Kai Yu

List of Publications by Year
in descending order

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133	12,272	57631	26548
papers	citations	44 h-index	107 g-index

136	136	136	17752
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A genome-wide association study identifies alleles in FGFR2 associated with risk of sporadic postmenopausal breast cancer. Nature Genetics, 2007, 39, 870-874.	9.4	1,370
2	Genome-wide association study of prostate cancer identifies a second risk locus at 8q24. Nature Genetics, 2007, 39, 645-649.	9.4	1,059
3	Multiple loci identified in a genome-wide association study of prostate cancer. Nature Genetics, 2008, 40, 310-315.	9.4	871
4	Genome-wide association study of circulating vitamin D levels. Human Molecular Genetics, 2010, 19, 2739-2745.	1.4	700
5	Genome-wide association study identifies variants in the ABO locus associated with susceptibility to pancreatic cancer. Nature Genetics, 2009, 41, 986-990.	9.4	597
6	A genome-wide association study identifies pancreatic cancer susceptibility loci on chromosomes 13q22.1, 1q32.1 and 5p15.33. Nature Genetics, 2010, 42, 224-228.	9.4	539
7	A Genome-wide Association Study of Lung Cancer Identifies a Region of Chromosome 5p15 Associated with Risk for Adenocarcinoma. American Journal of Human Genetics, 2009, 85, 679-691.	2.6	489
8	A multistage genome-wide association study in breast cancer identifies two new risk alleles at 1p11.2 and 14q24.1 (RAD51L1). Nature Genetics, 2009, 41, 579-584.	9.4	487
9	A shared susceptibility locus in PLCE1 at 10q23 for gastric adenocarcinoma and esophageal squamous cell carcinoma. Nature Genetics, 2010, 42, 764-767.	9.4	453
10	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	9.4	408
11	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. Nature Genetics, 2014, 46, 994-1000.	9.4	294
12	Pathway analysis by adaptive combination of Pâ€values. Genetic Epidemiology, 2009, 33, 700-709.	0.6	248
13	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	4.1	235
14	Genome-Wide and Candidate Gene Association Study of Cigarette Smoking Behaviors. PLoS ONE, 2009, 4, e4653.	1.1	226
15	HPV16 E7 Genetic Conservation Is Critical to Carcinogenesis. Cell, 2017, 170, 1164-1174.e6.	13.5	221
16	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. Nature Communications, 2018, 9, 556.	5.8	188
17	Joint analysis of three genome-wide association studies of esophageal squamous cell carcinoma in Chinese populations. Nature Genetics, 2014, 46, 1001-1006.	9.4	148
18	HPV16 Sublineage Associations With Histology-Specific Cancer Risk Using HPV Whole-Genome Sequences in 3200 Women. Journal of the National Cancer Institute, 2016, 108, djw100.	3.0	147

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19	Burden of Nonsynonymous Mutations among TCGA Cancers and Candidate Immune Checkpoint Inhibitor Responses. Cancer Research, 2016, 76, 3767-3772.	0.4	124
20	Improved correction for population stratification in genomeâ€wide association studies by identifying hidden population structures. Genetic Epidemiology, 2008, 32, 215-226.	0.6	123
21	Association of Coffee Drinking With Mortality by Genetic Variation in Caffeine Metabolism. JAMA Internal Medicine, 2018, 178, 1086.	2.6	120
22	Population Substructure and Control Selection in Genome-Wide Association Studies. PLoS ONE, 2008, 3, e2551.	1.1	111
23	Common Genetic Variants and Risk for HPV Persistence and Progression to Cervical Cancer. PLoS ONE, 2010, 5, e8667.	1.1	104
24	Pathway analysis of genome-wide association study data highlights pancreatic development genes as susceptibility factors for pancreatic cancer. Carcinogenesis, 2012, 33, 1384-1390.	1.3	102
25	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	2.6	101
26	Winner's Curse Correction and Variable Thresholding Improve Performance of Polygenic Risk Modeling Based on Genome-Wide Association Study Summary-Level Data. PLoS Genetics, 2016, 12, e1006493.	1.5	98
27	The association of telomere length and genetic variation in telomere biology genesa. Human Mutation, 2010, 31, 1050-1058.	1.1	93
28	Landscape of Combination Immunotherapy and Targeted Therapy to Improve Cancer Management. Cancer Research, 2017, 77, 3666-3671.	0.4	93
29	Two susceptibility loci identified for prostate cancer aggressiveness. Nature Communications, 2015, 6, 6889.	5.8	88
30	Three new pancreatic cancer susceptibility signals identified on chromosomes 1q32.1, 5p15.33 and 8q24.21. Oncotarget, 2016, 7, 66328-66343.	0.8	88
31	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	5.8	86
32	Deep sequencing of HPV16 genomes: A new high-throughput tool for exploring the carcinogenicity and natural history of HPV16 infection. Papillomavirus Research (Amsterdam, Netherlands), 2015, 1, 3-11.	4.5	75
33	Efficient Approximation of Pâ€value of the Maximum of Correlated Tests, with Applications to Genomeâ€Wide Association Studies. Annals of Human Genetics, 2008, 72, 397-406.	0.3	71
34	A comprehensive candidate gene approach identifies genetic variation associated with osteosarcoma. BMC Cancer, 2011, 11, 209.	1.1	69
35	Genetic variants in DNA repair pathway genes and risk of esophageal squamous cell carcinoma and gastric adenocarcinoma in a Chinese population. Carcinogenesis, 2013, 34, 1536-1542.	1.3	68
36	Endogenous Estrogens, Estrogen Metabolites, and Breast Cancer Risk in Postmenopausal Chinese Women. Journal of the National Cancer Institute, 2016, 108, djw103.	3.0	67

