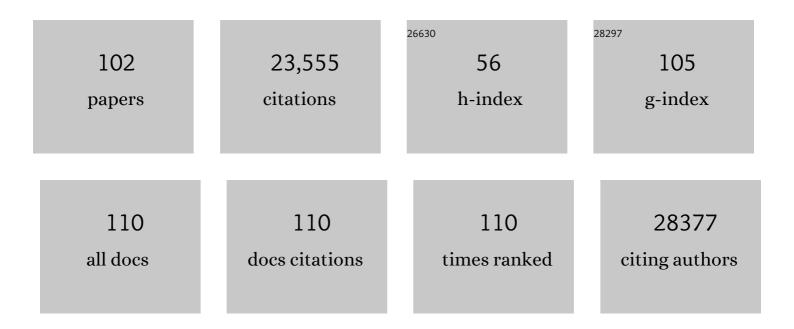


List of Publications by Year in descending order

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Μακιίι

#	Article	IF	CITATIONS
1	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	21.4	1,982
2	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
3	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	21.4	1,631
4	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
5	Genome-Wide Association Analysis Identifies Variants Associated with Nonalcoholic Fatty Liver Disease That Have Distinct Effects on Metabolic Traits. PLoS Genetics, 2011, 7, e1001324.	3.5	796
6	New loci associated with kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 376-384.	21.4	710
7	<i>APOL1</i> Risk Variants, Race, and Progression of Chronic Kidney Disease. New England Journal of Medicine, 2013, 369, 2183-2196.	27.0	654
8	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615
9	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	21.4	591
10	MYH9 is associated with nondiabetic end-stage renal disease in African Americans. Nature Genetics, 2008, 40, 1185-1192.	21.4	587
11	Multiple loci associated with indices of renal function and chronic kidney disease. Nature Genetics, 2009, 41, 712-717.	21.4	553
12	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	21.4	552
13	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
14	Association between C reactive protein and coronary heart disease: mendelian randomisation analysis based on individual participant data. BMJ: British Medical Journal, 2011, 342, d548-d548.	2.3	530
15	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	21.4	501
16	Common variants in KCNN3 are associated with lone atrial fibrillation. Nature Genetics, 2010, 42, 240-244.	21.4	438
17	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	3.5	419
18	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412

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19	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
20	Genome-wide association study of PR interval. Nature Genetics, 2010, 42, 153-159.	21.4	400
21	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. Diabetes, 2010, 59, 3229-3239.	0.6	387
22	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	21.4	365
23	Variants in ZFHX3 are associated with atrial fibrillation in individuals of European ancestry. Nature Genetics, 2009, 41, 879-881.	21.4	363
24	Common variants at ten loci modulate the QT interval duration in the QTSCD Study. Nature Genetics, 2009, 41, 407-414.	21.4	356
25	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
26	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
27	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
28	Reduced Neutrophil Count in People of African Descent Is Due To a Regulatory Variant in the Duffy Antigen Receptor for Chemokines Gene. PLoS Genetics, 2009, 5, e1000360.	3.5	335
29	Genome-Wide Association Identifies Nine Common Variants Associated With Fasting Proinsulin Levels and Provides New Insights Into the Pathophysiology of Type 2 Diabetes. Diabetes, 2011, 60, 2624-2634.	0.6	335
30	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	21.4	308
31	Multiple Genetic Loci Influence Serum Urate Levels and Their Relationship With Gout and Cardiovascular Disease Risk Factors. Circulation: Cardiovascular Genetics, 2010, 3, 523-530.	5.1	285
32	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	21.4	279
33	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
34	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	21.4	223
35	CUBN Is a Gene Locus for Albuminuria. Journal of the American Society of Nephrology: JASN, 2011, 22, 555-570.	6.1	208
36	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	2.5	197

