

Man Li

List of Publications by Citations

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

102
papers

18,022
citations

51
h-index

110
g-index

110
ext. papers

21,298
ext. citations

14.2
avg, IF

4.33
L-index

#	Paper	IF	Citations
102	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010 , 42, 105-16	36.3	1673
101	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012 , 44, 981-90	36.3	1482
100	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. <i>Nature Genetics</i> , 2010 , 42, 579-89	36.3	1449
99	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014 , 46, 234-44	36.3	784
98	Genome-wide association analysis identifies variants associated with nonalcoholic fatty liver disease that have distinct effects on metabolic traits. <i>PLoS Genetics</i> , 2011 , 7, e1001324	6	629
97	New loci associated with kidney function and chronic kidney disease. <i>Nature Genetics</i> , 2010 , 42, 376-84	36.3	599
96	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. <i>Nature Genetics</i> , 2010 , 42, 142-8	36.3	527
95	MYH9 is associated with nondiabetic end-stage renal disease in African Americans. <i>Nature Genetics</i> , 2008 , 40, 1185-92	36.3	518
94	APOL1 risk variants, race, and progression of chronic kidney disease. <i>New England Journal of Medicine</i> , 2013 , 369, 2183-96	59.2	492
93	Multiple loci associated with indices of renal function and chronic kidney disease. <i>Nature Genetics</i> , 2009 , 41, 712-7	36.3	469
92	Association between C reactive protein and coronary heart disease: mendelian randomisation analysis based on individual participant data. <i>BMJ, The</i> , 2011 , 342, d548	5.9	422
91	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. <i>Nature Genetics</i> , 2011 , 43, 1131-8	36.3	415
90	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017 , 66, 2888-2902	39.0	414
89	Common variants in KCNN3 are associated with lone atrial fibrillation. <i>Nature Genetics</i> , 2010 , 42, 240-4	36.3	362
88	Genome-wide association study of PR interval. <i>Nature Genetics</i> , 2010 , 42, 153-9	36.3	340
87	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011 , 43, 1005-11	36.3	338
86	Novel loci for adiponectin levels and their influence on type 2 diabetes and metabolic traits: a multi-ethnic meta-analysis of 45,891 individuals. <i>PLoS Genetics</i> , 2012 , 8, e1002607	6	326

85	Common variants at 10 genomic loci influence hemoglobin A1c levels via glyceemic and nonglyceemic pathways. <i>Diabetes</i> , 2010 , 59, 3229-39	0.9	314
84	Common variants at ten loci modulate the QT interval duration in the QTSCD Study. <i>Nature Genetics</i> , 2009 , 41, 407-14	36.3	308
83	Variants in ZFHX3 are associated with atrial fibrillation in individuals of European ancestry. <i>Nature Genetics</i> , 2009 , 41, 879-81	36.3	307
82	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016 , 7, 10023	17.4	295
81	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015 , 47, 1415-25	36.3	292
80	Genome-wide association identifies nine common variants associated with fasting proinsulin levels and provides new insights into the pathophysiology of type 2 diabetes. <i>Diabetes</i> , 2011 , 60, 2624-34	0.9	285
79	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018 , 50, 1225-1233	36.3	277
78	Reduced neutrophil count in people of African descent is due to a regulatory variant in the Duffy antigen receptor for chemokines gene. <i>PLoS Genetics</i> , 2009 , 5, e1000360	6	251
77	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. <i>Nature Genetics</i> , 2010 , 42, 1068-76	36.3	249
76	Multiple genetic loci influence serum urate levels and their relationship with gout and cardiovascular disease risk factors. <i>Circulation: Cardiovascular Genetics</i> , 2010 , 3, 523-30		243
75	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	11.6	223
74	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018 , 50, 559-571	36.3	221
73	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019 , 51, 957-972	36.3	217
72	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. <i>Nature Genetics</i> , 2017 , 49, 946-952	36.3	176
71	CUBN is a gene locus for albuminuria. <i>Journal of the American Society of Nephrology: JASN</i> , 2011 , 22, 555-567	17.0	170
70	Stratifying type 2 diabetes cases by BMI identifies genetic risk variants in LAMA1 and enrichment for risk variants in lean compared to obese cases. <i>PLoS Genetics</i> , 2012 , 8, e1002741	6	162
69	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. <i>Nature Genetics</i> , 2016 , 48, 1162-70	36.3	152
68	Meta-analysis of genome-wide association studies in African Americans provides insights into the genetic architecture of type 2 diabetes. <i>PLoS Genetics</i> , 2014 , 10, e1004517	6	151