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37	Serum Beta Carotene and Overall and Cause-Specific Mortality. Circulation Research, 2018, 123, 1339-1349.	2.0	67
38	Sleep Duration and Cancer in the NIH-AARP Diet and Health Study Cohort. PLoS ONE, 2016, 11, e0161561.	1.1	67
39	A Transcriptome-Wide Association Study Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer. Journal of the National Cancer Institute, 2020, 112, 1003-1012.	3.0	59
40	Massively parallel reporter assays of melanoma risk variants identify MX2 as a gene promoting melanoma. Nature Communications, 2020, 11, 2718.	5.8	53
41	Mutations in the HPV16 genome induced by APOBEC3 are associated with viral clearance. Nature Communications, 2020, 11, 886.	5.8	52
42	Integration of multiethnic fine-mapping and genomic annotation to prioritize candidate functional SNPs at prostate cancer susceptibility regions. Human Molecular Genetics, 2015, 24, 5603-5618.	1.4	50
43	Bayesian Subset Modeling for High-Dimensional Generalized Linear Models. Journal of the American Statistical Association, 2013, 108, 589-606.	1.8	49
44	Genome-wide association study of circulating vitamin Dâ€“binding protein. American Journal of Clinical Nutrition, 2014, 99, 1424-1431.	2.2	49
45	Flexible Design for Following Up Positive Findings. American Journal of Human Genetics, 2007, 81, 540-551.	2.6	47
46	High Prevalence of Screen Detected Prostate Cancer in West Africans: Implications for Racial Disparity of Prostate Cancer. Journal of Urology, 2014, 192, 730-736.	0.2	46
47	A GWAS Meta-analysis and Replication Study Identifies a Novel Locus within CLPTM1L/TERT Associated with Nasopharyngeal Carcinoma in Individuals of Chinese Ancestry. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 188-192.	1.1	45
48	Relationship Between Serum Alpha-Tocopherol and Overall and Cause-Specific Mortality. Circulation Research, 2019, 125, 29-40.	2.0	44
49	Association of <scp>HPV35</scp> with cervical carcinogenesis among women of African ancestry: Evidence of viralâ€host interaction with implications for disease intervention. International Journal of Cancer, 2020, 147, 2677-2686.	2.3	44
50	Fine mapping of a region of chromosome 11q13 reveals multiple independent loci associated with risk of prostate cancer. Human Molecular Genetics, 2011, 20, 2869-2878.	1.4	43
51	Using Principal Components of Genetic Variation for Robust and Powerful Detection of Gene-Gene Interactions in Case-Control and Case-Only Studies. American Journal of Human Genetics, 2010, 86, 331-342.	2.6	41
52	Pesticide Use Modifies the Association Between Genetic Variants on Chromosome 8q24 and Prostate Cancer. Cancer Research, 2010, 70, 9224-9233.	0.4	41
53	Single Nucleotide Polymorphisms in the PRDX3 and RPS19 and Risk of HPV Persistence and Cervical Precancer/Cancer. PLoS ONE, 2012, 7, e33619.	1.1	37
54	MAX-rank: a simple and robust genome-wide scan for case-control association studies. Human Genetics, 2008, 123, 617-623.	1.8	36

