Mark McCarthy

List of Publications by Citations

559 papers	125,249 citations	161 h-index	349 g-index
612 ext. papers	149,613 ext. citations	14.3 avg, IF	7.45 L-index

#	Paper	IF	Citations
559	Analysis of protein-coding genetic variation in 60,706 humans. *Nature*, **2016**, 536, 285-91	50.4	6940
558	Finding the missing heritability of complex diseases. *Nature*, **2009**, 461, 747-53	50.4	6084
557	The Genotype-Tissue Expression (GTEx) project. *Nature Genetics*, **2013**, 45, 580-5	36.3	4179
556	A common variant in the FTO gene is associated with body mass index and predisposes to childhood and adult obesity. *Science*, **2007**, 316, 889-94	33.3	3294
555	Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans. *Science*, **2015**, 348, 648-60	33.3	3242
554	Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*, **2010**, 466, 707-13	50.4	2742
553	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
552	Age-related clonal hematopoiesis associated with adverse outcomes. *New England Journal of Medicine*, **2014**, 371, 2488-98	59.2	2314
551	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics*, **2010**, 42, 937-48	36.3	2267
550	Genome-wide association studies for complex traits: consensus, uncertainty and challenges. *Nature Reviews Genetics*, **2008**, 9, 356-69	30.1	2126
549	Discovery and refinement of loci associated with lipid levels. *Nature Genetics*, **2013**, 45, 1274-1283	36.3	1904
548	Replication of genome-wide association signals in UK samples reveals risk loci for type 2 diabetes. *Science*, **2007**, 316, 1336-41	33.3	1823
547	10 Years of GWAS Discovery: Biology, Function, and Translation. *American Journal of Human Genetics*, **2017**, 101, 5-22	11	1651
546	Five years of GWAS discovery. *American Journal of Human Genetics*, **2012**, 90, 7-24	11	1635
545	Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature*, **2010**, 467, 832-8	50.4	1514
544	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. *Nature Genetics*, **2008**, 40, 638-45	36.3	1496
543	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

542	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. *Nature Genetics*, **2010**, 42, 579-89	36.3	1449
541	A reference panel of 64,976 haplotypes for genotype imputation. *Nature Genetics*, **2016**, 48, 1279-83	36.3	1447
540	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. *Nature Genetics*, **2009**, 41, 25-34	36.3	1368
539	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
538	Transcriptome and genome sequencing uncovers functional variation in humans. *Nature*, **2013**, 501, 506-11	50.4	1323
537	Common genetic determinants of vitamin D insufficiency: a genome-wide association study. *Lancet, The*, **2010**, 376, 180-8	40	1183
536	Large-scale association analysis identifies new risk loci for coronary artery disease. *Nature Genetics*, **2013**, 45, 25-33	36.3	1172
535	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. *Nature Genetics*, **2013**, 45, 1150-9	36.3	1153
534	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. *Nature Genetics*, **2007**, 39, 1329-37	36.3	1130
533	Common variants near MC4R are associated with fat mass, weight and risk of obesity. *Nature Genetics*, **2008**, 40, 768-75	36.3	1048
532	Genome-wide association study identifies eight loci associated with blood pressure. *Nature Genetics*, **2009**, 41, 666-76	36.3	970
531	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
530	Metabolic profiling reveals a contribution of gut microbiota to fatty liver phenotype in insulin-resistant mice. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 12511-6	11.5	854
529	A large-scale genome-wide association study of Asian populations uncovers genetic factors influencing eight quantitative traits. *Nature Genetics*, **2009**, 41, 527-34	36.3	822
528	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
527	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
526	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
525	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. *Nature Genetics*, **2009**, 41, 47-55	36.3	708

