Man Li

List of Publications by Year
in descending order

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102 papers	23,555 citations	26630 56 h-index	28297 105 g-index
110 all docs	110 docs citations	110 times ranked	28377 citing authors

#	Article	IF	Citations
1	Integrated Analysis Highlights the Immunosuppressive Role of TREM2+ Macrophages in Hepatocellular Carcinoma. Frontiers in Immunology, 2022, 13, 848367.	4.8	28
2	Low Colorectal Tumor Removal by E-Cadherin Destruction-Enabled Tumor Cell Dissociation. Nano Letters, 2022, 22, 2769-2779.	9.1	9
3	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
4	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	4.4	17
5	Machine Learning Based on MRI DWI Radiomics Features for Prognostic Prediction in Nasopharyngeal Carcinoma. Cancers, 2022, 14, 3201.	3.7	5
6	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	5.2	42
7	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
8	The effectiveness and safety of acupuncture therapy for Guillainâ€“BarrÃ© syndrome. Medicine (United) Tj ETQq0 0 0 rgBT /Overlock 10	1.0	4
9	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2020, 13, 387-395.	3.6	16
10	Analysis of putative cis-regulatory elements regulating blood pressure variation. Human Molecular Genetics, 2020, 29, 1922-1932.	2.9	7
11	The efficacy and safety of Health Qigong for ankylosing spondylitis. Medicine (United States), 2020, 99, e18734.	1.0	4
12	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
13	Genotyping Array Design and Data Quality Control in the Million Veteran Program. American Journal of Human Genetics, 2020, 106, 535-548.	6.2	118
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). Journal of the American Heart Association, 2019, 8, e013098.	3.7	10
15	Mapping eGFR loci to the renal transcriptome and phenome in the VA Million Veteran Program. Nature Communications, 2019, 10, 3842.	12.8	90
16	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	12.8	133
17	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
18	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549

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19	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
20	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
21	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
22	A null variant in the apolipoprotein L3 gene is associated with non-diabetic nephropathy. Nephrology Dialysis Transplantation, 2018, 33, 323-330.	0.7	25
23	A comprehensive evaluation of the genetic architecture of sudden cardiac arrest. European Heart Journal, 2018, 39, 3961-3969.	2.2	59
24	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
25	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	3.6	19
26	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
27	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. Genome Biology, 2018, 19, 87.	8.8	47
28	The VAAST Variant Prioritizer (VVP): ultrafast, easy to use whole genome variant prioritization tool. BMC Bioinformatics, 2018, 19, 57.	2.6	29
29	Advances in understanding the genetic basis of diabetic kidney disease. Acta Diabetologica, 2018, 55, 1093-1104.	2.5	16
30	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	21.4	552
31	Discovery of novel heart rate-associated loci using the Exome Chip. Human Molecular Genetics, 2017, 26, 2346-2363.	2.9	29
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	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	3.3	98
34	Genome-wide association study of 1,5-anhydroglucitol identifies novel genetic loci linked to glucose metabolism. Scientific Reports, 2017, 7, 2812.	3.3	26
35	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615
36	NFAT5 and SLC4A10 Loci Associate with Plasma Osmolality. Journal of the American Society of Nephrology: JASN, 2017, 28, 2311-2321.	6.1	24