67	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. <i>Nature Communications</i> , 2015 , 6, 5897	17.4	147
66	Association of eGFR-Related Loci Identified by GWAS with Incident CKD and ESRD. <i>PLoS Genetics</i> , 2011 , 7, e1002292	6	144
65	Genome-wide association and functional follow-up reveals new loci for kidney function. <i>PLoS Genetics</i> , 2012 , 8, e1002584	6	143
64	A genome-wide association search for type 2 diabetes genes in African Americans. <i>PLoS ONE</i> , 2012 , 7, e29202	3.7	138
63	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019 , 51, 1459-1474	36.3	122
62	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. <i>Diabetes</i> , 2016 , 65, 803-17	0.9	96
61	Leveraging cross-species transcription factor binding site patterns: from diabetes risk loci to disease mechanisms. <i>Cell</i> , 2014 , 156, 343-58	56.2	96
60	Identification of a sudden cardiac death susceptibility locus at 2q24.2 through genome-wide association in European ancestry individuals. <i>PLoS Genetics</i> , 2011 , 7, e1002158	6	95
59	Common genetic variants associate with serum phosphorus concentration. <i>Journal of the American Society of Nephrology: JASN</i> , 2010 , 21, 1223-32	12.7	93
58	Genetic association for renal traits among participants of African ancestry reveals new loci for renal function. <i>PLoS Genetics</i> , 2011 , 7, e1002264	6	91
57	Genome-Wide Association and Trans-ethnic Meta-Analysis for Advanced Diabetic Kidney Disease: Family Investigation of Nephropathy and Diabetes (FIND). <i>PLoS Genetics</i> , 2015 , 11, e1005352	6	84
56	Genome-wide association study of kidney function decline in individuals of European descent. <i>Kidney International</i> , 2015 , 87, 1017-29	9.9	83
55	Novel loci associated with usual sleep duration: the CHARGE Consortium Genome-Wide Association Study. <i>Molecular Psychiatry</i> , 2015 , 20, 1232-9	15.1	76
54	The MYH9/APOL1 region and chronic kidney disease in European-Americans. <i>Human Molecular Genetics</i> , 2011 , 20, 2450-6	5.6	74
53	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. <i>Scientific Reports</i> , 2017 , 7, 45040	4.9	70
52	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. <i>Human Molecular Genetics</i> , 2012 , 21, 5329-43	5.6	54
51	The trans-ancestral genomic architecture of glyceemic traits. <i>Nature Genetics</i> , 2021 , 53, 840-860	36.3	44
50	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019 , 10, 4130	17.4	43

