Mark McCarthy

List of Publications by Year in Descending Order

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	Four groups of type 2 diabetes contribute to the etiological and clinical heterogeneity in newly diagnosed individuals: An IMI DIRECT study.. *Cell Reports Medicine*, **2022**, 3, 100477	18	1
558	Polygenic Prediction of Type 2 Diabetes in Africa.. *Diabetes Care*, **2022**,	14.6	2
557	An effector index to predict target genes at GWAS loci.. *Human Genetics*, **2022**, 1	6.3	0
556	Integration of questionnaire-based risk factors improves polygenic risk scores for human coronary heart disease and type 2 diabetes.. *Communications Biology*, **2022**, 5, 158	6.7	0
555	Identification of genetic effects underlying type 2 diabetes in South Asian and European populations.. *Communications Biology*, **2022**, 5, 329	6.7	2
554	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. *Nature Genetics*, **2022**,	36.3	7
553	Genome-wide association analyses highlight etiological differences underlying newly defined subtypes of diabetes. *Nature Genetics*, **2021**, 53, 1534-1542	36.3	7
552	Responsible use of polygenic risk scores in the clinic: potential benefits, risks and gaps. *Nature Medicine*, **2021**, 27, 1876-1884	50.5	25
551	Association of Genetic Variant at Chromosome 12q23.1 With Neuropathic Pain Susceptibility. *JAMA Network Open*, **2021**, 4, e2136560	10.4	0
550	Processes Underlying Glycemic Deterioration in Type 2 Diabetes: An IMI DIRECT Study. *Diabetes Care*, **2021**, 44, 511-518	14.6	6
549	Genome-Wide Association Study of Peripheral Artery Disease. *Circulation Genomic and Precision Medicine*, **2021**, 14, e002862	5.2	3
548	Improving reporting standards for polygenic scores in risk prediction studies. *Nature*, **2021**, 591, 211-219	50.4	70
547	Analysis of overlapping genetic association in type 1 and type 2 diabetes. *Diabetologia*, **2021**, 64, 1342-1347	10.3	5
546	The trans-ancestral genomic architecture of glycemic traits. *Nature Genetics*, **2021**, 53, 840-860	36.3	44
545	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. *Nature Communications*, **2021**, 12, 3505	17.4	5
544	HIV infection and anaemia do not affect HbA for the detection of diabetes in black South Africans: Evidence from the Durban Diabetes Study. *Diabetic Medicine*, **2021**, 38, e14605	3.5	2
543	Genetic variation associated with thyroid autoimmunity shapes the systemic immune response to PD-1 checkpoint blockade. *Nature Communications*, **2021**, 12, 3355	17.4	5