524	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
523	Genomics, type 2 diabetes, and obesity. *New England Journal of Medicine*, **2010**, 363, 2339-50	59.2	696
522	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
521	Genome-wide association analysis identifies 20 loci that influence adult height. *Nature Genetics*, **2008**, 40, 575-83	36.3	654
520	Interaction between ERAP1 and HLA-B27 in ankylosing spondylitis implicates peptide handling in the mechanism for HLA-B27 in disease susceptibility. *Nature Genetics*, **2011**, 43, 761-7	36.3	646
519	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. *Nature*, **2010**, 464, 713-20	50.4	639
518	Identification of seven loci affecting mean telomere length and their association with disease. *Nature Genetics*, **2013**, 45, 422-7, 427e1-2	36.3	624
517	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
516	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. *Nature Genetics*, **2012**, 44, 659-69	36.3	615
515	Large-scale association studies of variants in genes encoding the pancreatic beta-cell KATP channel subunits Kir6.2 (KCNJ11) and SUR1 (ABCC8) confirm that the KCNJ11 E23K variant is associated with type 2 diabetes. *Diabetes*, **2003**, 52, 568-72	0.9	614
514	Common variants associated with plasma triglycerides and risk for coronary artery disease. *Nature Genetics*, **2013**, 45, 1345-52	36.3	597
513	Causal relationship between obesity and vitamin D status: bi-directional Mendelian randomization analysis of multiple cohorts. *PLoS Medicine*, **2013**, 10, e1001383	11.6	592
512	Genome-wide association analysis of metabolic traits in a birth cohort from a founder population. *Nature Genetics*, **2009**, 41, 35-46	36.3	588
511	Variants in MTNR1B influence fasting glucose levels. *Nature Genetics*, **2009**, 41, 77-81	36.3	584
510	Sequence variants at CHRNB3-CHRNA6 and CYP2A6 affect smoking behavior. *Nature Genetics*, **2010**, 42, 448-53	36.3	582
509	Mapping cis- and trans-regulatory effects across multiple tissues in twins. *Nature Genetics*, **2012**, 44, 1084-9	36.3	572
508	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. *Nature Genetics*, **2010**, 42, 142-8	36.3	527
507	Genome-wide association study for early-onset and morbid adult obesity identifies three new risk loci in European populations. *Nature Genetics*, **2009**, 41, 157-9	36.3	521

506	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. *Nature*, **2017**, 541, 81-86	50.4	511
505	Epigenome-wide scans identify differentially methylated regions for age and age-related phenotypes in a healthy ageing population. *PLoS Genetics*, **2012**, 8, e1002629	6	501
504	Meta-analysis of 28,141 individuals identifies common variants within five new loci that influence uric acid concentrations. *PLoS Genetics*, **2009**, 5, e1000504	6	495
503	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
502	Genetic Loci associated with C-reactive protein levels and risk of coronary heart disease. *JAMA - Journal of the American Medical Association*, **2009**, 302, 37-48	27.4	459
501	Assessment of cumulative evidence on genetic associations: interim guidelines. *International Journal of Epidemiology*, **2008**, 37, 120-32	7.8	451
500	Genome-wide association study identifies multiple loci influencing human serum metabolite levels. *Nature Genetics*, **2012**, 44, 269-76	36.3	441
499	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
498	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. *Nature Genetics*, **2011**, 43, 1131-8	36.3	415
497	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. *Diabetes*, **2017**, 66, 2888-2902	39	414
496	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
495	Genome-wide association study of ulcerative colitis identifies three new susceptibility loci, including the HNF4A region. *Nature Genetics*, **2009**, 41, 1330-4	36.3	411
494	What makes a good genetic association study?. *Lancet, The*, **2005**, 366, 1315-23	40	408
493	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
492	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. *Nature*, **2014**, 514, 92-97	50.4	401
491	The metabochip, a custom genotyping array for genetic studies of metabolic, cardiovascular, and anthropometric traits. *PLoS Genetics*, **2012**, 8, e1002793	6	395
490	Genome-wide association scan meta-analysis identifies three Loci influencing adiposity and fat distribution. *PLoS Genetics*, **2009**, 5, e1000508	6	393
489	Causal relationships among the gut microbiome, short-chain fatty acids and metabolic diseases. *Nature Genetics*, **2019**, 51, 600-605	36.3	378