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37	Urinary metabolites along with common and rareÂgenetic variations are associated with incidentÂchronic kidney disease. Kidney International, 2017, 91, 1426-1435.	5.2	49
38	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
39	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
40	Genome-Wide Association of Copy Number Polymorphisms and Kidney Function. PLoS ONE, 2017, 12, e0170815.	2.5	3
41	VARPRISM: incorporating variant prioritization in tests of de novo mutation association. Genome Medicine, 2016, 8, 91.	8.2	7
42	Genetic variants in RBFOX3 are associated with sleep latency. European Journal of Human Genetics, 2016, 24, 1488-1495.	2.8	27
43	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
44	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
45	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. Diabetes, 2016, 65, 803-817.	0.6	131
46	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
47	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
48	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
49	Racial Differences in Circulating Natriuretic Peptide Levels: The Atherosclerosis Risk in Communities Study. Journal of the American Heart Association, 2015, 4, .	3.7	53
50	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
51	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
52	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	21.4	365
53	Genome-wide association study of kidney function decline in individuals of European descent. Kidney International, 2015, 87, 1017-1029.	5.2	113
54	Novel loci associated with usual sleep duration: the CHARGE Consortium Genome-Wide Association Study. Molecular Psychiatry, 2015, 20, 1232-1239.	7.9	112

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55	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
56	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	2.5	64
57	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
58	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
59	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. Cell, 2014, 156, 343-358.	28.9	113
60	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
61	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
62	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
63	Host APOL1 genotype is independently associated with proteinuria in HIV infection. Kidney International, 2013, 84, 834-840.	5.2	31
64	APOL1 Risk Variants, Race, and Progression of Chronic Kidney Disease. New England Journal of Medicine, 2013, 369, 2183-2196.	27.0	654
65	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	3.5	166
66	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
67	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
68	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
69	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
70	Comprehensive evaluation of imputation performance in African Americans. Journal of Human Genetics, 2012, 57, 411-421.	2.3	14
71	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
72	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

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73	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	2.5	197
74	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	21.4	501
75	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
76	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
77	CUBN Is a Gene Locus for Albuminuria. Journal of the American Society of Nephrology: JASN, 2011, 22, 555-570.	6.1	208
78	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
79	The MYH9/APOL1 region and chronic kidney disease in European-Americans. Human Molecular Genetics, 2011, 20, 2450-2456.	2.9	88
80	Association of a Fasting Glucose Genetic Risk Score With Subclinical Atherosclerosis. Diabetes, 2011, 60, 331-335.	0.6	46
81	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
82	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
83	Genetic Association for Renal Traits among Participants of African Ancestry Reveals New Loci for Renal Function. PLoS Genetics, 2011, 7, e1002264.	3.5	109
84	Association of eGFR-Related Loci Identified by GWAS with Incident CKD and ESRD. PLoS Genetics, 2011, 7, e1002292.	3.5	172
85	Admixture Mapping of Obesityâ€related Traits in African Americans: The Atherosclerosis Risk in Communities (ARIC) Study. Obesity, 2010, 18, 563-572.	3.0	44
86	Genome-wide association study of PR interval. Nature Genetics, 2010, 42, 153-159.	21.4	400
87	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	21.4	591
88	Common variants in KCNN3 are associated with lone atrial fibrillation. Nature Genetics, 2010, 42, 240-244.	21.4	438
89	New loci associated with kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 376-384.	21.4	710
90	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	21.4	1,631

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91	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	21.4	308
92	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. Diabetes, 2010, 59, 3229-3239.	0.6	387
93	Common Genetic Variants Associate with Serum Phosphorus Concentration. Journal of the American Society of Nephrology: JASN, 2010, 21, 1223-1232.	6.1	123
94	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
95	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
96	Impact of repeated measures and sample selection on genomeâ€wide association studies of fasting glucose. Genetic Epidemiology, 2010, 34, 665-673.	1.3	30
97	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
98	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
99	Common variants at ten loci modulate the QT interval duration in the QTSCD Study. Nature Genetics, 2009, 41, 407-414.	21.4	356
100	Multiple loci associated with indices of renal function and chronic kidney disease. Nature Genetics, 2009, 41, 712-717.	21.4	553
101	Variants in ZFHX3 are associated with atrial fibrillation in individuals of European ancestry. Nature Genetics, 2009, 41, 879-881.	21.4	363
102	MYH9 is associated with nondiabetic end-stage renal disease in African Americans. Nature Genetics, 2008, 40, 1185-1192.	21.4	587