor-15 Concentration in Blood. <i>Frontiers in Genetics</i> , 2018 , 9, 97	4.5	19
132	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. <i>Nature Communications</i> , 2018 , 9, 2252	17.4	71
131	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018 , 50, 1225-1233	36.3	277
130	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , 2018 , 3, 4	4.8	16
129	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018 , 50, 26-41	36.3	186
128	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. <i>Nature Genetics</i> , 2018 , 50, 1505-1513	36.3	675
127	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018 , 50, 1412-1425	36.3	386
126	Guidance for the utility of linear models in meta-analysis of genetic association studies of binary phenotypes. <i>European Journal of Human Genetics</i> , 2017 , 25, 240-245	5.3	26
125	Genome-wide association study of nevirapine hypersensitivity in a sub-Saharan African HIV-infected population. <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 1152-1162	5.1	33
124	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017 , 542, 186-190	50.4	412
123	SCOPA and META-SCOPA: software for the analysis and aggregation of genome-wide association studies of multiple correlated phenotypes. <i>BMC Bioinformatics</i> , 2017 , 18, 25	3.6	12
122	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. <i>Nature Genetics</i> , 2017 , 49, 416-425	36.3	170
121	Improved imputation accuracy of rare and low-frequency variants using population-specific high-coverage WGS-based imputation reference panel. <i>European Journal of Human Genetics</i> , 2017 , 25, 869-876	5.3	82

120	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. <i>Nature Genetics</i> , 2017 , 49, 946-952	36.3	176
119	Copy number variations in "classical" obesity candidate genes are not frequently associated with severe early-onset obesity in children. <i>Journal of Pediatric Endocrinology and Metabolism</i> , 2017 , 30, 507-516	11.6	15
118	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017 , 8, 14977	17.4	105
117	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. <i>Nature Genetics</i> , 2017 , 49, 125-130	36.3	80
116	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. <i>Nature Communications</i> , 2017 , 8, 15805	17.4	50
115	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. <i>American Journal of Human Genetics</i> , 2017 , 100, 865-884	11	74
114	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017 , 66, 2888-2902	29.02	414
113	Discovery and fine-mapping of loci associated with MUFAs through trans-ethnic meta-analysis in Chinese and European populations. <i>Journal of Lipid Research</i> , 2017 , 58, 974-981	6.3	12
112	Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis. <i>American Journal of Human Genetics</i> , 2017 , 100, 51-63	11	30
111	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017 , 49, 1758-1766	36.6	310
110	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transeethnic genome-wide meta-analysis. <i>PLoS Medicine</i> , 2017 , 14, e1002383	11.6	223
109	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. <i>Hypertension</i> , 2017 ,	8.5	85
108	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 2017 , 8, 80	17.4	88
107	Variability of genome-wide DNA methylation and mRNA expression profiles in reproductive and endocrine disease related tissues. <i>Epigenetics</i> , 2017 , 12, 897-908	5.7	19
106	MARV: a tool for genome-wide multi-phenotype analysis of rare variants. <i>BMC Bioinformatics</i> , 2017 , 18, 110	3.6	12
105	Genetic and methylation variation in the CYP2B6 gene is related to circulating p,pRdde levels in a population-based sample. <i>Environment International</i> , 2017 , 98, 212-218	12.9	4
104	Personalized risk prediction for type 2 diabetes: the potential of genetic risk scores. <i>Genetics in Medicine</i> , 2017 , 19, 322-329	8.1	79
103	Genome-wide genetic analyses highlight mitogen-activated protein kinase (MAPK) signaling in the pathogenesis of endometriosis. <i>Human Reproduction</i> , 2017 , 32, 780-793	5.7	59

102	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017 , 4, 170179	8.2	22
101	Trans-ethnic meta-regression of genome-wide association studies accounting for ancestry increases power for discovery and improves fine-mapping resolution. <i>Human Molecular Genetics</i> , 2017 , 26, 3639-3650	5.6	67
100	Ranking and characterization of established BMI and lipid associated loci as candidates for gene-environment interactions. <i>PLoS Genetics</i> , 2017 , 13, e1006812	6	13
99	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. <i>Atherosclerosis</i> , 2017 , 266, 196-204	3.1	2
98	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016 , 7, 13357	17.4	46
97	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016 , 48, 1151-1161	36.3	181
96	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016 , 48, 1171-1184	36.3	251
95	Genome-Wide Association Study of the Modified Stumvoll Insulin Sensitivity Index Identifies BCL2 and FAM19A2 as Novel Insulin Sensitivity Loci. <i>Diabetes</i> , 2016 , 65, 3200-11	0.9	47
94	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. <i>Scientific Reports</i> , 2016 , 6, 35278	4.9	18
93	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. <i>Science Translational Medicine</i> , 2016 , 8, 341ra76	17.5	77
92	Trans-ethnic study design approaches for fine-mapping. <i>European Journal of Human Genetics</i> , 2016 , 24, 1330-6	5.3	48
91	Trans-ethnic Meta-analysis and Functional Annotation Illuminates the Genetic Architecture of Fasting Glucose and Insulin. <i>American Journal of Human Genetics</i> , 2016 , 99, 56-75	11	41
90	Genome-wide DNA methylation study identifies genes associated with the cardiovascular biomarker GDF-15. <i>Human Molecular Genetics</i> , 2016 , 25, 817-27	5.6	23
89	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016 , 7, 10495	17.4	180
88	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , 2016 , 7, 10494	17.4	107
87	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. <i>Human Molecular Genetics</i> , 2016 , 25, 2070-2081	5.6	20
86	Genetic Evidence for Causal Relationships Between Maternal Obesity-Related Traits and Birth Weight. <i>JAMA - Journal of the American Medical Association</i> , 2016 , 315, 1129-40	27.4	149
85	Investigating the Causal Relationship of C-Reactive Protein with 32 Complex Somatic and Psychiatric Outcomes: A Large-Scale Cross-Consortium Mendelian Randomization Study. <i>PLoS Medicine</i> , 2016 , 13, e1001976	11.6	100