542	Effects of apolipoprotein B on lifespan and risks of major diseases including type 2 diabetes: a mendelian randomisation analysis using outcomes in first-degree relatives. *The Lancet Healthy Longevity*, **2021**, 2, e317-e326	9.5	7
541	Profiles of Glucose Metabolism in Different Prediabetes Phenotypes, Classified by Fasting Glycemia, 2-Hour OGTT, Glycated Hemoglobin, and 1-Hour OGTT: An IMI DIRECT Study. *Diabetes*, **2021**, 70, 2092-2106	0.9	4
540	Genome-wide association study identifies 48 common genetic variants associated with handedness. *Nature Human Behaviour*, **2021**, 5, 59-70	12.8	33
539	Sex Differences in the Risk of Coronary Heart Disease Associated With Type 2 Diabetes: A Mendelian Randomization Analysis. *Diabetes Care*, **2021**, 44, 556-562	14.6	4
538	Genome-Wide Association Analysis of Pancreatic Beta-Cell Glucose Sensitivity. *Journal of Clinical Endocrinology and Metabolism*, **2021**, 106, 80-90	5.6	2
537	Genetics meets proteomics: perspectives for large population-based studies. *Nature Reviews Genetics*, **2021**, 22, 19-37	30.1	62
536	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. *Nature Communications*, **2021**, 12, 24	17.4	30
535	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. *Genome Biology*, **2021**, 22, 49	18.3	38
534	Identification of 371 genetic variants for age at first sex and birth linked to externalising behaviour. *Nature Human Behaviour*, **2021**,	12.8	5
533	Identification of rare loss of function genetic variation regulating body fat distribution. *Journal of Clinical Endocrinology and Metabolism*, **2021**,	5.6	1
532	A Multi-omic Integrative Scheme Characterizes Tissues of Action at Loci Associated with Type 2 Diabetes. *American Journal of Human Genetics*, **2020**, 107, 1011-1028	11	6
531	Unsupervised Clustering of Missense Variants in HNF1A Using Multidimensional Functional Data Aids Clinical Interpretation. *American Journal of Human Genetics*, **2020**, 107, 670-682	11	9
530	Identification of type 2 diabetes loci in 433,540 East Asian individuals. *Nature*, **2020**, 582, 240-245	50.4	89
529	Multifaceted genome-wide study identifies novel regulatory loci in SLC22A11 and ZNF45 for body mass index in Indians. *Molecular Genetics and Genomics*, **2020**, 295, 1013-1026	3.1	1
528	Mendelian randomization analysis does not support causal associations of birth weight with hypertension risk and blood pressure in adulthood. *European Journal of Epidemiology*, **2020**, 35, 685-697	12.1	2
527	Altered cortisol metabolism in individuals with HNF1A-MODY. *Clinical Endocrinology*, **2020**, 93, 269-279	3.4	3
526	RSPO3 impacts body fat distribution and regulates adipose cell biology in vitro. *Nature Communications*, **2020**, 11, 2797	17.4	15
525	Precision medicine in diabetes: a Consensus Report from the American Diabetes Association (ADA) and the European Association for the Study of Diabetes (EASD). *Diabetologia*, **2020**, 63, 1671-1693	10.3	33

524	Precision Medicine in Diabetes: A Consensus Report From the American Diabetes Association (ADA) and the European Association for the Study of Diabetes (EASD). *Diabetes Care*, **2020**, 43, 1617-1635	14.6	75
523	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts. *PLoS Medicine*, **2020**, 17, e1003149	11.6	18
522	The role of physical activity in metabolic homeostasis before and after the onset of type 2 diabetes: an IMI DIRECT study. *Diabetologia*, **2020**, 63, 744-756	10.3	4
521	Using human genetics to understand the disease impacts of testosterone in men and women. *Nature Medicine*, **2020**, 26, 252-258	50.5	121
520	A Multi-tissue Transcriptome Analysis of Human Metabolites Guides Interpretability of Associations Based on Multi-SNP Models for Gene Expression. *American Journal of Human Genetics*, **2020**, 106, 188-201	11	12
519	Common maternal and fetal genetic variants show expected polygenic effects on risk of small- or large-for-gestational-age (SGA or LGA), except in the smallest 3% of babies. *PLoS Genetics*, **2020**, 16, e1009191	6	5
518	Post-load glucose subgroups and associated metabolic traits in individuals with type 2 diabetes: An IMI-DIRECT study. *PLoS ONE*, **2020**, 15, e0242360	3.7	2
517	Deep learning models predict regulatory variants in pancreatic islets and refine type 2 diabetes association signals. *ELife*, **2020**, 9,	8.9	13
516	Genetic variant effects on gene expression in human pancreatic islets and their implications for T2D. *Nature Communications*, **2020**, 11, 4912	17.4	30
515	Cohort Profile: East London Genes & Health (ELGH), a community-based population genomics and health study in British Bangladeshi and British Pakistani people. *International Journal of Epidemiology*, **2020**, 49, 20-21i	7.8	19
514	A brief history of human disease genetics. *Nature*, **2020**, 577, 179-189	50.4	181
513	Analysis of Differentiation Protocols Defines a Common Pancreatic Progenitor Molecular Signature and Guides Refinement of Endocrine Differentiation. *Stem Cell Reports*, **2020**, 14, 138-153	8	13
512	Glutamine Links Obesity to Inflammation in Human White Adipose Tissue. *Cell Metabolism*, **2020**, 31, 375-390.e11	24.6	56
511	Novel loci for childhood body mass index and shared heritability with adult cardiometabolic traits. *PLoS Genetics*, **2020**, 16, e1008718	6	25
510	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
509	Whole blood co-expression modules associate with metabolic traits and type 2 diabetes: an IMI-DIRECT study. *Genome Medicine*, **2020**, 12, 109	14.4	3
508	Genome-wide association analysis of type 2 diabetes in the EPIC-InterAct study. *Scientific Data*, **2020**, 7, 393	8.2	7
507	Dietary metabolite profiling brings new insight into the relationship between nutrition and metabolic risk: An IMI DIRECT study. *EBioMedicine*, **2020**, 58, 102932	8.8	2

