

# Anubha Mahajan

## List of Publications by Year in descending order

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Version: 2024-02-01

177  
papers

34,963  
citations

10956

71  
h-index

4978

167  
g-index

220  
all docs

220  
docs citations

220  
times ranked

39520  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
2	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016, 48, 1279-1283.	9.4	2,421
3	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	9.4	1,818
4	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012, 44, 981-990.	9.4	1,748
5	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.	9.4	1,331
6	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	13.7	1,328
7	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014, 46, 234-244.	9.4	959
8	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	13.7	952
9	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	9.4	924
10	Causal relationships among the gut microbiome, short-chain fatty acids and metabolic diseases. <i>Nature Genetics</i> , 2019, 51, 600-605.	9.4	854
11	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.	9.4	746
12	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017, 66, 2888-2902.	0.3	615
13	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018, 50, 1225-1233.	9.4	552
14	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	9.4	549
15	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	13.7	544
16	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766.	9.4	470
17	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. <i>Nature Communications</i> , 2020, 11, 163.	5.8	466
18	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. <i>Nature Genetics</i> , 2014, 46, 357-363.	9.4	428

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19	Coding Variation in <i>ANGPTL4</i> , <i>LPL</i> and <i>SVEP1</i> and the Risk of Coronary Disease. <i>New England Journal of Medicine</i> , 2016, 374, 1134-1144.	13.9	427
20	Genome-wide associations for birth weight and correlations with adult disease. <i>Nature</i> , 2016, 538, 248-252.	13.7	406
21	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. <i>Nature Genetics</i> , 2019, 51, 804-814.	9.4	402
22	Using human genetics to understand the disease impacts of testosterone in men and women. <i>Nature Medicine</i> , 2020, 26, 252-258.	15.2	384
23	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015, 47, 1415-1425.	9.4	365
24	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018, 50, 559-571.	9.4	356
25	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	13.7	353
26	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.	9.4	350
27	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. <i>PLoS Medicine</i> , 2017, 14, e1002383.	3.9	341
28	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. <i>PLoS Genetics</i> , 2018, 14, e1007813.	1.5	341
29	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	9.4	341
30	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.	1.5	331
31	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , 2018, 103, 691-706.	2.6	326
32	The impact of low-frequency and rare variants on lipid levels. <i>Nature Genetics</i> , 2015, 47, 589-597.	9.4	310
33	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. <i>Lancet Diabetes and Endocrinology</i> , 2017, 5, 97-105.	5.5	298
34	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. <i>Nature Genetics</i> , 2013, 45, 76-82.	9.4	293
35	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.	9.4	286
36	Identification of type 2 diabetes loci in 433,540 East Asian individuals. <i>Nature</i> , 2020, 582, 240-245.	13.7	282

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37	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. <i>Human Molecular Genetics</i> , 2016, 25, 389-403.	1.4	275
38	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016, 48, 1151-1161.	9.4	261
39	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	9.4	251
40	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. <i>Nature Genetics</i> , 2022, 54, 560-572.	9.4	250
41	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019, 570, 71-76.	13.7	248
42	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016, 7, 10495.	5.8	245
43	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2017, 69, 823-836.	1.2	214
44	Genetic Risk Scores for Diabetes Diagnosis and Precision Medicine. <i>Endocrine Reviews</i> , 2019, 40, 1500-1520.	8.9	192
45	Genome-Wide Association Study for Type 2 Diabetes in Indians Identifies a New Susceptibility Locus at 2q21. <i>Diabetes</i> , 2013, 62, 977-986.	0.3	173
46	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.	1.4	170
47	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.	5.8	169
48	Impact of Common Variants of <i>PPARG</i> , <i>KCNJ11</i> , <i>TCF7L2</i> , <i>SLC30A8</i> , <i>HHEX</i> , <i>CDKN2A</i> , <i>IGF2BP2</i> , and <i>CDKAL1</i> on the Risk of Type 2 Diabetes in 5,164 Indians. <i>Diabetes</i> , 2010, 59, 2068-2074.	0.3	163
49	Genome-wide physical activity interactions in adiposity – A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	1.5	158
50	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , 2016, 7, 10494.	5.8	153
51	Regulatory variants at <i>KLF14</i> influence type 2 diabetes risk via a female-specific effect on adipocyte size and body composition. <i>Nature Genetics</i> , 2018, 50, 572-580.	9.4	143
52	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019, 10, 4130.	5.8	133
53	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, 70, .	1.3	123
54	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.	2.6	123