49	Trans-ethnic Meta-analysis and Functional Annotation Illuminates the Genetic Architecture of Fasting Glucose and Insulin. <i>American Journal of Human Genetics</i> , 2016 , 99, 56-75	11	41
48	Admixture mapping of obesity-related traits in African Americans: the Atherosclerosis Risk in Communities (ARIC) Study. <i>Obesity</i> , 2010 , 18, 563-72	8	41
47	Racial differences in circulating natriuretic peptide levels: the atherosclerosis risk in communities study. <i>Journal of the American Heart Association</i> , 2015 , 4,	6	40
46	Association of a fasting glucose genetic risk score with subclinical atherosclerosis: The Atherosclerosis Risk in Communities (ARIC) study. <i>Diabetes</i> , 2011 , 60, 331-5	0.9	39
45	Mapping eGFR loci to the renal transcriptome and phenome in the VA Million Veteran Program. <i>Nature Communications</i> , 2019 , 10, 3842	17.4	36
44	The association between APOL1 risk alleles and longitudinal kidney function differs by HIV viral suppression status. <i>Clinical Infectious Diseases</i> , 2015 , 60, 646-52	11.6	32
43	Urinary metabolites along with common and rare genetic variations are associated with incident chronic kidney disease. <i>Kidney International</i> , 2017 , 91, 1426-1435	9.9	31
42	Modulation of genetic associations with serum urate levels by body-mass-index in humans. <i>PLoS ONE</i> , 2015 , 10, e0119752	3.7	31
41	A comprehensive evaluation of the genetic architecture of sudden cardiac arrest. <i>European Heart Journal</i> , 2018 , 39, 3961-3969	9.5	31
40	and Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. <i>Journal of the American Society of Nephrology: JASN</i> , 2017 , 28, 981-994	12.7	30
39	Impact of repeated measures and sample selection on genome-wide association studies of fasting glucose. <i>Genetic Epidemiology</i> , 2010 , 34, 665-73	2.6	30
38	Genetic association and gene-gene interaction analyses in African American dialysis patients with nondiabetic nephropathy. <i>American Journal of Kidney Diseases</i> , 2012 , 59, 210-21	7.4	28
37	Common variants in Mendelian kidney disease genes and their association with renal function. <i>Journal of the American Society of Nephrology: JASN</i> , 2013 , 24, 2105-17	12.7	27
36	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. <i>Genome Biology</i> , 2018 , 19, 87	18.3	25
35	Host APOL1 genotype is independently associated with proteinuria in HIV infection. <i>Kidney International</i> , 2013 , 84, 834-40	9.9	25
34	Genotyping Array Design and Data Quality Control in the Million Veteran Program. <i>American Journal of Human Genetics</i> , 2020 , 106, 535-548	11	22
33	The VAAST Variant Prioritizer (VVP): ultrafast, easy to use whole genome variant prioritization tool. <i>BMC Bioinformatics</i> , 2018 , 19, 57	3.6	18
32	Genetic variants in RBF3X are associated with sleep latency. <i>European Journal of Human Genetics</i> , 2016 , 24, 1488-95	5.3	18

