Xin Sheng

List of Publications by Year
in descending order

77 papers	5,317 citations	186209 28 h-index	106281 65 g-index
85 all docs	85 docs citations	85 times ranked	9774 citing authors

#	Article	IF	Citations
1	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	13.7	679
2	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	9.4	652
3	Discovery of 318 new risk loci for type 2 diabetes and related vascular outcomes among 1.4 million participants in a multi-ancestry meta-analysis. Nature Genetics, 2020, 52, 680-691.	9.4	445
4	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	9.4	408
5	Mitochondrial Damage and Activation of the STING Pathway Lead to Renal Inflammation and Fibrosis. Cell Metabolism, 2019, 30, 784-799.e5.	7.2	320
6	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
7	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. Nature Genetics, 2021, 53, 65-75.	9.4	264
8	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	5.8	178
9	Renal tubule Cpt1a overexpression protects from kidney fibrosis by restoring mitochondrial homeostasis. Journal of Clinical Investigation, 2021, 131, .	3.9	147
10	The contribution of rare variation to prostate cancer heritability. Nature Genetics, 2016, 48, 30-35.	9.4	139
11	Prostate Cancer Susceptibility in Men of African Ancestry at 8q24. Journal of the National Cancer Institute, 2016, 108, djv431.	3.0	111
12	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	2.6	101
13	The Nuclear Receptor ESRRA Protects from Kidney Disease by Coupling Metabolism and Differentiation. Cell Metabolism, 2021, 33, 379-394.e8.	7.2	93
14	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	5.8	88
15	Mapping the genetic architecture of human traits to cell types in the kidney identifies mechanisms of disease and potential treatments. Nature Genetics, 2021, 53, 1322-1333.	9.4	87
16	Epigenomic and transcriptomic analyses define core cell types, genes and targetable mechanisms for kidney disease. Nature Genetics, 2022, 54, 950-962.	9.4	71
17	The key role of NLRP3 and STING in APOL1-associated podocytopathy. Journal of Clinical Investigation, 2021, 131, .	3.9	66
18	Urinary Single-Cell Profiling Captures the Cellular Diversity of the Kidney. Journal of the American Society of Nephrology: JASN, 2021, 32, 614-627.	3.0	64

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19	Kidney cytosine methylation changes improve renal function decline estimation in patients with diabetic kidney disease. Nature Communications, 2019, 10, 2461.	5.8	59
20	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. Journal of the National Cancer Institute, 2017, 109, .	3.0	57
21	Functional methylome analysis of human diabetic kidney disease. JCI Insight, 2019, 4, .	2.3	54
22	Transcriptome-wide association analysis identifies DACH1 as a kidney disease risk gene that contributes to fibrosis. Journal of Clinical Investigation, 2021, 131, .	3.9	49
23	Systematic integrated analysis of genetic and epigenetic variation in diabetic kidney disease. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 29013-29024.	3.3	46
24	Replication and validation of genetic polymorphisms associated with survival after allogeneic blood or marrow transplant. Blood, 2017, 130, 1585-1596.	0.6	45
25	Germline variation at 8q24 and prostate cancer risk in men of European ancestry. Nature Communications, 2018, 9, 4616.	5.8	43
26	Germline Sequencing DNA Repair Genes in 5545 Men With Aggressive and Nonaggressive Prostate Cancer. Journal of the National Cancer Institute, 2021, 113, 616-625.	3.0	40
27	Combined Effect of a Polygenic Risk Score and Rare Genetic Variants on Prostate Cancer Risk. European Urology, 2021, 80, 134-138.	0.9	39
28	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. International Journal of Cancer, 2021, 148, 307-319.	2.3	35
29	Replication of associations between genetic polymorphisms and chronic graft-versus-host disease. Blood, 2016, 128, 2450-2456.	0.6	32
30	A Germline Variant at 8q24 Contributes to Familial Clustering of Prostate Cancer in Men of African Ancestry. European Urology, 2020, 78, 316-320.	0.9	32
31	Role of microRNAs in the resistance of colorectalÃ¯Â¿Â½cancer to chemoradiotherapy (Review). Molecular and Clinical Oncology, 2018, 8, 523-527.	0.4	30
32	Pathogenic Variants in Cancer Predisposition Genes and Prostate Cancer Risk in Men of African Ancestry. JCO Precision Oncology, 2020, 4, 32-43.	1.5	30
33	Kidney disease genetic risk variants alter lysosomal beta-mannosidase (MANBA) expression and disease severity. Science Translational Medicine, 2021, 13, .	5.8	30
34	Downregulation of EB virus miR-BART4 inhibits proliferation and aggressiveness while promoting radiosensitivity of nasopharyngeal carcinoma. Biomedicine and Pharmacotherapy, 2018, 108, 741-751.	2.5	29
35	Population-specific reference panels are crucial for genetic analyses: an example of the CREBRF locus in Native Hawaiians. Human Molecular Genetics, 2020, 29, 2275-2284.	1.4	27
36	Whole-exome sequencing of over 4100 men of African ancestry and prostate cancer risk. Human Molecular Genetics, 2016, 25, 371-381.	1.4	26