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55	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.	9.4	116
56	Causal relationships between obesity and the leading causes of death in women and men. <i>PLoS Genetics</i> , 2019, 15, e1008405.	1.5	113
57	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. <i>Nature Communications</i> , 2019, 10, 29.	5.8	113
58	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.	9.4	112
59	A novel common variant in DCST2 is associated with length in early life and height in adulthood. <i>Human Molecular Genetics</i> , 2015, 24, 1155-1168.	1.4	109
60	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. <i>Nature Communications</i> , 2015, 6, 8658.	5.8	108
61	Clinical and Genetic Correlates of Growth Differentiation Factor 15 in the Community. <i>Clinical Chemistry</i> , 2012, 58, 1582-1591.	1.5	106
62	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.	1.5	105
63	Genome-wide association study of toxic metals and trace elements reveals novel associations. <i>Human Molecular Genetics</i> , 2015, 24, 4739-4745.	1.4	104
64	Integration of human pancreatic islet genomic data refines regulatory mechanisms at Type 2 Diabetes susceptibility loci. <i>ELife</i> , 2018, 7, .	2.8	103
65	A Genome-Wide Association Study of IVGTT-Based Measures of First-Phase Insulin Secretion Refines the Underlying Physiology of Type 2 Diabetes Variants. <i>Diabetes</i> , 2017, 66, 2296-2309.	0.3	102
66	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. <i>Nature Communications</i> , 2018, 9, 2252.	5.8	99
67	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. <i>PLoS Genetics</i> , 2015, 11, e1004876.	1.5	95
68	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. <i>Nature Communications</i> , 2017, 8, 15805.	5.8	95
69	Identification and validation of N-acetyltransferase 2 as an insulin sensitivity gene. <i>Journal of Clinical Investigation</i> , 2015, 125, 1739-1751.	3.9	94
70	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.	9.4	91
71	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.	9.4	89
72	Genetic variant effects on gene expression in human pancreatic islets and their implications for T2D. <i>Nature Communications</i> , 2020, 11, 4912.	5.8	89

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73	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021, 12, 24.	5.8	87
74	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	5.8	84
75	Association of vitamin D with risk of type 2 diabetes: A Mendelian randomisation study in European and Chinese adults. <i>PLoS Medicine</i> , 2018, 15, e1002566.	3.9	82
76	Genome-wide association analyses highlight etiological differences underlying newly defined subtypes of diabetes. <i>Nature Genetics</i> , 2021, 53, 1534-1542.	9.4	81
77	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. <i>PLoS Genetics</i> , 2015, 11, e1005230.	1.5	77
78	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, 13357.	5.8	74
79	Genome-Wide and Abdominal MRI Data Provide Evidence That a Genetically Determined Favorable Adiposity Phenotype Is Characterized by Lower Ectopic Liver Fat and Lower Risk of Type 2 Diabetes, Heart Disease, and Hypertension. <i>Diabetes</i> , 2019, 68, 207-219.	0.3	72
80	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.	5.2	69
81	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. <i>American Journal of Human Genetics</i> , 2016, 99, 636-646.	2.6	67
82	High-Sensitivity C-Reactive Protein Levels and Type 2 Diabetes in Urban North Indians. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2009, 94, 2123-2127.	1.8	65
83	Common variants of FTO and the risk of obesity and type 2 diabetes in Indians. <i>Journal of Human Genetics</i> , 2011, 56, 720-726.	1.1	63
84	Identification of 371 genetic variants for age at first sex and birth linked to externalising behaviour. <i>Nature Human Behaviour</i> , 2021, 5, 1717-1730.	6.2	62
85	Type 2 diabetes risk alleles in PAM impact insulin release from human pancreatic $\beta$ -cells. <i>Nature Genetics</i> , 2018, 50, 1122-1131.	9.4	59
86	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020, 11, 2542.	5.8	59
87	Genome-wide association study of type 2 diabetes in Africa. <i>Diabetologia</i> , 2019, 62, 1204-1211.	2.9	56
88	Variants in the fetal genome near pro-inflammatory cytokine genes on 2q13 associate with gestational duration. <i>Nature Communications</i> , 2019, 10, 3927.	5.8	49
89	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475,000 Individuals. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	48
90	A Low-Frequency Inactivating <i>AKT2</i> Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017, 66, 2019-2032.	0.3	47