488	Pancreatic islet enhancer clusters enriched in type 2 diabetes risk-associated variants. *Nature Genetics*, **2014**, 46, 136-143	36.3	366
487	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. *Nature Genetics*, **2014**, 46, 357-63	36.3	351
486	Bayesian refinement of association signals for 14 loci in 3 common diseases. *Nature Genetics*, **2012**, 44, 1294-301	36.3	347
485	Human β cell transcriptome analysis uncovers lncRNAs that are tissue-specific, dynamically regulated, and abnormally expressed in type 2 diabetes. *Cell Metabolism*, **2012**, 16, 435-48	24.6	345
484	The architecture of gene regulatory variation across multiple human tissues: the MuTHER study. *PLoS Genetics*, **2011**, 7, e1002003	6	336
483	Genomic inflation factors under polygenic inheritance. *European Journal of Human Genetics*, **2011**, 19, 807-12	5.3	335
482	A genome-wide association study identifies protein quantitative trait loci (pQTLs). *PLoS Genetics*, **2008**, 4, e1000072	6	331
481	A common variant of HMGA2 is associated with adult and childhood height in the general population. *Nature Genetics*, **2007**, 39, 1245-50	36.3	330
480	Coding Variation in ANGPTL4, LPL, and SVEP1 and the Risk of Coronary Disease. *New England Journal of Medicine*, **2016**, 374, 1134-44	59.2	325
479	Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. *Nature*, **2011**, 478, 97-102	50.4	322
478	Concept, design and implementation of a cardiovascular gene-centric 50 k SNP array for large-scale genomic association studies. *PLoS ONE*, **2008**, 3, e3583	3.7	321
477	Common variants near ATM are associated with glycemic response to metformin in type 2 diabetes. *Nature Genetics*, **2011**, 43, 117-20	36.3	319
476	Common variants at 10 genomic loci influence hemoglobin A(C) levels via glycemic and nonglycemic pathways. *Diabetes*, **2010**, 59, 3229-39	0.9	314
475	The human pancreatic islet transcriptome: expression of candidate genes for type 1 diabetes and the impact of pro-inflammatory cytokines. *PLoS Genetics*, **2012**, 8, e1002552	6	313
474	Integrative genomic analysis implicates limited peripheral adipose storage capacity in the pathogenesis of human insulin resistance. *Nature Genetics*, **2017**, 49, 17-26	36.3	312
473	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
472	FTO genotype is associated with phenotypic variability of body mass index. *Nature*, **2012**, 490, 267-72	50.4	304
471	Common variants in WFS1 confer risk of type 2 diabetes. *Nature Genetics*, **2007**, 39, 951-3	36.3	296

470	Improved detection of common variants associated with schizophrenia by leveraging pleiotropy with cardiovascular-disease risk factors. *American Journal of Human Genetics*, **2013**, 92, 197-209	11	293
469	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. *Nature Genetics*, **2015**, 47, 1415-25	36.3	292
468	A genome-wide association meta-analysis identifies new childhood obesity loci. *Nature Genetics*, **2012**, 44, 526-31	36.3	292
467	Mapping of a gene for type 2 diabetes associated with an insulin secretion defect by a genome scan in Finnish families. *Nature Genetics*, **1996**, 14, 90-4	36.3	290
466	Genome-wide association identifies nine common variants associated with fasting proinsulin levels and provides new insights into the pathophysiology of type 2 diabetes. *Diabetes*, **2011**, 60, 2624-34	0.9	285
465	Rare MTNR1B variants impairing melatonin receptor 1B function contribute to type 2 diabetes. *Nature Genetics*, **2012**, 44, 297-301	36.3	279
464	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
463	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. *PLoS Genetics*, **2013**, 9, e1003500	6	277
462	A genomewide scan for loci predisposing to type 2 diabetes in a U.K. population (the Diabetes UK Warren 2 Repository): analysis of 573 pedigrees provides independent replication of a susceptibility locus on chromosome 1q. *American Journal of Human Genetics*, **2001**, 69, 553-69	11	271
461	Global analysis of DNA methylation variation in adipose tissue from twins reveals links to disease-associated variants in distal regulatory elements. *American Journal of Human Genetics*, **2013**, 93, 876-90	11	269
460	Genome-wide associations for birth weight and correlations with adult disease. *Nature*, **2016**, 538, 248-252	52.4	266
459	Genome-wide association studies: potential next steps on a genetic journey. *Human Molecular Genetics*, **2008**, 17, R156-65	5.6	263
458	Common variation in the FTO gene alters diabetes-related metabolic traits to the extent expected given its effect on BMI. *Diabetes*, **2008**, 57, 1419-26	0.9	260
457	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. *Nature Genetics*, **2017**, 49, 834-841	36.3	257
456	Research capacity. Enabling the genomic revolution in Africa. *Science*, **2014**, 344, 1346-8	33.3	256
455	Linkage and association of insulin gene VNTR regulatory polymorphism with polycystic ovary syndrome. *Lancet, The*, **1997**, 349, 986-90	40	254
454	Identification of an imprinted master trans regulator at the KLF14 locus related to multiple metabolic phenotypes. *Nature Genetics*, **2011**, 43, 561-4	36.3	253
453	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