506	Large-Scale Analyses Provide No Evidence for Gene-Gene Interactions Influencing Type 2 Diabetes Risk. *Diabetes*, **2020**, 69, 2518-2522	0.9	2
505	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. *Circulation Genomic and Precision Medicine*, **2020**, 13, e002769	5.2	1
504	Endocrine-Exocrine Signaling Drives Obesity-Associated Pancreatic Ductal Adenocarcinoma. *Cell*, **2020**, 181, 832-847.e18	56.2	34
503	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts **2020**, 17, e1003149		
502	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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499	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts **2020**, 17, e1003149		
498	GWAS on longitudinal growth traits reveals different genetic factors influencing infant, child, and adult BMI. *Science Advances*, **2019**, 5, eaaw3095	14.3	39
497	Integrative analysis of prognostic biomarkers derived from multiomics panels helps discrimination of chronic kidney disease trajectories in people with type 2 diabetes. *Kidney International*, **2019**, 96, 1381-1388	9.9	15
496	Variants in the fetal genome near pro-inflammatory cytokine genes on 2q13 associate with gestational duration. *Nature Communications*, **2019**, 10, 3927	17.4	21
495	Genetic Risk Scores for Diabetes Diagnosis and Precision Medicine. *Endocrine Reviews*, **2019**, 40, 1500-1520	27.2	94
494	Discovery of biomarkers for glycaemic deterioration before and after the onset of type 2 diabetes: descriptive characteristics of the epidemiological studies within the IMI DIRECT Consortium. *Diabetologia*, **2019**, 62, 1601-1615	10.3	14
493	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. *American Journal of Human Genetics*, **2019**, 105, 15-28	11	12
492	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. *Nature*, **2019**, 570, 71-76	50.4	129
491	Genome-wide association study of type 2 diabetes in Africa. *Diabetologia*, **2019**, 62, 1204-1211	10.3	36
490	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
489	The Early Growth Genetics (EGG) and EArly Genetics and Lifecourse Epidemiology (EAGLE) consortia: design, results and future prospects. *European Journal of Epidemiology*, **2019**, 34, 279-300	12.1	18

