Anubha Mahajan

List of Publications by Year
in descending order

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177 papers	34,963 citations	10986 71 h-index	4991 167 g-index
220 all docs	220 docs citations	220 times ranked	39520 citing authors

#	Article	IF	Citations
1	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.	6.5	39
2	Identification of genetic effects underlying type 2 diabetes in South Asian and European populations. Communications Biology, 2022, 5, 329.	4.4	21
3	Evaluating human genetic support for hypothesized metabolic disease genes. Cell Metabolism, 2022, 34, 661-666.	16.2	14
4	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
5	Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. Kidney International, 2022, 102, 624-639.	5.2	18
6	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	4.4	17
7	Sex Differences in the Risk of Coronary Heart Disease Associated With Type 2 Diabetes: A Mendelian Randomization Analysis. Diabetes Care, 2021, 44, 556-562.	8.6	21
8	Genome-Wide Association Analysis of Pancreatic Beta-Cell Glucose Sensitivity. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 80-90.	3.6	5
9	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
10	Analysis of overlapping genetic association in type 1 and type 2 diabetes. Diabetologia, 2021, 64, 1342-1347.	6.3	20
11	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
12	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.	4.6	41
13	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.	0.6	17
14	Identification of 371 genetic variants for age at first sex and birth linked to externalising behaviour. Nature Human Behaviour, 2021, 5, 1717-1730.	12.0	62
15	The genomics of heart failure: design and rationale of the HERMES consortium. ESC Heart Failure, 2021, 8, 5531-5541.	3.1	11
16	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. Journal of Human Genetics, 2021, 66, 625-636.	2.3	40
17	Processes Underlying Glycemic Deterioration in Type 2 Diabetes: An IMI DIRECT Study. Diabetes Care, 2021, 44, 511-518.	8.6	16
18	Genome-Wide Association Study of Peripheral Artery Disease. Circulation Genomic and Precision Medicine, 2021, 14, e002862.	3.6	24

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19	Type 2 diabetes sex-specific effects associated with E167K coding variant in TM6SF2. IScience, 2021, 24, 103196.	4.1	10
20	Genome-wide association analyses highlight etiological differences underlying newly defined subtypes of diabetes. Nature Genetics, 2021, 53, 1534-1542.	21.4	81
21	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
22	Elevated risk of invasive group A streptococcal disease and host genetic variation in the human leucocyte antigen locus. Genes and Immunity, 2020, 21, 63-70.	4.1	5
23	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	12.8	466
24	A Polygenic and Phenotypic Risk Prediction for Polycystic Ovary Syndrome Evaluated by Phenome-Wide Association Studies. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 1918-1936.	3.6	40
25	Fine-scale population structure in the UK Biobank: implications for genome-wide association studies. Human Molecular Genetics, 2020, 29, 2803-2811.	2.9	20
26	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	21.4	91
27	Whole blood co-expression modules associate with metabolic traits and type 2 diabetes: an IMI-DIRECT study. Genome Medicine, 2020, 12, 109.	8.2	8
28	Dietary metabolite profiling brings new insight into the relationship between nutrition and metabolic risk: An IMI DIRECT study. EBioMedicine, 2020, 58, 102932.	6.1	3
29	Chronic obstructive pulmonary disease and related phenotypes: polygenic risk scores in population-based and case-control cohorts. Lancet Respiratory Medicine,the, 2020, 8, 696-708.	10.7	69
30	Large-Scale Analyses Provide No Evidence for Gene-Gene Interactions Influencing Type 2 Diabetes Risk. Diabetes, 2020, 69, 2518-2522.	0.6	7
31	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.6	26
32	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. Circulation Genomic and Precision Medicine, 2020, 13, e002769.	3.6	5
33	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.	6.2	23
34	Unsupervised Clustering of Missense Variants in HNF1A Using Multidimensional Functional Data Aids Clinical Interpretation. American Journal of Human Genetics, 2020, 107, 670-682.	6.2	25
35	Early Metabolic Features of Genetic Liability to Type 2 Diabetes: Cohort Study With Repeated Metabolomics Across Early Life. Diabetes Care, 2020, 43, 1537-1545.	8.6	29
36	Identification of type 2 diabetes loci in 433,540 East Asian individuals. Nature, 2020, 582, 240-245.	27.8	282