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91	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts. <i>PLoS Medicine</i> , 2020, 17, e1003149.	3.9	47
92	Variation in the Plasma Membrane Monoamine Transporter (PMAT) (Encoded by <i>SLC29A4</i> ) and Organic Cation Transporter 1 (OCT1) (Encoded by <i>SLC22A1</i> ) and Gastrointestinal Intolerance to Metformin in Type 2 Diabetes: An IMI DIRECT Study. <i>Diabetes Care</i> , 2019, 42, 1027-1033.	4.3	43
93	Genetic Predisposition to Type 2 Diabetes and Risk of Subclinical Atherosclerosis and Cardiovascular Diseases Among 160,000 Chinese Adults. <i>Diabetes</i> , 2019, 68, 2155-2164.	0.3	42
94	Evaluation of type 2 diabetes genetic risk variants in Chinese adults: findings from 93,000 individuals from the China Kadoorie Biobank. <i>Diabetologia</i> , 2016, 59, 1446-1457.	2.9	41
95	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. <i>The Lancet Healthy Longevity</i> , 2021, 2, e317-e326.	2.0	41
96	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.	1.4	40
97	A Polygenic and Phenotypic Risk Prediction for Polycystic Ovary Syndrome Evaluated by Phenome-Wide Association Studies. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, 1918-1936.	1.8	40
98	Variation in the SERPINA6/SERPINA1 locus alters morning plasma cortisol, hepatic corticosteroid binding globulin expression, gene expression in peripheral tissues, and risk of cardiovascular disease. <i>Journal of Human Genetics</i> , 2021, 66, 625-636.	1.1	40
99	Four groups of type 2 diabetes contribute to the etiological and clinical heterogeneity in newly diagnosed individuals: An IMI DIRECT study. <i>Cell Reports Medicine</i> , 2022, 3, 100477.	3.3	39
100	Association of variants in genes involved in pancreatic $\beta$ -cell development and function with type 2 diabetes in North Indians. <i>Journal of Human Genetics</i> , 2011, 56, 695-700.	1.1	37
101	Habitual coffee consumption and cognitive function: a Mendelian randomization meta-analysis in up to 415,530 participants. <i>Scientific Reports</i> , 2018, 8, 7526.	1.6	36
102	Oligonucleotide properties determination and primer designing: a critical examination of predictions. <i>Bioinformatics</i> , 2005, 21, 3918-3925.	1.8	34
103	Elevated levels of C-reactive protein as a risk factor for Metabolic Syndrome in Indians. <i>Atherosclerosis</i> , 2012, 220, 275-281.	0.4	34
104	Homogeneity in the association of body mass index with type 2 diabetes across the UK Biobank: A Mendelian randomization study. <i>PLoS Medicine</i> , 2019, 16, e1002982.	3.9	34
105	RSPO3 impacts body fat distribution and regulates adipose cell biology in vitro. <i>Nature Communications</i> , 2020, 11, 2797.	5.8	34
106	Developing a network view of type 2 diabetes risk pathways through integration of genetic, genomic and functional data. <i>Genome Medicine</i> , 2019, 11, 19.	3.6	33
107	Genome-wide DNA methylation study identifies genes associated with the cardiovascular biomarker GDF-15. <i>Human Molecular Genetics</i> , 2016, 25, 817-827.	1.4	32
108	Obesity-dependent association of TNF-LTA locus with type 2 diabetes in North Indians. <i>Journal of Molecular Medicine</i> , 2010, 88, 515-522.	1.7	31