488	Variation in the Plasma Membrane Monoamine Transporter (PMAT) (Encoded by) and Organic Cation Transporter 1 (OCT1) (Encoded by) and Gastrointestinal Intolerance to Metformin in Type 2 Diabetes: An IMI DIRECT Study. *Diabetes Care*, **2019**, 42, 1027-1033	14.6	20
487	The Genetic Basis of Metabolic Disease. *Cell*, **2019**, 177, 146-161	56.2	51
486	Dissecting features of epigenetic variants underlying cardiometabolic risk using full-resolution epigenome profiling in regulatory elements. *Nature Communications*, **2019**, 10, 1209	17.4	9
485	Developing a network view of type 2 diabetes risk pathways through integration of genetic, genomic and functional data. *Genome Medicine*, **2019**, 11, 19	14.4	18
484	Genetic Predisposition to Type 2 Diabetes and Risk of Subclinical Atherosclerosis and Cardiovascular Diseases Among 160,000 Chinese Adults. *Diabetes*, **2019**, 68, 2155-2164	0.9	20
483	Fostering improved human islet research: a European perspective. *Diabetologia*, **2019**, 62, 1514-1516	10.3	9
482	A trans-ancestral meta-analysis of genome-wide association studies reveals loci associated with childhood obesity. *Human Molecular Genetics*, **2019**, 28, 3327-3338	5.6	30
481	Genome-Wide Association Study of Diabetic Kidney Disease Highlights Biology Involved in Glomerular Basement Membrane Collagen. *Journal of the American Society of Nephrology: JASN*, **2019**, 30, 2000-2016	12.7	66
480	Associations of autozygosity with a broad range of human phenotypes. *Nature Communications*, **2019**, 10, 4957	17.4	40
479	Loss of ZnT8 function protects against diabetes by enhanced insulin secretion. *Nature Genetics*, **2019**, 51, 1596-1606	36.3	45
478	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
477	Causal relationships among the gut microbiome, short-chain fatty acids and metabolic diseases. *Nature Genetics*, **2019**, 51, 600-605	36.3	378
476	Homogeneity in the association of body mass index with type 2 diabetes across the UK Biobank: A Mendelian randomization study. *PLoS Medicine*, **2019**, 16, e1002982	11.6	15
475	A novel rare CUBN variant and three additional genes identified in Europeans with and without diabetes: results from an exome-wide association study of albuminuria. *Diabetologia*, **2019**, 62, 292-305	10.3	17
474	Plasma Fucosylated Glycans and C-Reactive Protein as Biomarkers of HNF1A-MODY in Young Adult-Onset Nonautoimmune Diabetes. *Diabetes Care*, **2019**, 42, 17-26	14.6	23
473	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
472	Homogeneity in the association of body mass index with type 2 diabetes across the UK Biobank: A Mendelian randomization study **2019**, 16, e1002982		
471	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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469	Homogeneity in the association of body mass index with type 2 diabetes across the UK Biobank: A Mendelian randomization study **2019**, 16, e1002982		
468	Homogeneity in the association of body mass index with type 2 diabetes across the UK Biobank: A Mendelian randomization study **2019**, 16, e1002982		
467	Genome-wide association study of offspring birth weight in 86 577 women identifies five novel loci and highlights maternal genetic effects that are independent of fetal genetics. *Human Molecular Genetics*, **2018**, 27, 742-756	5.6	98
466	Patterns of differential gene expression in a cellular model of human islet development, and relationship to type 2 diabetes predisposition. *Diabetologia*, **2018**, 61, 1614-1622	10.3	9
465	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
464	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
463	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. *Nature Communications*, **2018**, 9, 711	17.4	35
462	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
461	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
460	Toppar: an interactive browser for viewing association study results. *Bioinformatics*, **2018**, 34, 1922-1924	7.2	5
459	A Genome-Wide Association Study of Diabetic Kidney Disease in Subjects With Type 2 Diabetes. *Diabetes*, **2018**, 67, 1414-1427	0.9	71
458	Characterising -regulatory variation in the transcriptome of histologically normal and tumour-derived pancreatic tissues. *Gut*, **2018**, 67, 521-533	19.2	16
457	Metabolite ratios as potential biomarkers for type 2 diabetes: a DIRECT study. *Diabetologia*, **2018**, 61, 117-129	10.3	21
456	Association of vitamin D with risk of type 2 diabetes: A Mendelian randomisation study in European and Chinese adults. *PLoS Medicine*, **2018**, 15, e1002566	11.6	48
455	Type 2 diabetes risk alleles in PAM impact insulin release from human pancreatic β-cells. *Nature Genetics*, **2018**, 50, 1122-1131	36.3	35
454	Understanding human fetal pancreas development using subpopulation sorting, RNA sequencing and single-cell profiling. *Development (Cambridge)*, **2018**, 145,	6.6	42
453	Validation of Plasma Biomarker Candidates for the Prediction of eGFR Decline in Patients With Type 2 Diabetes. *Diabetes Care*, **2018**, 41, 1947-1954	14.6	25