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37	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.	2.1	8
38	RSPO3 impacts body fat distribution and regulates adipose cell biology in vitro. Nature Communications, 2020, 11, 2797.	12.8	34
39	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
40	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.	8.4	47
41	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.	6.3	12
42	Using human genetics to understand the disease impacts of testosterone in men and women. Nature Medicine, 2020, 26, 252-258.	30.7	384
43	Genetic variant effects on gene expression in human pancreatic islets and their implications for T2D. Nature Communications, 2020, 11, 4912.	12.8	89
44	Deep learning models predict regulatory variants in pancreatic islets and refine type 2 diabetes association signals. ELife, 2020, 9, .	6.0	28
45	Post-load glucose subgroups and associated metabolic traits in individuals with type 2 diabetes: An IMI-DIRECT study. PLoS ONE, 2020, 15, e0242360.	2.5	7
46	Title is missing!. , 2020, 17, e1003149.		0
47	Title is missing!. , 2020, 17, e1003149.		0
48	Title is missing!. , 2020, 17, e1003149.		0
49	Title is missing!. , 2020, 17, e1003149.		0
50	Title is missing!. , 2020, 17, e1003149.		0
51	Genetic Predisposition to Type 2 Diabetes and Risk of Subclinical Atherosclerosis and Cardiovascular Diseases Among 160,000 Chinese Adults. Diabetes, 2019, 68, 2155-2164.	0.6	42
52	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. BMC Cardiovascular Disorders, 2019, 19, 240.	1.7	22
53	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
54	Causal relationships between obesity and the leading causes of death in women and men. PLoS Genetics, 2019, 15, e1008405.	3.5	113

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55	Variants in the fetal genome near pro-inflammatory cytokine genes on 2q13 associate with gestational duration. Nature Communications, 2019, 10, 3927.	12.8	49
56	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	12.8	133
57	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
58	Genetic Risk Scores for Diabetes Diagnosis and Precision Medicine. Endocrine Reviews, 2019, 40, 1500-1520.	20.1	192
59	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.	6.3	22
60	Genetic studies of abdominal MRI data identify genes regulating hepcidin as major determinants of liver iron concentration. Journal of Hepatology, 2019, 71, 594-602.	3.7	23
61	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	6.2	21
62	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
63	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	27.8	248
64	Genome-wide association study of type 2 diabetes in Africa. Diabetologia, 2019, 62, 1204-1211.	6.3	56
65	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	21.4	402
66	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.	5.7	26
67	Variation in the Plasma Membrane Monoamine Transporter (PMAT) (Encoded by SLC29A4) and Organic Cation Transporter 1 (OCT1) (Encoded by SLC22A1) and Gastrointestinal Intolerance to Metformin in Type 2 Diabetes: An IMI DIRECT Study. Diabetes Care, 2019, 42, 1027-1033.	8.6	43
68	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
69	Developing a network view of type 2 diabetes risk pathways through integration of genetic, genomic and functional data. Genome Medicine, 2019, 11, 19.	8.2	33
70	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. Nature Genetics, 2019, 51, 481-493.	21.4	350
71	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
72	Causal relationships among the gut microbiome, short-chain fatty acids and metabolic diseases. Nature Genetics, 2019, 51, 600-605.	21.4	854

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73	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.	8.4	34
74	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. Nature Communications, 2019, 10, 29.	12.8	113
75	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. Diabetes, 2019, 68, 207-219.	0.6	72
76	Causal relationships between obesity and the leading causes of death in women and men. , 2019, 15, e1008405.		0
77	Causal relationships between obesity and the leading causes of death in women and men. , 2019, 15, e1008405.		0
78	Causal relationships between obesity and the leading causes of death in women and men. , 2019, 15, e1008405.		0
79	Causal relationships between obesity and the leading causes of death in women and men. , 2019, 15, e1008405.		0
80	Title is missing!. , 2019, 16, e1002982.		0
81	Title is missing!. , 2019, 16, e1002982.		0
82	Title is missing!. , 2019, 16, e1002982.		0
83	Title is missing!. , 2019, 16, e1002982.		0
84	Title is missing!. , 2019, 16, e1002982.		0
85	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	21.4	356
86	Regulatory variants at KLF14 influence type 2 diabetes risk via a female-specific effect on adipocyte size and body composition. Nature Genetics, 2018, 50, 572-580.	21.4	143
87	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	6.2	123
88	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. PLoS Genetics, 2018, 14, e1007813.	3.5	341
89	Genome-Wide Association Studies of Estimated Fatty Acid Desaturase Activity in Serum and Adipose Tissue in Elderly Individuals: Associations with Insulin Sensitivity. Nutrients, 2018, 10, 1791.	4.1	18
90	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. Nature Genetics, 2018, 50, 1505-1513.	21.4	1,331