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109	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, 170179.	2.4	31
110	Early Metabolic Features of Genetic Liability to Type 2 Diabetes: Cohort Study With Repeated Metabolomics Across Early Life. <i>Diabetes Care</i> , 2020, 43, 1537-1545.	4.3	29
111	Deep learning models predict regulatory variants in pancreatic islets and refine type 2 diabetes association signals. <i>ELife</i> , 2020, 9, .	2.8	28
112	Evaluation of DOK5 as a susceptibility gene for type 2 diabetes and obesity in North Indian population. <i>BMC Medical Genetics</i> , 2010, 11, 35.	2.1	26
113	A Meta-Analysis of Genome-Wide Association Studies of Growth Differentiation Factor-15 Concentration in Blood. <i>Frontiers in Genetics</i> , 2018, 9, 97.	1.1	26
114	The Early Growth Genetics (EGG) and EARly Genetics and Lifecourse Epidemiology (EAGLE) consortia: design, results and future prospects. <i>European Journal of Epidemiology</i> , 2019, 34, 279-300.	2.5	26
115	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. <i>Diabetes</i> , 2020, 69, 2806-2818.	0.3	26
116	Bone mineral density and risk of type 2 diabetes and coronary heart disease: A Mendelian randomization study. <i>Wellcome Open Research</i> , 2017, 2, 68.	0.9	26
117	Unsupervised Clustering of Missense Variants in HNF1A Using Multidimensional Functional Data Aids Clinical Interpretation. <i>American Journal of Human Genetics</i> , 2020, 107, 670-682.	2.6	25
118	Genome-Wide Association Study of Peripheral Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e002862.	1.6	24
119	Genetic Association, Post-translational Modification, and Protein-Protein Interactions in Type 2 Diabetes Mellitus. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1029-1037.	2.5	23
120	Genetic studies of abdominal MRI data identify genes regulating hepcidin as major determinants of liver iron concentration. <i>Journal of Hepatology</i> , 2019, 71, 594-602.	1.8	23
121	A Multi-omic Integrative Scheme Characterizes Tissues of Action at Loci Associated with Type 2 Diabetes. <i>American Journal of Human Genetics</i> , 2020, 107, 1011-1028.	2.6	23
122	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. <i>BMC Cardiovascular Disorders</i> , 2019, 19, 240.	0.7	22
123	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. <i>Diabetologia</i> , 2019, 62, 1601-1615.	2.9	22
124	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. <i>Human Molecular Genetics</i> , 2016, 25, 2070-2081.	1.4	21
125	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. <i>American Journal of Human Genetics</i> , 2019, 105, 15-28.	2.6	21
126	Sex Differences in the Risk of Coronary Heart Disease Associated With Type 2 Diabetes: A Mendelian Randomization Analysis. <i>Diabetes Care</i> , 2021, 44, 556-562.	4.3	21