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37	A genomeâ€wide association study of prostate cancer in Latinos. International Journal of Cancer, 2020, 146, 1819-1826.	2.3	24
38	Genetic discovery and risk characterization in type 2 diabetes across diverse populations. Human Genetics and Genomics Advances, 2021, 2, 100029.	1.0	23
39	The Four-Kallikrein Panel Is Effective in Identifying Aggressive Prostate Cancer in a Multiethnic Population. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1381-1388.	1.1	22
40	Association of Genetic Risk Score With NAFLD in An Ethnically Diverse Cohort. Hepatology Communications, 2021, 5, 1689-1703.	2.0	22
41	A Rare Germline HOXB13 Variant Contributes to Risk of Prostate Cancer in Men of African Ancestry. European Urology, 2022, 81, 458-462.	0.9	22
42	Exome chip analyses identify genes affecting mortality after HLA-matched unrelated-donor blood and marrow transplantation. Blood, 2018, 131, 2490-2499.	0.6	21
43	A Meta-analysis of Multiple Myeloma Risk Regions in African and European Ancestry Populations Identifies Putatively Functional Loci. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1609-1618.	1.1	18
44	MTD: a mammalian transcriptomic database to explore gene expression and regulation. Briefings in Bioinformatics, 2017, 18, 28-36.	3.2	18
45	Identification of novel epithelial ovarian cancer loci in women of African ancestry. International Journal of Cancer, 2020, 146, 2987-2998.	2.3	18
46	Genetic analyses of gynecological disease identify genetic relationships between uterine fibroids and endometrial cancer, and a novel endometrial cancer genetic risk region at the WNT4 1p36.12 locus. Human Genetics, 2021, 140, 1353-1365.	1.8	18
47	A meta-analysis of genome-wide association studies of multiple myeloma among men and women of African ancestry. Blood Advances, 2020, 4, 181-190.	2.5	16
48	Genome-wide meta-analysis and omics integration identifies novel genes associated with diabetic kidney disease. Diabetologia, 2022, 65, 1495-1509.	2.9	16
49	Genetic association with B-cell acute lymphoblastic leukemia in allogeneic transplant patients differs by age and sex. Blood Advances, 2017, 1, 1717-1728.	2.5	15
50	Validation of a multi-ancestry polygenic risk score and age-specific risks of prostate cancer: A meta-analysis within diverse populations. ELife, 0, 11, .	2.8	15
51	Genome-wide association studies identify the role of caspase-9 in kidney disease. Science Advances, 2021, 7, eabi8051.	4.7	14
52	Dnmt3a and Dnmt3b-Decommissioned Fetal Enhancers are Linked to Kidney Disease. Journal of the American Society of Nephrology: JASN, 2020, 31, 765-782.	3.0	13
53	The kidney transcriptome, from single cells to whole organs and back. Current Opinion in Nephrology and Hypertension, 2019, 28, 219-226.	1.0	11
54	Replication and Genetic Risk Score Analysis for Pancreatic Cancer in a Diverse Multiethnic Population. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 2686-2692.	1.1	11