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91	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	6.2	326
92	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
93	Habitual coffee consumption and cognitive function: a Mendelian randomization meta-analysis in up to 415,530 participants. Scientific Reports, 2018, 8, 7526.	3.3	36
94	Integration of human pancreatic islet genomic data refines regulatory mechanisms at Type 2 Diabetes susceptibility loci. ELife, 2018, 7, .	6.0	103
95	Association of vitamin D with risk of type 2 diabetes: A Mendelian randomisation study in European and Chinese adults. PLoS Medicine, 2018, 15, e1002566.	8.4	82
96	Type 2 diabetes risk alleles in PAM impact insulin release from human pancreatic Î²-cells. Nature Genetics, 2018, 50, 1122-1131.	21.4	59
97	A Meta-Analysis of Genome-Wide Association Studies of Growth Differentiation Factor-15 Concentration in Blood. Frontiers in Genetics, 2018, 9, 97.	2.3	26
98	The value of genetic risk scores in precision medicine for diabetes. Expert Review of Precision Medicine and Drug Development, 2018, 3, 279-281.	0.7	15
99	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. Nature Communications, 2018, 9, 2252.	12.8	99
100	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	21.4	552
101	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
102	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 2018, 3, 4.	1.8	19
103	Integrative network analysis highlights biological processes underlying GLP-1 stimulated insulin secretion: A DIRECT study. PLoS ONE, 2018, 13, e0189886.	2.5	9
104	Guidance for the utility of linear models in meta-analysis of genetic association studies of binary phenotypes. European Journal of Human Genetics, 2017, 25, 240-245.	2.8	40
105	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
106	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	2.8	214
107	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.	0.6	102
108	Copy number variations in â€œclassicalâ€•obesity candidate genes are not frequently associated with severe early-onset obesity in children. Journal of Pediatric Endocrinology and Metabolism, 2017, 30, 507-515.	0.9	0

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109	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
110	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2017, 5, 97-105.	11.4	298
111	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. Nature Genetics, 2017, 49, 125-130.	21.4	116
112	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	12.8	95
113	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615
114	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.6	47
115	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
116	New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48
117	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	2.7	123
118	Genetic and methylation variation in the CYP2B6 gene is related to circulating p,pâ€²-dde levels in a population-based sample. Environment International, 2017, 98, 212-218.	10.0	5
119	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
120	Trans-ethnic meta-regression of genome-wide association studies accounting for ancestry increases power for discovery and improves fine-mapping resolution. Human Molecular Genetics, 2017, 26, 3639-3650.	2.9	170
121	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. PLoS Medicine, 2017, 14, e1002383.	8.4	341
122	Bone mineral density and risk of type 2 diabetes and coronary heart disease: A Mendelian randomization study. Wellcome Open Research, 2017, 2, 68.	1.8	26
123	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
124	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
125	Coding Variation inANGPTL4,LPL,andSVEP1and the Risk of Coronary Disease. New England Journal of Medicine, 2016, 374, 1134-1144.	27.0	427
126	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.	6.3	41

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127	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. American Journal of Human Genetics, 2016, 99, 636-646.	6.2	67
128	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	27.8	406
129	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	21.4	2,421
130	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
131	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
132	Genome-wide DNA methylation study identifies genes associated with the cardiovascular biomarker GDF-15. Human Molecular Genetics, 2016, 25, 817-827.	2.9	32
133	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	12.8	245
134	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	12.8	153
135	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. Human Molecular Genetics, 2016, 25, 2070-2081.	2.9	21
136	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. Human Molecular Genetics, 2016, 25, 389-403.	2.9	275
137	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	3.5	331
138	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. PLoS Genetics, 2015, 11, e1005230.	3.5	77
139	Identification and validation of N-acetyltransferase 2 as an insulin sensitivity gene. Journal of Clinical Investigation, 2015, 125, 1739-1751.	8.2	94
140	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	12.8	108
141	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
142	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
143	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. PLoS Genetics, 2015, 11, e1004876.	3.5	95
144	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	21.4	310

