

Yong Li

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

4,573
citations

136950

32
h-index

233421

45
g-index

45
all docs

45
docs citations

45
times ranked

8486
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetics of osteopontin in patients with chronic kidney disease: The German Chronic Kidney Disease study. <i>PLoS Genetics</i> , 2022, 18, e1010139.	3.5	5
2	Genome-wide studies reveal factors associated with circulating uromodulin and its relationships to complex diseases. <i>JCI Insight</i> , 2022, 7, .	5.0	12
3	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022, 5, .	4.4	17
4	Rare genetic variants affecting urine metabolite levels link population variation to inborn errors of metabolism. <i>Nature Communications</i> , 2021, 12, 964.	12.8	20
5	Discovery and prioritization of variants and genes for kidney function in >1.2 million individuals. <i>Nature Communications</i> , 2021, 12, 4350.	12.8	125
6	Therapeutic Effects of Inhibition of Sphingosine-1-Phosphate Signaling in HIF-2 α Inhibitor-Resistant Clear Cell Renal Cell Carcinoma. <i>Cancers</i> , 2021, 13, 4801.	3.7	6
7	Genetic studies of urinary metabolites illuminate mechanisms of detoxification and excretion in humans. <i>Nature Genetics</i> , 2020, 52, 167-176.	21.4	101
8	Mapping eGFR loci to the renal transcriptome and phenome in the VA Million Veteran Program. <i>Nature Communications</i> , 2019, 10, 3842.	12.8	90
9	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019, 10, 4130.	12.8	133
10	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	21.4	251
11	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	21.4	549
12	ETR1/RDO3 Regulates Seed Dormancy by Relieving the Inhibitory Effect of the ERF12-TPL Complex on <i>DELAY OF GERMINATION1</i> Expression. <i>Plant Cell</i> , 2019, 31, 832-847.	6.6	62
13	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. <i>Nature Communications</i> , 2018, 9, 4455.	12.8	181
14	Large-scale whole-exome sequencing association studies identify rare functional variants influencing serum urate levels. <i>Nature Communications</i> , 2018, 9, 4228.	12.8	43
15	Genetics of serum urate concentrations and gout in a high-risk population, patients with chronic kidney disease. <i>Scientific Reports</i> , 2018, 8, 13184.	3.3	12
16	Genetic risk variants for membranous nephropathy: extension of and association with other chronic kidney disease aetiologies. <i>Nephrology Dialysis Transplantation</i> , 2017, 32, 325-332.	0.7	63
17	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. <i>Scientific Reports</i> , 2017, 7, 45040.	3.3	98
18	SOS2 and ACP1 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.	6.1	39

