Kai Yu

List of Publications by Year
in descending order

133 papers	12,272 citations	57758 44 h-index	26613 107 g-index
136 all docs	136 docs citations	136 times ranked	17752 citing authors

#	Article	IF	Citations
1	Integrative analysis of multiple caseâ€control studies. Biometrics, 2022, 78, 1080-1091.	1.4	2
2	Prediagnostic Serum Vitamin D, Vitamin D Binding Protein Isoforms, and Cancer Survival. JNCI Cancer Spectrum, 2022, 6, .	2.9	9
3	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.	0.9	0
4	Comprehensive analysis based in silico study of organophosphate flame retardants - environmental explanation of bladder cancer progression. Environmental Toxicology and Pharmacology, 2022, 92, 103851.	4.0	7
5	Relationship between chocolate consumption and overall and cause-specific mortality, systematic review and updated meta-analysis. European Journal of Epidemiology, 2022, 37, 321-333.	5.7	7
6	Retrospective versus prospective score tests for genetic association with caseâ€control data. Biometrics, 2021, 77, 102-112.	1.4	3
7	ABO genotypes and the risk of esophageal and gastric cancers. BMC Cancer, 2021, 21, 589.	2.6	8
8	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.	4.7	9
9	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.	6.2	9
10	Phylogenomic Analysis of Human Papillomavirus Type 31 and Cervical Carcinogenesis: A Study of 2093 Viral Genomes. Viruses, 2021, 13, 1948.	3.3	7
11	Association between serum retinol and overall and cause-specific mortality in a 30-year prospective cohort study. Nature Communications, 2021, 12, 6418.	12.8	15
12	A Prospective Study of Serum Vitamin E and 28-Year Risk of Lung Cancer. Journal of the National Cancer Institute, 2020, 112, 191-199.	6.3	18
13	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.	2.9	15
14	On Mendelian randomization analysis of caseâ€control study. Biometrics, 2020, 76, 380-391.	1.4	7
15	Approximation of bias and meanâ€squared error in twoâ€sample Mendelian randomization analyses. Biometrics, 2020, 76, 369-379.	1.4	7
16	A Transcriptome-Wide Association Study Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer. Journal of the National Cancer Institute, 2020, 112, 1003-1012.	6.3	59
17	Pathway Analysis of Renal Cell Carcinoma Genome-Wide Association Studies Identifies Novel Associations. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 2065-2069.	2.5	6
18	Mendelian Randomization Analysis of n-6 Polyunsaturated Fatty Acid Levels and Pancreatic Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 2735-2739.	2.5	6

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19	Generalized integration model for improved statistical inference by leveraging external summary data. Biometrika, 2020, 107, 689-703.	2.4	26
20	Massively parallel reporter assays of melanoma risk variants identify MX2 as a gene promoting melanoma. Nature Communications, 2020, 11, 2718.	12.8	53
21	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.	5.1	44
22	Genome-Wide Association Study Data Reveal Genetic Susceptibility to Chronic Inflammatory Intestinal Diseases and Pancreatic Ductal Adenocarcinoma Risk. Cancer Research, 2020, 80, 4004-4013.	0.9	5
23	Mutations in the HPV16 genome induced by APOBEC3 are associated with viral clearance. Nature Communications, 2020, 11, 886.	12.8	52
24	Power calculation for the general twoâ€sample Mendelian randomization analysis. Genetic Epidemiology, 2020, 44, 290-299.	1.3	25
25	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.	0.3	0
26	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.	2.5	5
27	Relationship Between Serum Alpha-Tocopherol and Overall and Cause-Specific Mortality. Circulation Research, 2019, 125, 29-40.	4.5	44
28	Diurnal variation of metabolites in three individual participants. Chronobiology International, 2019, 36, 332-342.	2.0	10
29	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.	6.3	21
30	Automated Cervical Screening and Triage, Based on HPV Testing and Computer-Interpreted Cytology. Journal of the National Cancer Institute, 2018, 110, 1222-1228.	6.3	12
31	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. Nature Communications, 2018, 9, 556.	12.8	188
32	A multi-locus genetic association test for a dichotomous trait and its secondary phenotype. Statistical Methods in Medical Research, 2018, 27, 1464-1475.	1.5	0
33	Proper joint analysis of summary association statistics requires the adjustment of heterogeneity in SNP coverage pattern. Briefings in Bioinformatics, 2018, 19, 1337-1343.	6.5	2
34	Serum Beta Carotene and Overall and Cause-Specific Mortality. Circulation Research, 2018, 123, 1339-1349.	4.5	67
35	Association of Coffee Drinking With Mortality by Genetic Variation in Caffeine Metabolism. JAMA Internal Medicine, 2018, 178, 1086.	5.1	120
36	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.	5.7	32