31	Discovery of novel heart rate-associated loci using the Exome Chip. <i>Human Molecular Genetics</i> , 2017 , 26, 2346-2363	5.6	17
30	A null variant in the apolipoprotein L3 gene is associated with non-diabetic nephropathy. <i>Nephrology Dialysis Transplantation</i> , 2018 , 33, 323-330	4.3	17
29	Genome-wide association study of 1,5-anhydroglucitol identifies novel genetic loci linked to glucose metabolism. <i>Scientific Reports</i> , 2017 , 7, 2812	4.9	16
28	Admixture mapping scans identify a locus affecting retinal vascular caliber in hypertensive African Americans: the Atherosclerosis Risk in Communities (ARIC) study. <i>PLoS Genetics</i> , 2010 , 6, e1000908	6	15
27	and Loci Associate with Plasma Osmolality. <i>Journal of the American Society of Nephrology: JASN</i> , 2017 , 28, 2311-2321	12.7	14
26	Genetics of Plasma Soluble Receptor for Advanced Glycation End-Products and Cardiovascular Outcomes in a Community-based Population: Results from the Atherosclerosis Risk in Communities Study. <i>PLoS ONE</i> , 2015 , 10, e0128452	3.7	14
25	ExomeChip-Wide Analysis of 95 626 Individuals Identifies 10 Novel Loci Associated With QT and JT Intervals. <i>Circulation Genomic and Precision Medicine</i> , 2018 , 11, e001758	5.2	14
24	Re-Sequencing of the APOL1-APOL4 and MYH9 Gene Regions in African Americans Does Not Identify Additional Risks for CKD Progression. <i>American Journal of Nephrology</i> , 2015 , 42, 99-106	4.6	12
23	Genome-Wide Association Study of Serum Fructosamine and Glycated Albumin in Adults Without Diagnosed Diabetes: Results From the Atherosclerosis Risk in Communities Study. <i>Diabetes</i> , 2018 , 67, 1684-1696	0.9	12
22	Comprehensive evaluation of imputation performance in African Americans. <i>Journal of Human Genetics</i> , 2012 , 57, 411-21	4.3	11
21	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. <i>Circulation Genomic and Precision Medicine</i> , 2018 , 11, e002037	5.2	11
20	Advances in understanding the genetic basis of diabetic kidney disease. <i>Acta Diabetologica</i> , 2018 , 55, 1093-1104	3.9	8
19	The detection of vascular endothelial growth factor in serum of patients with hemorrhagic fever with renal syndrome. <i>Inflammation</i> , 2013 , 36, 962-7	5.1	7
18	Strength of association for incident diabetes risk factors according to diabetes case definitions: the Atherosclerosis Risk in Communities Study. <i>American Journal of Epidemiology</i> , 2012 , 175, 466-72	3.8	6
17	Type-specific detection of human papillomaviruses in Kazakh esophageal squamous cell carcinoma by genotyping both E6 and L1 genes with MALDI-TOF mass spectrometry. <i>International Journal of Clinical and Experimental Pathology</i> , 2015 , 8, 13156-65	1.4	6
16	VARPRISM: incorporating variant prioritization in tests of de novo mutation association. <i>Genome Medicine</i> , 2016 , 8, 91	14.4	6
15	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. <i>Kidney International</i> , 2021 , 99, 926-939	9.9	6
14	Effect of Baseline Kidney Function on the Risk of Recurrent Stroke and on Effects of Intensive Blood Pressure Control in Patients With Previous Lacunar Stroke: A Post Hoc Analysis of the SPS3 Trial (Secondary Prevention of Small Subcortical Strokes). <i>Journal of the American Heart Association</i> , 2019 , 8, e018088	6	5

13	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes		4
12	Tissue-Specific Alteration of Metabolic Pathways Influences Glycemic Regulation		4
11	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, 387-395	5.2	4
10	Rare variants in SLC5A10 are associated with serum 1,5-anhydroglucitol (1,5-AG) in the Atherosclerosis Risk in Communities (ARIC) Study. <i>Scientific Reports</i> , 2019 , 9, 5941	4.9	3
9	Association of West African ancestry and blood pressure control among African Americans taking antihypertensive medication in the Jackson Heart Study. <i>Journal of Clinical Hypertension</i> , 2020 , 22, 157-166	4.2	3
8	Genome-Wide Association of Copy Number Polymorphisms and Kidney Function. <i>PLoS ONE</i> , 2017 , 12, e0170815	3.7	3
7	The efficacy and safety of Health Qigong for ankylosing spondylitis: Protocol for a systematic review and meta-analysis. <i>Medicine (United States)</i> , 2020 , 99, e18734	1.8	2
6	West African Ancestry and Nocturnal Blood Pressure in African Americans: The Jackson Heart Study. <i>American Journal of Hypertension</i> , 2018 , 31, 706-714	2.3	2
5	The effectiveness and safety of acupuncture therapy for Guillain-Barré syndrome: A systematic review and meta-analysis protocol. <i>Medicine (United States)</i> , 2020 , 99, e18619	1.8	2
4	Integrated Analysis Highlights the Immunosuppressive Role of TREM2 Macrophages in Hepatocellular Carcinoma.. <i>Frontiers in Immunology</i> , 2022 , 13, 848367	8.4	2
3	The Trans-Ancestral Genomic Architecture of Glycaemic Traits		1
2	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022 , 5,	6.7	1
1	Analysis of putative cis-regulatory elements regulating blood pressure variation. <i>Human Molecular Genetics</i> , 2020 , 29, 1922-1932	5.6	0