452	Variation in TCF7L2 influences therapeutic response to sulfonylureas: a GoDARTs study. *Diabetes*, **2007**, 56, 2178-82	0.9	251
451	Association of vitamin D status with arterial blood pressure and hypertension risk: a mendelian randomisation study. *Lancet Diabetes and Endocrinology,the*, **2014**, 2, 719-29	18.1	250
450	Two new Loci for body-weight regulation identified in a joint analysis of genome-wide association studies for early-onset extreme obesity in French and german study groups. *PLoS Genetics*, **2010**, 6, e1000916	6	250
449	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
448	Assessing the combined impact of 18 common genetic variants of modest effect sizes on type 2 diabetes risk. *Diabetes*, **2008**, 57, 3129-35	0.9	245
447	Distribution and medical impact of loss-of-function variants in the Finnish founder population. *PLoS Genetics*, **2014**, 10, e1004494	6	243
446	Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. *Nature Genetics*, **2018**, 50, 956-967	36.3	239
445	Regulation of Fto/Ftm gene expression in mice and humans. *American Journal of Physiology - Regulatory Integrative and Comparative Physiology*, **2008**, 294, R1185-96	3.2	238
444	Impact of type 2 diabetes susceptibility variants on quantitative glycemic traits reveals mechanistic heterogeneity. *Diabetes*, **2014**, 63, 2158-71	0.9	235
443	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. *Nature Genetics*, **2013**, 45, 76-82	36.3	232
442	The impact of low-frequency and rare variants on lipid levels. *Nature Genetics*, **2015**, 47, 589-97	36.3	229
441	Association Between Low-Density Lipoprotein Cholesterol-Lowering Genetic Variants and Risk of Type 2 Diabetes: A Meta-analysis. *JAMA - Journal of the American Medical Association*, **2016**, 316, 1383-1391	27.4	225
440	Detection of human adaptation during the past 2000 years. *Science*, **2016**, 354, 760-764	33.3	224
439	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. *Nature Genetics*, **2015**, 47, 1282-1293	36.3	223
438	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
437	Association analysis of 6,736 U.K. subjects provides replication and confirms TCF7L2 as a type 2 diabetes susceptibility gene with a substantial effect on individual risk. *Diabetes*, **2006**, 55, 2640-4	0.9	222
436	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
435	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