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37	Measuring serum melatonin in postmenopausal women: Implications for epidemiologic studies and breast cancer studies. PLoS ONE, 2018, 13, e0195666.	2.5	5
38	Landscape of Combination Immunotherapy and Targeted Therapy to Improve Cancer Management. Cancer Research, 2017, 77, 3666-3671.	0.9	93
39	HPV16 E7 Genetic Conservation Is Critical to Carcinogenesis. Cell, 2017, 170, 1164-1174.e6.	28.9	221
40	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.	5.1	28
41	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.	5.1	19
42	Three new pancreatic cancer susceptibility signals identified on chromosomes 1q32.1, 5p15.33 and 8q24.21. Oncotarget, 2016, 7, 66328-66343.	1.8	88
43	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	2.5	12
44	Calibration and seasonal adjustment for matched caseâ€“control studies of vitamin D and cancer. Statistics in Medicine, 2016, 35, 2133-2148.	1.6	28
45	Endogenous Estrogens, Estrogen Metabolites, and Breast Cancer Risk in Postmenopausal Chinese Women. Journal of the National Cancer Institute, 2016, 108, djw103.	6.3	67
46	Burden of Nonsynonymous Mutations among TCGA Cancers and Candidate Immune Checkpoint Inhibitor Responses. Cancer Research, 2016, 76, 3767-3772.	0.9	124
47	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.	6.3	147
48	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	12.8	86
49	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.	1.9	19
50	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.	2.5	45
51	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.	3.5	34
52	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.	3.5	98
53	Sleep Duration and Cancer in the NIH-AARP Diet and Health Study Cohort. PLoS ONE, 2016, 11, e0161561.	2.5	67
54	A hybrid parametric and empirical likelihood model for evaluating interactions in case-control studies. Statistics and Its Interface, 2016, 9, 147-158.	0.3	1

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55	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
56	Vitamin D Metabolic Pathway Genes and Pancreatic Cancer Risk. PLoS ONE, 2015, 10, e0117574.	2.5	29
57	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	6.2	101
58	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.	2.5	20
59	Using covariate-specific disease prevalence information to increase the power of case-control studies. Biometrika, 2015, 102, 169-180.	2.4	36
60	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
61	A robust association test for detecting genetic variants with heterogeneous effects. Biostatistics, 2015, 16, 5-16.	1.5	1
62	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.	2.9	50
63	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.	5.1	16
64	Two susceptibility loci identified for prostate cancer aggressiveness. Nature Communications, 2015, 6, 6889.	12.8	88
65	Common genetic variants in epigenetic machinery genes and risk of upper gastrointestinal cancers. International Journal of Epidemiology, 2015, 44, 1341-1352.	1.9	13
66	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	7.9	235
67	Human Leukocyte Antigen Class I and II Alleles and Cervical Adenocarcinoma. Frontiers in Oncology, 2014, 4, 119.	2.8	23
68	A fast and powerful tree-based association test for detecting complex joint effects in caseâ€"control studies. Bioinformatics, 2014, 30, 2171-2178.	4.1	4
69	Variants Associated with Susceptibility to Pancreatic Cancer and Melanoma Do Not Reciprocally Affect Risk. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1121-1124.	2.5	14
70	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
71	A fast multilocus test with adaptive SNP selection for large-scale genetic-association studies. European Journal of Human Genetics, 2014, 22, 696-702.	2.8	19
72	Stochastic approximation Monte Carlo importance sampling for approximating exact conditional probabilities. Statistics and Computing, 2014, 24, 505-520.	1.5	3