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55	Using covariate-specific disease prevalence information to increase the power of case-control studies. Biometrika, 2015, 102, 169-180.	1.3	36
56	Adolescent age at first pregnancy and subsequent obesity. Paediatric and Perinatal Epidemiology, 1997, 11, 130-141.	0.8	34
57	A Powerful Procedure for Pathway-Based Meta-analysis Using Summary Statistics Identifies 43 Pathways Associated with Type II Diabetes in European Populations. PLoS Genetics, 2016, 12, e1006122.	1.5	34
58	Individual Variations in Serum Melatonin Levels through Time: Implications for Epidemiologic Studies. PLoS ONE, 2013, 8, e83208.	1.1	32
59	Circulating 25-hydroxyvitamin D up to 3Âdecades prior to diagnosis in relation to overall and organ-specific cancer survival. European Journal of Epidemiology, 2018, 33, 1087-1099.	2.5	32
60	Genetic variants in sex hormone metabolic pathway genes and risk of esophageal squamous cell carcinoma. Carcinogenesis, 2013, 34, 1062-1068.	1.3	31
61	Vitamin D Metabolic Pathway Genes and Pancreatic Cancer Risk. PLoS ONE, 2015, 10, e0117574.	1.1	29
62	Large-scale fine mapping of the HNF1B locus and prostate cancer risk. Human Molecular Genetics, 2011, 20, 3322-3329.	1.4	28
63	Calibration and seasonal adjustment for matched caseâ€“control studies of vitamin D and cancer. Statistics in Medicine, 2016, 35, 2133-2148.	0.8	28
64	Inherited variation in circadian rhythm genes and risks of prostate cancer and three other cancer sites in combined cancer consortia. International Journal of Cancer, 2017, 141, 1794-1802.	2.3	28
65	Telomere length and variation in telomere biology genes in individuals with osteosarcoma. International Journal of Molecular Epidemiology and Genetics, 2011, 2, 19-29.	0.4	27
66	Genetic variants in fas signaling pathway genes and risk of gastric cancer. International Journal of Cancer, 2014, 134, 822-831.	2.3	26
67	Generalized integration model for improved statistical inference by leveraging external summary data. Biometrika, 2020, 107, 689-703.	1.3	26
68	Power calculation for the general twoâ€sample Mendelian randomization analysis. Genetic Epidemiology, 2020, 44, 290-299.	0.6	25
69	Using Tree-Based Recursive Partitioning Methods to Group Haplotypes for Increased Power in Association Studies. Annals of Human Genetics, 2005, 69, 577-589.	0.3	24
70	Human Leukocyte Antigen Class I and II Alleles and Cervical Adenocarcinoma. Frontiers in Oncology, 2014, 4, 119.	1.3	23
71	A partially linear tree-based regression model for assessing complex joint geneâ€“gene and geneâ€“environment effects. Genetic Epidemiology, 2007, 31, 238-251.	0.6	22
72	Robust Tests for Singleâ€marker Analysis in Caseâ€Control Genetic Association Studies. Annals of Human Genetics, 2009, 73, 245-252.	0.3	21

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73	Agnostic Pathway/Gene Set Analysis of Genome-Wide Association Data Identifies Associations for Pancreatic Cancer. Journal of the National Cancer Institute, 2019, 111, 557-567.	3.0	21
74	A Flexible Bayesian Model for Studying Geneâ€“Environment Interaction. PLoS Genetics, 2012, 8, e1002482.	1.5	20
75	Vitamin Dâ€“Associated Genetic Variation and Risk of Breast Cancer in the Breast and Prostate Cancer Cohort Consortium (BPC3). Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 627-630.	1.1	20
76	Genetic background comparison using distanceâ€based regression, with applications in population stratification evaluation and adjustment. Genetic Epidemiology, 2009, 33, 432-441.	0.6	19
77	A fast multilocus test with adaptive SNP selection for large-scale genetic-association studies. European Journal of Human Genetics, 2014, 22, 696-702.	1.4	19
78	Pathway,in silicoand tissue-specific expression quantitative analyses of oesophageal squamous cell carcinoma genome-wide association studies data. International Journal of Epidemiology, 2016, 45, 206-220.	0.9	19
79	Proof-of-principle study of a novel cervical screening and triage strategy: Computer-analyzed cytology to decide which HPV-positive women are likely to have â‰¥CIN2. International Journal of Cancer, 2017, 140, 718-725.	2.3	19
80	A Prospective Study of Serum Vitamin E and 28-Year Risk of Lung Cancer. Journal of the National Cancer Institute, 2020, 112, 191-199.	3.0	18
81	Genetic Variants in Epidermal Growth Factor Receptor Pathway Genes and Risk of Esophageal Squamous Cell Carcinoma and Gastric Cancer in a Chinese Population. PLoS ONE, 2013, 8, e68999.	1.1	17
82	Robust joint analysis allowing for model uncertainty in two-stage genetic association studies. BMC Bioinformatics, 2011, 12, 9.	1.2	16
83	Efficient p-value evaluation for resampling-based tests. Biostatistics, 2011, 12, 582-593.	0.9	16
84	Prospective study of <scp>H</scp>elicobacter pylori antigens and gastric noncardia cancer risk in the nutrition intervention trial cohort. International Journal of Cancer, 2015, 137, 1938-1946.	2.3	16
85	Genetic Admixture and Population Substructure in Guanacaste Costa Rica. PLoS ONE, 2010, 5, e13336.	1.1	16
86	Tuberculosis infection and lung adenocarcinoma: Mendelian randomization and pathway analysis of genome-wide association study data from never-smoking Asian women. Genomics, 2020, 112, 1223-1232.	1.3	15
87	Association between serum retinol and overall and cause-specific mortality in a 30-year prospective cohort study. Nature Communications, 2021, 12, 6418.	5.8	15
88	Variants Associated with Susceptibility to Pancreatic Cancer and Melanoma Do Not Reciprocally Affect Risk. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1121-1124.	1.1	14
89	Common genetic variants in epigenetic machinery genes and risk of upper gastrointestinal cancers. International Journal of Epidemiology, 2015, 44, 1341-1352.	0.9	13
90	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	1.1	12