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19	Genetic loci associated with renal function measures and chronic kidney disease in children: the Pediatric Investigation for Genetic Factors Linked with Renal Progression Consortium. <i>Nephrology Dialysis Transplantation</i> , 2016, 31, gfv342.	0.7	35
20	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. <i>Diabetes</i> , 2016, 65, 803-817.	0.6	131
21	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016, 7, 10023.	12.8	412
22	Histone H2B Monoubiquitination Mediated by HISTONE MONOUBIQUITINATION1 and HISTONE MONOUBIQUITINATION2 Is Involved in Anther Development by Regulating Tapetum Degradation-Related Genes in Rice <i>Å</i> . <i>Plant Physiology</i> , 2015, 168, 1389-1405.	4.8	78
23	Cardiometabolic effects of genetic upregulation of the interleukin 1 receptor antagonist: a Mendelian randomisation analysis. <i>Lancet Diabetes and Endocrinology</i> , 2015, 3, 243-253.	11.4	115
24	Genome-Wide Meta-Analyses of Plasma Renin Activity and Concentration Reveal Association With the Kininogen 1 and Prekallikrein Genes. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 131-140.	5.1	24
25	A Genetic Risk Score for Thyroid Peroxidase Antibodies Associates With Clinical Thyroid Disease in Community-Based Populations. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2015, 100, E799-E807.	3.6	38
26	The Structural Features of Thousands of T-DNA Insertion Sites Are Consistent with a Double-Strand Break Repair-Based Insertion Mechanism. <i>Molecular Plant</i> , 2015, 8, 1651-1664.	8.3	80
27	Analysis of gene expression during parabolic flights reveals distinct early gravity responses in <i>Arabidopsis</i> roots. <i>Plant Biology</i> , 2014, 16, 129-141.	3.8	33
28	HISTONE DEACETYLASE 9 represses seedling traits in <i>Arabidopsis thaliana</i> dry seeds. <i>Plant Journal</i> , 2014, 80, 475-488.	5.7	107
29	Genetic Investigations of Kidney Disease: Core Curriculum 2013. <i>American Journal of Kidney Diseases</i> , 2013, 61, 832-844.	1.9	6
30	E-cadherin is required for the proper activation of the Lifr/Gp130 signaling pathway in mouse embryonic stem cells. <i>Development (Cambridge)</i> , 2013, 140, 1684-1692.	2.5	55
31	<i>Arabidopsis</i> Paired Amphipathic Helix Proteins SNL1 and SNL2 Redundantly Regulate Primary Seed Dormancy via Abscisic Acid-Ethylene Antagonism Mediated by Histone Deacetylation. <i>Plant Cell</i> , 2013, 25, 149-166.	6.6	140
32	Control and consequences of chromatin compaction during seed maturation in <i>Arabidopsis thaliana</i> . <i>Plant Signaling and Behavior</i> , 2012, 7, 338-341.	2.4	23
33	A novel role for histone methyltransferase KYP/SUVH4 in the control of <i>Arabidopsis</i> primary seed dormancy. <i>New Phytologist</i> , 2012, 193, 605-616.	7.3	104
34	Identification of the <i>Arabidopsis</i> REDUCED DORMANCY 2 Gene Uncovers a Role for the Polymerase Associated Factor 1 Complex in Seed Dormancy. <i>PLoS ONE</i> , 2011, 6, e22241.	2.5	77
35	T-DNA-mediated transfer of <i>Agrobacterium tumefaciens</i> chromosomal DNA into plants. <i>Nature Biotechnology</i> , 2008, 26, 1015-1017.	17.5	64
36	GABI-Kat SimpleSearch: an <i>Arabidopsis thaliana</i> T-DNA mutant database with detailed information for confirmed insertions. <i>Nucleic Acids Research</i> , 2007, 35, D874-D878.	14.5	50

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37	Analysis of T-DNA insertion site distribution patterns in <i>Arabidopsis thaliana</i> reveals special features of genes without insertions. <i>Genomics</i> , 2006, 87, 645-652.	2.9	38
38	The inositol oxygenase gene family of <i>Arabidopsis</i> is involved in the biosynthesis of nucleotide sugar precursors for cell-wall matrix polysaccharides. <i>Planta</i> , 2005, 221, 243-254.	3.2	135
39	SWI3 Subunits of Putative SWI/SNF Chromatin-Remodeling Complexes Play Distinct Roles during <i>Arabidopsis</i> Development. <i>Plant Cell</i> , 2005, 17, 2454-2472.	6.6	124
40	Site Preferences of Insertional Mutagenesis Agents in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2005, 137, 168-175.	4.8	47
41	Tic32, an Essential Component in Chloroplast Biogenesis. <i>Journal of Biological Chemistry</i> , 2004, 279, 34756-34762.	3.4	95
42	An <i>Arabidopsis thaliana</i> T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics. <i>Plant Molecular Biology</i> , 2003, 53, 247-259.	3.9	666
43	GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in <i>Arabidopsis thaliana</i> . <i>Bioinformatics</i> , 2003, 19, 1441-1442.	4.1	61
44	High-throughput generation of sequence indexes from T-DNA mutagenized <i>Arabidopsis thaliana</i> lines. <i>BioTechniques</i> , 2003, 35, 1164-1168.	1.8	27