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145	Genome-wide association study of plasma levels of polychlorinated biphenyls disclose an association with the CYP2B6 gene in a population-based sample. Environmental Research, 2015, 140, 95-101.	7.5	10
146	Genome-wide association study of toxic metals and trace elements reveals novel associations. Human Molecular Genetics, 2015, 24, 4739-4745.	2.9	104
147	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	21.4	365
148	A novel common variant in DCST2 is associated with length in early life and height in adulthood. Human Molecular Genetics, 2015, 24, 1155-1168.	2.9	109
149	Genome Wide Association Identifies Common Variants at the SERPINA6/SERPINA1 Locus Influencing Plasma Cortisol and Corticosteroid Binding Globulin. PLoS Genetics, 2014, 10, e1004474.	3.5	105
150	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
151	Genetic variation in the CYP2B6 Gene is related to circulating 2,2â€™,4,4â€™-tetrabromodiphenyl ether (BDE-47) concentrations: an observational population-based study. Environmental Health, 2014, 13, 34.	4.0	10
152	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	21.4	959
153	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. Nature Genetics, 2014, 46, 357-363.	21.4	428
154	Abstract 49: A Genome-wide Meta-analysis of the Combined Influence of Physical Activity and Genetic Variants on Body Fat Distribution in 94,779 Individuals of European Descent. Circulation, 2014, 129, .	1.6	0
155	Genome-Wide Association Study for Type 2 Diabetes in Indians Identifies a New Susceptibility Locus at 2q21. Diabetes, 2013, 62, 977-986.	0.6	173
156	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. Nature Genetics, 2013, 45, 76-82.	21.4	293
157	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	21.4	746
158	Elevated levels of C-reactive protein as a risk factor for Metabolic Syndrome in Indians. Atherosclerosis, 2012, 220, 275-281.	0.8	34
159	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	21.4	1,748
160	Clinical and Genetic Correlates of Growth Differentiation Factor 15 in the Community. Clinical Chemistry, 2012, 58, 1582-1591.	3.2	106
161	Common variants of SLAMF1 and ITLN1 on 1q21 are associated with type 2 diabetes in Indian population. Journal of Human Genetics, 2012, 57, 184-190.	2.3	16
162	Association of variants in genes involved in pancreatic Î²-cell development and function with type 2 diabetes in North Indians. Journal of Human Genetics, 2011, 56, 695-700.	2.3	37

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163	Common variants of FTO and the risk of obesity and type 2 diabetes in Indians. Journal of Human Genetics, 2011, 56, 720-726.	2.3	63
164	Protein molecular function influences mutation rates in human genetic diseases with allelic heterogeneity. Biochemical and Biophysical Research Communications, 2011, 412, 716-722.	2.1	2
165	No association of TNFRSF1B variants with type 2 diabetes in Indians of Indo-European origin. BMC Medical Genetics, 2011, 12, 110.	2.1	14
166	Common Variants in CRP and LEPR Influence High Sensitivity C-Reactive Protein Levels in North Indians. PLoS ONE, 2011, 6, e24645.	2.5	14
167	Obesity-dependent association of TNF-LTA locus with type 2 diabetes in North Indians. Journal of Molecular Medicine, 2010, 88, 515-522.	3.9	31
168	Evaluation of DOK5 as a susceptibility gene for type 2 diabetes and obesity in North Indian population. BMC Medical Genetics, 2010, 11, 35.	2.1	26
169	Impact of Common Variants of PPARG, KCNJ11, TCF7L2, SLC30A8, HHEX, CDKN2A, IGF2BP2, and CDKAL1 on the Risk of Type 2 Diabetes in 5,164 Indians. Diabetes, 2010, 59, 2068-2074.	0.6	163
170	High-Sensitivity C-Reactive Protein Levels and Type 2 Diabetes in Urban North Indians. Journal of Clinical Endocrinology and Metabolism, 2009, 94, 2123-2127.	3.6	65
171	Association analysis of TNFRSF1B polymorphisms with type 2 diabetes and its related traits in North India. Genomic Medicine, 2008, 2, 93-100.	0.3	16
172	Allelic heterogeneity of molecular events in human coagulation factor IX in Asian Indians. Human Mutation, 2007, 28, 526-526.	2.5	8
173	Oligonucleotide properties determination and primer designing: a critical examination of predictions. Bioinformatics, 2005, 21, 3918-3925.	4.1	34
174	Genetic Association, Post-translational Modification, and Protein-Protein Interactions in Type 2 Diabetes Mellitus. Molecular and Cellular Proteomics, 2005, 4, 1029-1037.	3.8	23
175	Molecular characterization of hemophilia B in North Indian families: identification of novel and recurrent molecular events in the factor IX gene. Haematologica, 2004, 89, 1498-503.	3.5	8
176	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	1.8	11
177	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	1.8	1