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91	Automated Cervical Screening and Triage, Based on HPV Testing and Computer-Interpreted Cytology. Journal of the National Cancer Institute, 2018, 110, 1222-1228.	3.0	12
92	Does changing paternity contribute to the risk of intrauterine growth retardation?. Paediatric and Perinatal Epidemiology, 1997, 11, 41-47.	0.8	11
93	A Haplotype Similarity Based Transmission/Disequilibrium Test under Founder Heterogeneity. Annals of Human Genetics, 2005, 69, 455-467.	0.3	11
94	A Partially Linear Treeâ€based Regression Model for Multivariate Outcomes. Biometrics, 2010, 66, 89-96.	0.8	11
95	Diurnal variation of metabolites in three individual participants. Chronobiology International, 2019, 36, 332-342.	0.9	10
96	Using Hierarchical Cluster Models to Systematically Identify Groups of Jobs With Similar Occupational Questionnaire Response Patterns to Assist Rule-Based Expert Exposure Assessment in Population-Based Studies. Annals of Occupational Hygiene, 2015, 59, 455-66.	1.9	9
97	Hepcidin-regulating iron metabolism genes and pancreatic ductal adenocarcinoma: a pathway analysis of genome-wide association studies. American Journal of Clinical Nutrition, 2021, 114, 1408-1417.	2.2	9
98	Altered regulation of DPF3, a member of the SWI/SNF complexes, underlies the 14q24 renal cancer susceptibility locus. American Journal of Human Genetics, 2021, 108, 1590-1610.	2.6	9
99	Prediagnostic Serum Vitamin D, Vitamin D Binding Protein Isoforms, and Cancer Survival. JNCI Cancer Spectrum, 2022, 6, .	1.4	9
100	Two-sample Comparison Based on Prediction Error, with Applications to Candidate Gene Association Studies. Annals of Human Genetics, 2007, 71, 107-118.	0.3	8
101	The association between inflammationâ€related genes and serum androgen levels in men: The prostate, lung, colorectal, and ovarian study. Prostate, 2012, 72, 65-71.	1.2	8
102	ABO genotypes and the risk of esophageal and gastric cancers. BMC Cancer, 2021, 21, 589.	1.1	8
103	Global transmission/disequilibrium tests based on haplotype sharing in multiple candidate genes. Genetic Epidemiology, 2005, 29, 323-335.	0.6	7
104	Comparison of Ordinal and Nominal Classification Trees to Predict Ordinal Expert-Based Occupational Exposure Estimates in a Caseâ€“Control Study. Annals of Occupational Hygiene, 2014, 59, 324-35.	1.9	7
105	On Mendelian randomization analysis of caseâ€control study. Biometrics, 2020, 76, 380-391.	0.8	7
106	Approximation of bias and meanâ€squared error in twoâ€sample Mendelian randomization analyses. Biometrics, 2020, 76, 369-379.	0.8	7
107	Phylogenomic Analysis of Human Papillomavirus Type 31 and Cervical Carcinogenesis: A Study of 2093 Viral Genomes. Viruses, 2021, 13, 1948.	1.5	7
108	Comprehensive analysis based in silico study of organophosphate flame retardants - environmental explanation of bladder cancer progression. Environmental Toxicology and Pharmacology, 2022, 92, 103851.	2.0	7