452	NKX6.1 induced pluripotent stem cell reporter lines for isolation and analysis of functionally relevant neuronal and pancreas populations. *Stem Cell Research*, **2018**, 29, 220-231	1.6	14
451	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. *Nature Communications*, **2018**, 9, 2252	17.4	71
450	Human Genetics of Obesity and Type 2 Diabetes Mellitus: Past, Present, and Future. *Circulation Genomic and Precision Medicine*, **2018**, 11, e002090	5.2	41
449	Maturity onset diabetes of the young due to variants in Croatia. *Biochemia Medica*, **2018**, 28, 020703	2.5	12
448	DOLORisk: study protocol for a multi-centre observational study to understand the risk factors and determinants of neuropathic pain. *Wellcome Open Research*, **2018**, 3, 63	4.8	12
447	DOLORisk: study protocol for a multi-centre observational study to understand the risk factors and determinants of neuropathic pain. *Wellcome Open Research*, **2018**, 3, 63	4.8	11
446	Integrative network analysis highlights biological processes underlying GLP-1 stimulated insulin secretion: A DIRECT study. *PLoS ONE*, **2018**, 13, e0189886	3.7	5
445	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
444	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
443	A variant within the FTO confers susceptibility to diabetic nephropathy in Japanese patients with type 2 diabetes. *PLoS ONE*, **2018**, 13, e0208654	3.7	12
442	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
441	A Global Overview of Precision Medicine in Type 2 Diabetes. *Diabetes*, **2018**, 67, 1911-1922	0.9	52
440	A genome-wide association study suggests new evidence for an association of the NADPH Oxidase 4 (NOX4) gene with severe diabetic retinopathy in type 2 diabetes. *Acta Ophthalmologica*, **2018**, 96, e811-e819	3.7	36
439	Association of Genetically Enhanced Lipoprotein Lipase-Mediated Lipolysis and Low-Density Lipoprotein Cholesterol-Lowering Alleles With Risk of Coronary Disease and Type 2 Diabetes. *JAMA Cardiology*, **2018**, 3, 957-966	16.2	30
438	Derivation and molecular characterization of pancreatic differentiated MODY1-iPSCs. *Stem Cell Research*, **2018**, 31, 16-26	1.6	13
437	Integration of human pancreatic islet genomic data refines regulatory mechanisms at Type 2 Diabetes susceptibility loci. *ELife*, **2018**, 7,	8.9	70
436	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
435	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412

434	Decreased STARD10 Expression Is Associated with Defective Insulin Secretion in Humans and Mice. *American Journal of Human Genetics*, **2017**, 100, 238-256	11	50
433	Painting a new picture of personalised medicine for diabetes. *Diabetologia*, **2017**, 60, 793-799	10.3	102
432	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
431	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
430	A Genome-Wide Association Study of IVGTT-Based Measures of First-Phase Insulin Secretion Refines the Underlying Physiology of Type 2 Diabetes Variants. *Diabetes*, **2017**, 66, 2296-2309	0.9	69
429	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
428	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. *American Journal of Human Genetics*, **2017**, 100, 865-884	11	74
427	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. *Diabetes*, **2017**, 66, 2888-2902	8.9	414
426	How Can Genetic Studies Help Us to Understand Links Between Birth Weight and Type 2 Diabetes?. *Current Diabetes Reports*, **2017**, 17, 22	5.6	23
425	Genetics of T2DM in 2016: Biological and translational insights from T2DM genetics. *Nature Reviews Endocrinology*, **2017**, 13, 71-72	15.2	8
424	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. *Nature*, **2017**, 541, 81-86	50.4	511
423	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
422	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475 000 Individuals. *Circulation: Cardiovascular Genetics*, **2017**, 10,		33
421	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
420	Genes Associated with Pancreas Development and Function Maintain Open Chromatin in iPSCs Generated from Human Pancreatic Beta Cells. *Stem Cell Reports*, **2017**, 9, 1395-1405	8	10
419	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. *Nature Communications*, **2017**, 8, 16015	17.4	80
418	10 Years of GWAS Discovery: Biology, Function, and Translation. *American Journal of Human Genetics*, **2017**, 101, 5-22	11	1651
417	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