434	Genome-wide association and genetic functional studies identify autism susceptibility candidate 2 gene (AUTS2) in the regulation of alcohol consumption. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 7119-24	11.5	218
433	Genome-wide association of polycystic ovary syndrome implicates alterations in gonadotropin secretion in European ancestry populations. *Nature Communications*, **2015**, 6, 7502	17.4	214
432	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
431	Combining information from common type 2 diabetes risk polymorphisms improves disease prediction. *PLoS Medicine*, **2006**, 3, e374	11.6	214
430	Genetic Predisposition to an Impaired Metabolism of the Branched-Chain Amino Acids and Risk of Type 2 Diabetes: A Mendelian Randomisation Analysis. *PLoS Medicine*, **2016**, 13, e1002179	11.6	214
429	Detailed physiologic characterization reveals diverse mechanisms for novel genetic Loci regulating glucose and insulin metabolism in humans. *Diabetes*, **2010**, 59, 1266-75	0.9	211
428	Genetic loci influencing kidney function and chronic kidney disease. *Nature Genetics*, **2010**, 42, 373-5	36.3	205
427	Type 2 diabetes: new genes, new understanding. *Trends in Genetics*, **2008**, 24, 613-21	8.5	204
426	Common variants of the novel type 2 diabetes genes CDKAL1 and HHEX/IDE are associated with decreased pancreatic beta-cell function. *Diabetes*, **2007**, 56, 3101-4	0.9	203
425	Early life factors and blood pressure at age 31 years in the 1966 northern Finland birth cohort. *Hypertension*, **2004**, 44, 838-46	8.5	203
424	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. *Human Molecular Genetics*, **2016**, 25, 389-403	5.6	202
423	A bivariate genome-wide approach to metabolic syndrome: STAMPEED consortium. *Diabetes*, **2011**, 60, 1329-39	0.9	194
422	Integrated genetic and epigenetic analysis identifies haplotype-specific methylation in the FTO type 2 diabetes and obesity susceptibility locus. *PLoS ONE*, **2010**, 5, e14040	3.7	193
421	Mosaic PPM1D mutations are associated with predisposition to breast and ovarian cancer. *Nature*, **2013**, 493, 406-10	50.4	191
420	A coherent approach for analysis of the Illumina HumanMethylation450 BeadChip improves data quality and performance in epigenome-wide association studies. *Genome Biology*, **2015**, 16, 37	18.3	186
419	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
418	Gene expression changes with age in skin, adipose tissue, blood and brain. *Genome Biology*, **2013**, 14, R75	18.3	185
417	Variants in ADCY5 and near CCNL1 are associated with fetal growth and birth weight. *Nature Genetics*, **2010**, 42, 430-5	36.3	184

416	Development of polycystic ovary syndrome: involvement of genetic and environmental factors. *Journal of Developmental and Physical Disabilities*, **2006**, 29, 278-85; discussion 286-90		184
415	Evidence that a locus for familial psoriasis maps to chromosome 4q. *Nature Genetics*, **1996**, 14, 231-3	36.3	182
414	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
413	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
412	A brief history of human disease genetics. *Nature*, **2020**, 577, 179-189	50.4	181
411	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180
410	Remapping the insulin gene/IDDM2 locus in type 1 diabetes. *Diabetes*, **2004**, 53, 1884-9	0.9	180
409	Genome-wide association study identifies variants in TMPRSS6 associated with hemoglobin levels. *Nature Genetics*, **2009**, 41, 1170-2	36.3	179
408	Dissection of the genetics of Parkinson's disease identifies an additional association 5' of SNCA and multiple associated haplotypes at 17q21. *Human Molecular Genetics*, **2011**, 20, 345-53	5.6	178
407	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. *Nature Communications*, **2018**, 9, 260	17.4	174
406	RNA sequencing identifies dysregulation of the human pancreatic islet transcriptome by the saturated fatty acid palmitate. *Diabetes*, **2014**, 63, 1978-93	0.9	174
405	Reduced insulin exocytosis in human pancreatic β-cells with gene variants linked to type 2 diabetes. *Diabetes*, **2012**, 61, 1726-33	0.9	174
404	Genome-wide association studies in type 2 diabetes. *Current Diabetes Reports*, **2009**, 9, 164-71	5.6	174
403	Human genomics. Effect of predicted protein-truncating genetic variants on the human transcriptome. *Science*, **2015**, 348, 666-9	33.3	170
402	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. *American Journal of Human Genetics*, **2014**, 94, 233-45	11	170
401	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. *PLoS Genetics*, **2018**, 14, e1007813	6	166
400	The genetic and epigenetic basis of type 2 diabetes and obesity. *Clinical Pharmacology and Therapeutics*, **2012**, 92, 707-15	6.1	162
399	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