84	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016 , 536, 41-47	50.4	704
83	Multi-ethnic genome-wide association study identifies novel locus for type 2 diabetes susceptibility. <i>European Journal of Human Genetics</i> , 2016 , 24, 1175-80	5.3	54
82	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. <i>American Journal of Human Genetics</i> , 2016 , 99, 636-646	11	44
81	Cystatin C and Cardiovascular Disease: A Mendelian Randomization Study. <i>Journal of the American College of Cardiology</i> , 2016 , 68, 934-45	15.1	65
80	Genome-wide associations for birth weight and correlations with adult disease. <i>Nature</i> , 2016 , 538, 248-254	52.4	266
79	Beyond Endometriosis Genome-Wide Association Study: From Genomics to Phenomics to the Patient. <i>Seminars in Reproductive Medicine</i> , 2016 , 34, 242-54	1.4	50
78	Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations. <i>Nature Genetics</i> , 2015 , 47, 979-986	36.3	1278
77	Identification and functional characterization of G6PC2 coding variants influencing glycemc traits define an effector transcript at the G6PC2-ABCB11 locus. <i>PLoS Genetics</i> , 2015 , 11, e1004876	6	76
76	The impact of low-frequency and rare variants on lipid levels. <i>Nature Genetics</i> , 2015 , 47, 589-97	36.3	229
75	Genome-wide association study of plasma levels of polychlorinated biphenyls disclose an association with the CYP2B6 gene in a population-based sample. <i>Environmental Research</i> , 2015 , 140, 95-101	7.9	10
74	Genome-wide enrichment analysis between endometriosis and obesity-related traits reveals novel susceptibility loci. <i>Human Molecular Genetics</i> , 2015 , 24, 1185-99	5.6	57
73	Novel insights into the genetics of smoking behaviour, lung function, and chronic obstructive pulmonary disease (UK BiLEVE): a genetic association study in UK Biobank. <i>Lancet Respiratory Medicine</i> , 2015 , 3, 769-81	35.1	245
72	Genome-wide association study of toxic metals and trace elements reveals novel associations. <i>Human Molecular Genetics</i> , 2015 , 24, 4739-45	5.6	75
71	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. <i>Human Molecular Genetics</i> , 2015 , 24, 5955-64	5.6	48
70	The UK10K project identifies rare variants in health and disease. <i>Nature</i> , 2015 , 526, 82-90	50.4	776
69	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , 2015 , 47, 1121-1130	36.3	1290
68	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015 , 47, 1415-25	36.3	292
67	Mutagenesis. Smoking is associated with mosaic loss of chromosome Y. <i>Science</i> , 2015 , 347, 81-3	33.3	108

66	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015 , 20, 647-656	15.1	167
65	A Bayesian Approach to the Overlap Analysis of Epidemiologically Linked Traits. <i>Genetic Epidemiology</i> , 2015 , 39, 624-34	2.6	3
64	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015 , 11, e1005378	6	220
63	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. <i>PLoS Genetics</i> , 2015 , 11, e1005230	6	59
62	Genetic burden associated with varying degrees of disease severity in endometriosis. <i>Molecular Human Reproduction</i> , 2015 , 21, 594-602	4.4	22
61	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. <i>Nature Communications</i> , 2015 , 6, 8658	17.4	79
60	Association between endometriosis and the interleukin 1A (IL1A) locus. <i>Human Reproduction</i> , 2015 , 30, 239-48	5.7	49
59	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015 , 518, 187-196	50.4	920
58	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015 , 518, 197-206	50.4	2687
57	GWAS-identified loci for coronary heart disease are associated with intima-media thickness and plaque presence at the carotid artery bulb. <i>Atherosclerosis</i> , 2015 , 239, 304-10	3.1	26
56	Evaluating the Performance of Fine-Mapping Strategies at Common Variant GWAS Loci. <i>PLoS Genetics</i> , 2015 , 11, e1005535	6	49
55	Mosaic loss of chromosome Y in peripheral blood is associated with shorter survival and higher risk of cancer. <i>Nature Genetics</i> , 2014 , 46, 624-8	36.3	213
54	Genome-wide association analysis identifies six new loci associated with forced vital capacity. <i>Nature Genetics</i> , 2014 , 46, 669-77	36.3	104
53	Genetic variants underlying risk of endometriosis: insights from meta-analysis of eight genome-wide association and replication datasets. <i>Human Reproduction Update</i> , 2014 , 20, 702-16	15.8	131
52	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014 , 46, 1173-86	36.3	1339
51	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014 , 46, 234-44	36.3	784
50	Trans-ethnic meta-analysis of white blood cell phenotypes. <i>Human Molecular Genetics</i> , 2014 , 23, 6944-605.6		45
49	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. <i>Nature Genetics</i> , 2014 , 46, 357-636.3	36.3	351