416	The Genetic Landscape of Renal Complications in Type 1 Diabetes. *Journal of the American Society of Nephrology: JASN*, **2017**, 28, 557-574	12.7	69
415	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
414	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
413	Bone mineral density and risk of type 2 diabetes and coronary heart disease: A Mendelian randomization study. *Wellcome Open Research*, **2017**, 2, 68	4.8	17
412	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. *PLoS Genetics*, **2017**, 13, e1006528	6	103
411	A reference panel of 64,976 haplotypes for genotype imputation. *Nature Genetics*, **2016**, 48, 1279-83	36.3	1447
410	Systematic Functional Characterization of Candidate Causal Genes for Type 2 Diabetes Risk Variants. *Diabetes*, **2016**, 65, 3805-3811	0.9	61
409	Analysis of protein-coding genetic variation in 60,706 humans. *Nature*, **2016**, 536, 285-91	50.4	6940
408	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. *Nature Communications*, **2016**, 7, 13357	17.4	46
407	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
406	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
405	Diabetes and Cause-Specific Mortality in Mexico City. *New England Journal of Medicine*, **2016**, 375, 1961-1971	59.1	144
404	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
403	Trans-ethnic study design approaches for fine-mapping. *European Journal of Human Genetics*, **2016**, 24, 1330-6	5.3	48
402	A null mutation in ANGPTL8 does not associate with either plasma glucose or type 2 diabetes in humans. *BMC Endocrine Disorders*, **2016**, 16, 7	3.3	8
401	Insights into islet development and biology through characterization of a human iPSC-derived endocrine pancreas model. *Islets*, **2016**, 8, 83-95	2	18
400	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180
399	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

398	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
397	Loss-of-Function Mutations in the Cell-Cycle Control Gene CDKN2A Impact on Glucose Homeostasis in Humans. *Diabetes*, **2016**, 65, 527-33	0.9	28
396	Harmonising and linking biomedical and clinical data across disparate data archives to enable integrative cross-biobank research. *European Journal of Human Genetics*, **2016**, 24, 521-8	5.3	19
395	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. *Human Molecular Genetics*, **2016**, 25, 389-403	5.6	202
394	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
393	Burden of Diabetes and First Evidence for the Utility of HbA1c for Diagnosis and Detection of Diabetes in Urban Black South Africans: The Durban Diabetes Study. *PLoS ONE*, **2016**, 11, e0161966	3.7	25
392	The Importance of Context: Uncovering Species- and Tissue-Specific Effects of Genetic Risk Variants for Type 2 Diabetes. *Frontiers in Endocrinology*, **2016**, 7, 112	5.7	2
391	A Protein Domain and Family Based Approach to Rare Variant Association Analysis. *PLoS ONE*, **2016**, 11, e0153803	3.7	5
390	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
389	Higher chylomicron remnants and LDL particle numbers associate with CD36 SNPs and DNA methylation sites that reduce CD36. *Journal of Lipid Research*, **2016**, 57, 2176-2184	6.3	20
388	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
387	Evaluation of type 2 diabetes genetic risk variants in Chinese adults: findings from 93,000 individuals from the China Kadoorie Biobank. *Diabetologia*, **2016**, 59, 1446-1457	10.3	37
386	Detection of human adaptation during the past 2000 years. *Science*, **2016**, 354, 760-764	33.3	224
385	Genome-wide associations for birth weight and correlations with adult disease. *Nature*, **2016**, 538, 248-252	38.4	266
384	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
383	Exposing the exposures responsible for type 2 diabetes and obesity. *Science*, **2016**, 354, 69-73	33.3	138
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21	The genetics of non-insulin-dependent diabetes mellitus in south India: an overview. *Annals of Medicine*, **1992**, 24, 491-7	1.5	18

20	Type 2 diabetes mellitus344-358	
19	Aetiological differences between novel subtypes of diabetes derived from genetic associations	2
18	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes	4
17	Analysis of overlapping genetic association in type 1 and type 2 diabetes	1
16	An Effector Index to Predict Causal Genes at GWAS Loci	3
15	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes	1
14	Rare Non-coding Variation Identified by Large Scale Whole Genome Sequencing Reveals Unexplained Heritability of Type 2 Diabetes	2
13	Fine-mapping of an expanded set of type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps	18
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11	Genetic discovery and translational decision support from exome sequencing of 20,791 type 2 diabetes cases and 24,440 controls from five ancestries	2
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