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37	Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. PLoS Genetics, 2014, 10, e1004517.	3.5	191
38	Stratifying Type 2 Diabetes Cases by BMI Identifies Genetic Risk Variants in LAMA1 and Enrichment for Risk Variants in Lean Compared to Obese Cases. PLoS Genetics, 2012, 8, e1002741.	3.5	190
39	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
40	Association of eGFR-Related Loci Identified by GWAS with Incident CKD and ESRD. PLoS Genetics, 2011, 7, e1002292.	3.5	172
41	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	3.5	166
42	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	12.8	133
43	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. Diabetes, 2016, 65, 803-817.	0.6	131
44	Common Genetic Variants Associate with Serum Phosphorus Concentration. Journal of the American Society of Nephrology: JASN, 2010, 21, 1223-1232.	6.1	123
45	Genome-Wide Association and Trans-ethnic Meta-Analysis for Advanced Diabetic Kidney Disease: Family Investigation of Nephropathy and Diabetes (FIND). PLoS Genetics, 2015, 11, e1005352.	3.5	118
46	Genotyping Array Design and Data Quality Control in the Million Veteran Program. American Journal of Human Genetics, 2020, 106, 535-548.	6.2	118
47	Identification of a Sudden Cardiac Death Susceptibility Locus at 2q24.2 through Genome-Wide Association in European Ancestry Individuals. PLoS Genetics, 2011, 7, e1002158.	3.5	117
48	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. Cell, 2014, 156, 343-358.	28.9	113
49	Genome-wide association study of kidney function decline in individuals of European descent. Kidney International, 2015, 87, 1017-1029.	5.2	113
50	Novel loci associated with usual sleep duration: the CHARGE Consortium Genome-Wide Association Study. Molecular Psychiatry, 2015, 20, 1232-1239.	7.9	112
51	Genetic Association for Renal Traits among Participants of African Ancestry Reveals New Loci for Renal Function. PLoS Genetics, 2011, 7, e1002264.	3.5	109
52	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	3.3	98
53	Mapping eGFR loci to the renal transcriptome and phenome in the VA Million Veteran Program. Nature Communications, 2019, 10, 3842.	12.8	90
54	The MYH9/APOL1 region and chronic kidney disease in European-Americans. Human Molecular Genetics, 2011, 20, 2450-2456.	2.9	88

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55	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. Human Molecular Genetics, 2012, 21, 5329-5343.	2.9	64
56	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	2.5	64
57	A comprehensive evaluation of the genetic architecture of sudden cardiac arrest. European Heart Journal, 2018, 39, 3961-3969.	2.2	59
58	Trans-ethnic Meta-analysis and Functional Annotation Illuminates theÂGenetic Architecture of Fasting Glucose and Insulin. American Journal of Human Genetics, 2016, 99, 56-75.	6.2	55
59	Racial Differences in Circulating Natriuretic Peptide Levels: The Atherosclerosis Risk in Communities Study. Journal of the American Heart Association, 2015, 4, .	3.7	53
60	Urinary metabolites along with common and rareÂgenetic variations are associated with incidentÂchronic kidney disease. Kidney International, 2017, 91, 1426-1435.	5.2	49
61	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. Genome Biology, 2018, 19, 87.	8.8	47
62	Association of a Fasting Glucose Genetic Risk Score With Subclinical Atherosclerosis. Diabetes, 2011, 60, 331-335.	0.6	46
63	Admixture Mapping of Obesityâ€related Traits in African Americans: The Atherosclerosis Risk in Communities (ARIC) Study. Obesity, 2010, 18, 563-572.	3.0	44
64	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	5.2	42
65	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. Journal of the American Society of Nephrology: JASN, 2017, 28, 981-994.	6.1	39
66	The Association Between APOL1 Risk Alleles and Longitudinal Kidney Function Differs by HIV Viral Suppression Status. Clinical Infectious Diseases, 2015, 60, 646-652.	5.8	38
67	Genetic Association and Gene-Gene Interaction Analyses in African American Dialysis Patients With Nondiabetic Nephropathy. American Journal of Kidney Diseases, 2012, 59, 210-221.	1.9	34
68	Common Variants in Mendelian Kidney Disease Genes and Their Association with Renal Function. Journal of the American Society of Nephrology: JASN, 2013, 24, 2105-2117.	6.1	33
69	Host APOL1 genotype is independently associated with proteinuria in HIV infection. Kidney International, 2013, 84, 834-840.	5.2	31
70	Impact of repeated measures and sample selection on genomeâ€wide association studies of fasting glucose. Genetic Epidemiology, 2010, 34, 665-673.	1.3	30
71	Discovery of novel heart rate-associated loci using the Exome Chip. Human Molecular Genetics, 2017, 26, 2346-2363.	2.9	29
72	The VAAST Variant Prioritizer (VVP): ultrafast, easy to use whole genome variant prioritization tool. BMC Bioinformatics, 2018, 19, 57.	2.6	29