398	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. *Nature Communications*, **2014**, 5, 5068	17.4	160
397	Evaluation of common variants in the six known maturity-onset diabetes of the young (MODY) genes for association with type 2 diabetes. *Diabetes*, **2007**, 56, 685-93	0.9	160
396	Meta-analysis and a large association study confirm a role for calpain-10 variation in type 2 diabetes susceptibility. *American Journal of Human Genetics*, **2003**, 73, 1208-12	11	155
395	Studies of association between the gene for calpain-10 and type 2 diabetes mellitus in the United Kingdom. *American Journal of Human Genetics*, **2001**, 69, 544-52	11	154
394	Genetic evidence that raised sex hormone binding globulin (SHBG) levels reduce the risk of type 2 diabetes. *Human Molecular Genetics*, **2010**, 19, 535-44	5.6	150
393	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
392	Gene-lifestyle interaction and type 2 diabetes: the EPIC interact case-cohort study. *PLoS Medicine*, **2014**, 11, e1001647	11.6	149
391	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. *Journal of the American College of Cardiology*, **2017**, 69, 823-836	15.1	146
390	The miRNA profile of human pancreatic islets and beta-cells and relationship to type 2 diabetes pathogenesis. *PLoS ONE*, **2013**, 8, e55272	3.7	146
389	Diabetes and Cause-Specific Mortality in Mexico City. *New England Journal of Medicine*, **2016**, 375, 1961-1971	59.1	144
388	The role of adiposity in cardiometabolic traits: a Mendelian randomization analysis. *PLoS Medicine*, **2013**, 10, e1001474	11.6	144
387	Association between common variation at the FTO locus and changes in body mass index from infancy to late childhood: the complex nature of genetic association through growth and development. *PLoS Genetics*, **2011**, 7, e1001307	6	141
386	Exploring the developmental overnutrition hypothesis using parental-offspring associations and FTO as an instrumental variable. *PLoS Medicine*, **2008**, 5, e33	11.6	139
385	Genome-wide association and longitudinal analyses reveal genetic loci linking pubertal height growth, pubertal timing and childhood adiposity. *Human Molecular Genetics*, **2013**, 22, 2735-47	5.6	138
384	Transcript Expression Data from Human Islets Links Regulatory Signals from Genome-Wide Association Studies for Type 2 Diabetes and Glycemic Traits to Their Downstream Effectors. *PLoS Genetics*, **2015**, 11, e1005694	6	138
383	A genome-wide association search for type 2 diabetes genes in African Americans. *PLoS ONE*, **2012**, 7, e29202	3.7	138
382	Exposing the exposures responsible for type 2 diabetes and obesity. *Science*, **2016**, 354, 69-73	33.3	138
381	Genome-wide association study for type 2 diabetes in Indians identifies a new susceptibility locus at 2q21. *Diabetes*, **2013**, 62, 977-86	0.9	132

380	Reduced-function SLC22A1 polymorphisms encoding organic cation transporter 1 and glycemic response to metformin: a GoDARTS study. *Diabetes*, **2009**, 58, 1434-9	0.9	132
379	eVOC: a controlled vocabulary for unifying gene expression data. *Genome Research*, **2003**, 13, 1222-30	9.7	132
378	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. *Nature*, **2019**, 570, 71-76	50.4	129
377	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
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9	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts **2020**, 17, e1003149		
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6	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts **2020**, 17, e1003149		
5	Homogeneity in the association of body mass index with type 2 diabetes across the UK Biobank: A Mendelian randomization study **2019**, 16, e1002982		
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1 Homogeneity in the association of body mass index with type 2 diabetes across the UK Biobank: A Mendelian randomization study **2019**, 16, e1002982