48	Genetic variation in the CYP1A1 gene is related to circulating PCB118 levels in a population-based sample. <i>Environmental Research</i> , 2014 , 133, 135-40	7.9	10
47	Large-scale genome-wide association studies and meta-analyses of longitudinal change in adult lung function. <i>PLoS ONE</i> , 2014 , 9, e100776	3.7	42
46	An integrated epigenomic analysis for type 2 diabetes susceptibility loci in monozygotic twins. <i>Nature Communications</i> , 2014 , 5, 5719	17.4	85
45	Gene-lifestyle interaction and type 2 diabetes: the EPIC interact case-cohort study. <i>PLoS Medicine</i> , 2014 , 11, e1001647	11.6	149
44	Genome wide association identifies common variants at the SERPINA6/SERPINA1 locus influencing plasma cortisol and corticosteroid binding globulin. <i>PLoS Genetics</i> , 2014 , 10, e1004474	6	71
43	Genetic analysis of dyslexia candidate genes in the European cross-linguistic NeuroDys cohort. <i>European Journal of Human Genetics</i> , 2014 , 22, 675-80	5.3	46
42	Pleiotropic genes for metabolic syndrome and inflammation. <i>Molecular Genetics and Metabolism</i> , 2014 , 112, 317-38	3.7	81
41	Genome-wide association study identifies a novel locus contributing to type 2 diabetes susceptibility in Sikhs of Punjabi origin from India. <i>Diabetes</i> , 2013 , 62, 1746-55	0.9	129
40	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013 , 45, 501-12	36.3	437
39	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012 , 44, 981-90	36.3	1482
38	Conditional and joint multiple-SNP analysis of GWAS summary statistics identifies additional variants influencing complex traits. <i>Nature Genetics</i> , 2012 , 44, 369-75, S1-3	36.3	813
37	Discovery and fine mapping of serum protein loci through transethnic meta-analysis. <i>American Journal of Human Genetics</i> , 2012 , 91, 744-53	11	58
36	A genome-wide association search for type 2 diabetes genes in African Americans. <i>PLoS ONE</i> , 2012 , 7, e29202	3.7	138
35	The metabochip, a custom genotyping array for genetic studies of metabolic, cardiovascular, and anthropometric traits. <i>PLoS Genetics</i> , 2012 , 8, e1002793	6	395
34	Stratifying type 2 diabetes cases by BMI identifies genetic risk variants in LAMA1 and enrichment for risk variants in lean compared to obese cases. <i>PLoS Genetics</i> , 2012 , 8, e1002741	6	162
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. <i>PLoS Genetics</i> , 2012 , 8, e1002607	6	326
32	Bayesian refinement of association signals for 14 loci in 3 common diseases. <i>Nature Genetics</i> , 2012 , 44, 1294-301	36.3	347
31	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , 2012 , 44, 991-1005	36.3	621

30	Meta-analysis of genome-wide association studies identifies eight new loci for type 2 diabetes in east Asians. <i>Nature Genetics</i> , 2011 , 44, 67-72	36.3	475
29	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2011 , 43, 984-9	36.3	406
28	Transethnic meta-analysis of genomewide association studies. <i>Genetic Epidemiology</i> , 2011 , 35, 809-22	2.6	218
27	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. <i>Nature Genetics</i> , 2010 , 42, 579-89	36.3	1449
26	Genome-wide association analyses identifies a susceptibility locus for tuberculosis on chromosome 18q11.2. <i>Nature Genetics</i> , 2010 , 42, 739-741	36.3	276
25	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010 , 42, 949-60	36.3	724
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22	GWAMA: software for genome-wide association meta-analysis. <i>BMC Bioinformatics</i> , 2010 , 11, 288	3.6	342
21	An evaluation of statistical approaches to rare variant analysis in genetic association studies. <i>Genetic Epidemiology</i> , 2010 , 34, 188-93	2.6	402
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19	Meta-analysis of sex-specific genome-wide association studies. <i>Genetic Epidemiology</i> , 2010 , 34, 846-53	2.6	69
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6	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , 3, 4	4.8	1
5	Obesity as a cause of kidney disease [Insights from Mendelian randomisation studies]		1
4	Trans-ethnic Mendelian randomization study reveals causal relationships between cardio-metabolic factors and chronic kidney disease		1
3	Identification of type 2 diabetes loci in 433,540 East Asian individuals		4
2	Tissue-Specific Alteration of Metabolic Pathways Influences Glycemic Regulation		4
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