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73	Integrated Analysis Highlights the Immunosuppressive Role of TREM2+ Macrophages in Hepatocellular Carcinoma. Frontiers in Immunology, 2022, 13, 848367.	4.8	28
74	Genetic variants in RBFOX3 are associated with sleep latency. European Journal of Human Genetics, 2016, 24, 1488-1495.	2.8	27
75	ExomeChip-Wide Analysis of 95 626 Individuals Identifies 10 Novel Loci Associated With QT and JT Intervals. Circulation Genomic and Precision Medicine, 2018, 11, e001758.	3.6	27
76	Genome-wide association study of 1,5-anhydroglucitol identifies novel genetic loci linked to glucose metabolism. Scientific Reports, 2017, 7, 2812.	3.3	26
77	A null variant in the apolipoprotein L3 gene is associated with non-diabetic nephropathy. Nephrology Dialysis Transplantation, 2018, 33, 323-330.	0.7	25
78	NFAT5 and SLC4A10 Loci Associate with Plasma Osmolality. Journal of the American Society of Nephrology: JASN, 2017, 28, 2311-2321.	6.1	24
79	Admixture Mapping Scans Identify a Locus Affecting Retinal Vascular Caliber in Hypertensive African Americans: the Atherosclerosis Risk in Communities (ARIC) Study. PLoS Genetics, 2010, 6, e1000908.	3.5	19
80	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. PLoS ONE, 2015, 10, e0128452.	2.5	19
81	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	3.6	19
82	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
83	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	4.4	17
84	Genome-Wide Association Study of Serum Fructosamine and Glycated Albumin in Adults Without Diagnosed Diabetes: Results From the Atherosclerosis Risk in Communities Study. Diabetes, 2018, 67, 1684-1696.	0.6	16
85	Advances in understanding the genetic basis of diabetic kidney disease. Acta Diabetologica, 2018, 55, 1093-1104.	2.5	16
86	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2020, 13, 387-395.	3.6	16
87	Comprehensive evaluation of imputation performance in African Americans. Journal of Human Genetics, 2012, 57, 411-421.	2.3	14
88	Re-Sequencing of the <i>APOL1</i> - <i>APOL4</i> and <i>MYH9</i> Gene Regions in African Americans Does Not Identify Additional Risks for CKD Progression. American Journal of Nephrology, 2015, 42, 99-106.	3.1	13
89	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). Journal of the American Heart Association, 2019. 8. e013098.	3.7	10
90	Rare variants in SLC5A10 are associated with serum 1,5-anhydroglucitol (1,5-AG) in the Atherosclerosis Risk in Communities (ARIC) Study. Scientific Reports, 2019, 9, 5941.	3.3	9

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91	Low Colorectal Tumor Removal by E-Cadherin Destruction-Enabled Tumor Cell Dissociation. Nano Letters, 2022, 22, 2769-2779.	9.1	9
92	The Detection of Vascular Endothelial Growth Factor in Serum of Patients with Hemorrhagic Fever with Renal Syndrome. Inflammation, 2013, 36, 962-967.	3.8	8
93	VARPRISM: incorporating variant prioritization in tests of de novo mutation association. Genome Medicine, 2016, 8, 91.	8.2	7
94	Analysis of putative cis-regulatory elements regulating blood pressure variation. Human Molecular Genetics, 2020, 29, 1922-1932.	2.9	7
95	Type-specific detection of human papillomaviruses in Kazakh esophageal squamous cell carcinoma by genotyping both E6 and L1 genes with MALDI-TOF mass spectrometry. International Journal of Clinical and Experimental Pathology, 2015, 8, 13156-65.	0.5	7
96	Strength of Association for Incident Diabetes Risk Factors According to Diabetes Case Definitions: The Atherosclerosis Risk in Communities Study. American Journal of Epidemiology, 2012, 175, 466-472.	3.4	6
97	Machine Learning Based on MRI DWI Radiomics Features for Prognostic Prediction in Nasopharyngeal Carcinoma. Cancers, 2022, 14, 3201.	3.7	5
98	West African Ancestry and Nocturnal Blood Pressure in African Americans: The Jackson Heart Study. American Journal of Hypertension, 2018, 31, 706-714.	2.0	4
99	The effectiveness and safety of acupuncture therapy for Guillain–Barré syndrome. Medicine (United) Tj ETQq	1 1 0.7843 1.0	314 rgBT /○
100	The efficacy and safety of Health Qigong for ankylosing spondylitis. Medicine (United States), 2020, 99, e18734.	1.0	4
101	Association of West African ancestry and blood pressure control among African Americans taking antihypertensive medication in the Jackson Heart Study. Journal of Clinical Hypertension, 2020, 22, 157-166.	2.0	3
102	Genome-Wide Association of Copy Number Polymorphisms and Kidney Function. PLoS ONE, 2017, 12, e0170815.	2.5	3