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127	Identification of genetic effects underlying type 2 diabetes in South Asian and European populations. <i>Communications Biology</i> , 2022, 5, 329.	2.0	21
128	Fine-scale population structure in the UK Biobank: implications for genome-wide association studies. <i>Human Molecular Genetics</i> , 2020, 29, 2803-2811.	1.4	20
129	Analysis of overlapping genetic association in type 1 and type 2 diabetes. <i>Diabetologia</i> , 2021, 64, 1342-1347.	2.9	20
130	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , 2018, 3, 4.	0.9	19
131	Genome-Wide Association Studies of Estimated Fatty Acid Desaturase Activity in Serum and Adipose Tissue in Elderly Individuals: Associations with Insulin Sensitivity. <i>Nutrients</i> , 2018, 10, 1791.	1.7	18
132	Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. <i>Kidney International</i> , 2022, 102, 624-639.	2.6	18
133	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. <i>Diabetes</i> , 2021, 70, 2092-2106.	0.3	17
134	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022, 5, .	2.0	17
135	Association analysis of TNFRSF1B polymorphisms with type 2 diabetes and its related traits in North India. <i>Genomic Medicine</i> , 2008, 2, 93-100.	0.6	16
136	Common variants of SLAMF1 and ITLN1 on 1q21 are associated with type 2 diabetes in Indian population. <i>Journal of Human Genetics</i> , 2012, 57, 184-190.	1.1	16
137	Processes Underlying Glycemic Deterioration in Type 2 Diabetes: An IMI DIRECT Study. <i>Diabetes Care</i> , 2021, 44, 511-518.	4.3	16
138	The value of genetic risk scores in precision medicine for diabetes. <i>Expert Review of Precision Medicine and Drug Development</i> , 2018, 3, 279-281.	0.4	15
139	No association of TNFRSF1B variants with type 2 diabetes in Indians of Indo-European origin. <i>BMC Medical Genetics</i> , 2011, 12, 110.	2.1	14
140	Common Variants in CRP and LEPR Influence High Sensitivity C-Reactive Protein Levels in North Indians. <i>PLoS ONE</i> , 2011, 6, e24645.	1.1	14
141	Evaluating human genetic support for hypothesized metabolic disease genes. <i>Cell Metabolism</i> , 2022, 34, 661-666.	7.2	14
142	The role of physical activity in metabolic homeostasis before and after the onset of type 2 diabetes: an IMI DIRECT study. <i>Diabetologia</i> , 2020, 63, 744-756.	2.9	12
143	The genomics of heart failure: design and rationale of the HERMES consortium. <i>ESC Heart Failure</i> , 2021, 8, 5531-5541.	1.4	11
144	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , 0, 3, 4.	0.9	11

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145	Genetic variation in the CYP2B6 Gene is related to circulating 2,2,4,4-tetrabromodiphenyl ether (BDE-47) concentrations: an observational population-based study. <i>Environmental Health</i> , 2014, 13, 34.	1.7	10
146	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.	3.7	10
147	Type 2 diabetes sex-specific effects associated with E167K coding variant in TM6SF2. <i>IScience</i> , 2021, 24, 103196.	1.9	10
148	Integrative network analysis highlights biological processes underlying GLP-1 stimulated insulin secretion: A DIRECT study. <i>PLoS ONE</i> , 2018, 13, e0189886.	1.1	9
149	Allelic heterogeneity of molecular events in human coagulation factor IX in Asian Indians. <i>Human Mutation</i> , 2007, 28, 526-526.	1.1	8
150	Whole blood co-expression modules associate with metabolic traits and type 2 diabetes: an IMI-DIRECT study. <i>Genome Medicine</i> , 2020, 12, 109.	3.6	8
151	Multifaceted genome-wide study identifies novel regulatory loci in SLC22A11 and ZNF45 for body mass index in Indians. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1013-1026.	1.0	8
152	Molecular characterization of hemophilia B in North Indian families: identification of novel and recurrent molecular events in the factor IX gene. <i>Haematologica</i> , 2004, 89, 1498-503.	1.7	8
153	Large-Scale Analyses Provide No Evidence for Gene-Gene Interactions Influencing Type 2 Diabetes Risk. <i>Diabetes</i> , 2020, 69, 2518-2522.	0.3	7
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164	Causal relationships between obesity and the leading causes of death in women and men. , 2019, 15, e1008405.		0
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