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55	Validation of genetic associations with acute GVHD and nonrelapse mortality in DISCOVeRY-BMT. Blood Advances, 2019, 3, 2337-2341.	2.5	8
56	Genome-Wide Association Analyses Identify Variants in IRF4 Associated With Acute Myeloid Leukemia and Myelodysplastic Syndrome Susceptibility. Frontiers in Genetics, 2021, 12, 554948.	1.1	8
57	Novel genetic variants associated with mortality after unrelated donor allogeneic hematopoietic cell transplantation. EClinicalMedicine, 2021, 40, 101093.	3.2	8
58	Multiple functional variants in the IL1RL1 region are pretransplant markers for risk of GVHD and infection deaths. Blood Advances, 2019, 3, 2512-2524.	2.5	7
59	Combined Donor and Recipient Non-HLA Genotypes Show Evidence of Genome Wide Association with Transplant Related Mortality (TRM) after HLA-Matched Unrelated Donor Blood and Marrow Transplantation (URD-BMT) (DISCOVeRY-BMT study). Blood, 2015, 126, 61-61.	0.6	7
60	Pre-HCT mosaicism increases relapse risk and lowers survival in acute lymphoblastic leukemia patients postâ€“unrelated HCT. Blood Advances, 2021, 5, 66-70.	2.5	6
61	Evidence for Heterogeneous Genetic Associations with Acute Lymphoblastic Leukemia (ALL) By Cytogenetics and Sex in High-Risk Patients Treated with Matched Unrelated Donor Allogeneic Blood or Marrow Transplant (URD-BMT). Blood, 2015, 126, 2621-2621.	0.6	5
62	Prognostic impact of pre-transplant chromosomal aberrations in peripheral blood of patients undergoing unrelated donor hematopoietic cell transplant for acute myeloid leukemia. Scientific Reports, 2021, 11, 15004.	1.6	4
63	Genetic Variants Associated With Mineral Metabolism Traits in Chronic Kidney Disease. Journal of Clinical Endocrinology and Metabolism, 2022, 107, e3866-e3876.	1.8	3
64	Genome-wide association study of pancreatic fat: The Multiethnic Cohort Adiposity Phenotype Study. PLoS ONE, 2021, 16, e0249615.	1.1	2
65	De Novo and Therapy-Related Acute Myeloid Leukemia and Myelodysplastic Syndrome: Similarities and Differences in SNP-Array Detected Chromosomal Aberrations in Pre-Transplant Blood Samples. Blood, 2019, 134, 1430-1430.	0.6	2
66	HLA Haplotypes Are Associated with Multiple Myeloma Risk in the African American Multiple Myeloma Study (AAMMS). Blood, 2016, 128, 3250-3250.	0.6	1
67	Genome-Wide Association Study of Overall and Progression-Free Survival after HLA-Matched Unrelated Donor Blood and Marrow Transplantation (DISCOVeRY-BMT study). Blood, 2015, 126, 397-397.	0.6	1
68	Abstract LB011: Meta-analysis in more than 80,000 men of African ancestry identified nine novel variants associated with prostate cancer. , 2021, , .		0
69	Replication of Candidate SNP Survival Analyses and Gene-Based Tests of Association with Survival Outcomes after an Unrelated Donor Blood or Marrow Transplant: Results from the Discovery-BMT Study. Blood, 2016, 128, 71-71.	0.6	0
70	Exome Array Analyses Identify New Genes Influencing Survival Outcomes after HLA-Matched Unrelated Donor Blood and Marrow Transplantation. Blood, 2016, 128, 518-518.	0.6	0
71	Exome Array Analyses Identify Low-Frequency Germline Variants Associated with Increased Risk of AML in a HLA-Matched Unrelated Donor Blood and Marrow Transplant Population. Blood, 2016, 128, 42-42.	0.6	0
72	Comprehensive Investigation of White Blood Cell and Gene Expression Profiles As Risk Factors for Multiple Myeloma in African Americans. Blood, 2019, 134, 4379-4379.	0.6	0

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73	Genome Wide Interaction Analysis Identifies Expression Quantitative Trait Loci Associated with Reduced Survival after Reduced Intensity Conditioning HLA-Matched Unrelated Donor Allogeneic Hematopoietic Cell Transplant. Blood, 2019, 134, 4595-4595.	0.6	0
74	Meta-Analysis of Genome-Wide Association Studies of Acute Myeloid Leukemia (AML) Patients Identifies Variants Associated with Risk of 11q23/KMT2A-Translocated and Core-Binding Factor (CBF) AML and Suggests a Role for Transcription Elongation in Leukemogenesis. Blood, 2020, 136, 29-30.	0.6	0
75	Population Distribution of GvL and GvH Minor Histocompatibility Antigens. Blood, 2020, 136, 23-25.	0.6	0
76	Associations of Clinical Outcomes after Allogeneic Hematopoietic Cell Transplantation with Number of Predicted Class II Restricted mHA. Blood, 2020, 136, 2-2.	0.6	0
77	Pre-Transplant Clonal Mosaicism Is Associated with Increased Relapse and Lower Survival in Acute Lymphoblastic Leukemia Patients Undergoing Allogeneic Hematopoietic Cell Transplant. Blood, 2020, 136, 9-10.	0.6	0