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109	Relationship between chocolate consumption and overall and cause-specific mortality, systematic review and updated meta-analysis. European Journal of Epidemiology, 2022, 37, 321-333.	2.5	7
110	Pathway Analysis of Renal Cell Carcinoma Genome-Wide Association Studies Identifies Novel Associations. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 2065-2069.	1.1	6
111	Mendelian Randomization Analysis of n-6 Polyunsaturated Fatty Acid Levels and Pancreatic Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 2735-2739.	1.1	6
112	Statistical inference on the penetrances of rare genetic mutations based on a case-family design. Biostatistics, 2010, 11, 519-532.	0.9	5
113	Measuring serum melatonin in postmenopausal women: Implications for epidemiologic studies and breast cancer studies. PLoS ONE, 2018, 13, e0195666.	1.1	5
114	Evaluation of Rare and Common Variants from Suspected Familial or Sporadic Nasopharyngeal Carcinoma (NPC) Susceptibility Genes in Sporadic NPC. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 1682-1686.	1.1	5
115	Genome-Wide Association Study Data Reveal Genetic Susceptibility to Chronic Inflammatory Intestinal Diseases and Pancreatic Ductal Adenocarcinoma Risk. Cancer Research, 2020, 80, 4004-4013.	0.4	5
116	Age-Dependent Cancer Risk Is Not Different in betweenMSH2andMLH1Mutation Carriers. Journal of Cancer Epidemiology, 2009, 2009, 1-6.	0.5	4
117	Polymorphisms in genes related to one-carbon metabolism are not related to pancreatic cancer in PanScan and PanC4. Cancer Causes and Control, 2013, 24, 595-602.	0.8	4
118	A fast and powerful tree-based association test for detecting complex joint effects in caseâ€“control studies. Bioinformatics, 2014, 30, 2171-2178.	1.8	4
119	Inference of non-centrality parameter of a truncated non-central chi-squared distribution. Journal of Statistical Planning and Inference, 2009, 139, 2431-2444.	0.4	3
120	Stochastic approximation Monte Carlo importance sampling for approximating exact conditional probabilities. Statistics and Computing, 2014, 24, 505-520.	0.8	3
121	Retrospective versus prospective score tests for genetic association with caseâ€control data. Biometrics, 2021, 77, 102-112.	0.8	3
122	The limiting bound of Efron's W-formula for hypothesis testing when a nuisance parameter is present only under the alternative. Journal of Statistical Planning and Inference, 2010, 140, 1610-1617.	0.4	2
123	Proper joint analysis of summary association statistics requires the adjustment of heterogeneity in SNP coverage pattern. Briefings in Bioinformatics, 2018, 19, 1337-1343.	3.2	2
124	Integrative analysis of multiple caseâ€control studies. Biometrics, 2022, 78, 1080-1091.	0.8	2
125	Approximating probabilities of correlated events. Science China Mathematics, 2010, 53, 2937-2948.	0.8	1
126	Improved genetic association tests for an ordinal outcome representing the disease progression process. Genetic Epidemiology, 2011, 35, n/a-n/a.	0.6	1

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127	A robust association test for detecting genetic variants with heterogeneous effects. Biostatistics, 2015, 16, 5-16.	0.9	1
128	A hybrid parametric and empirical likelihood model for evaluating interactions in case-control studies. Statistics and Its Interface, 2016, 9, 147-158.	0.2	1
129	Semiparametric inference on the penetrances of rare genetic mutations based on a case-family design. Journal of Statistical Planning and Inference, 2013, 143, 368-377.	0.4	0
130	A multi-locus genetic association test for a dichotomous trait and its secondary phenotype. Statistical Methods in Medical Research, 2018, 27, 1464-1475.	0.7	0
131	A Pathway Analysis of Hereditary Hemochromatosis-related Genes and Pancreatic Ductal Adenocarcinoma Risk (FS11-05-19). Current Developments in Nutrition, 2019, 3, nzz037.FS11-05-19.	0.1	0
132	Serum 25â€hydroxyvitamin D and lung cancer risk. FASEB Journal, 2011, 25, 214.7.	0.2	0
133	Abstract P3-01-26: Mammographic density in relation to breast cancer risk factors among Chinese women. Cancer Research, 2022, 82, P3-01-26-P3-01-26.	0.4	0