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73	Genetic variants in fas signaling pathway genes and risk of gastric cancer. International Journal of Cancer, 2014, 134, 822-831.	5.1	26
74	Genome-wide association study of circulating vitamin Dâ€"binding protein. American Journal of Clinical Nutrition, 2014, 99, 1424-1431.	4.7	49
75	Joint analysis of three genome-wide association studies of esophageal squamous cell carcinoma in Chinese populations. Nature Genetics, 2014, 46, 1001-1006.	21.4	148
76	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. Nature Genetics, 2014, 46, 994-1000.	21.4	294
77	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	21.4	408
78	High Prevalence of Screen Detected Prostate Cancer in West Africans: Implications for Racial Disparity of Prostate Cancer. Journal of Urology, 2014, 192, 730-736.	0.4	46
79	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.	2.8	68
80	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.	0.6	0
81	Bayesian Subset Modeling for High-Dimensional Generalized Linear Models. Journal of the American Statistical Association, 2013, 108, 589-606.	3.1	49
82	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.	1.8	4
83	Genetic variants in sex hormone metabolic pathway genes and risk of esophageal squamous cell carcinoma. Carcinogenesis, 2013, 34, 1062-1068.	2.8	31
84	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.	2.5	17
85	Individual Variations in Serum Melatonin Levels through Time: Implications for Epidemiologic Studies. PLoS ONE, 2013, 8, e83208.	2.5	32
86	A Flexible Bayesian Model for Studying Geneâ€"Environment Interaction. PLoS Genetics, 2012, 8, e1002482.	3.5	20
87	Pathway analysis of genome-wide association study data highlights pancreatic development genes as susceptibility factors for pancreatic cancer. Carcinogenesis, 2012, 33, 1384-1390.	2.8	102
88	The association between inflammationâ€related genes and serum androgen levels in men: The prostate, lung, colorectal, and ovarian study. Prostate, 2012, 72, 65-71.	2.3	8
89	Single Nucleotide Polymorphisms in the PRDX3 and RPS19 and Risk of HPV Persistence and Cervical Precancer/Cancer. PLoS ONE, 2012, 7, e33619.	2.5	37
90	A comprehensive candidate gene approach identifies genetic variation associated with osteosarcoma. BMC Cancer, 2011, 11, 209.	2.6	69

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91	Robust joint analysis allowing for model uncertainty in two-stage genetic association studies. BMC Bioinformatics, 2011, 12, 9.	2.6	16
92	Improved genetic association tests for an ordinal outcome representing the disease progression process. Genetic Epidemiology, 2011, 35, n/a-n/a.	1.3	1
93	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.	2.9	43
94	Large-scale fine mapping of the HNF1B locus and prostate cancer risk. Human Molecular Genetics, 2011, 20, 3322-3329.	2.9	28
95	Efficient p-value evaluation for resampling-based tests. Biostatistics, 2011, 12, 582-593.	1.5	16
96	Serum 25â€hydroxyvitamin D and lung cancer risk. FASEB Journal, 2011, 25, 214.7.	0.5	0
97	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
98	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.	6.2	41
99	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.	0.6	2
100	Approximating probabilities of correlated events. Science China Mathematics, 2010, 53, 2937-2948.	1.7	1
101	The association of telomere length and genetic variation in telomere biology genesa. Human Mutation, 2010, 31, 1050-1058.	2.5	93
102	A Partially Linear Treeâ€based Regression Model for Multivariate Outcomes. Biometrics, 2010, 66, 89-96.	1.4	11
103	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.	21.4	539
104	A shared susceptibility locus in PLCE1 at 10q23 for gastric adenocarcinoma and esophageal squamous cell carcinoma. Nature Genetics, 2010, 42, 764-767.	21.4	453
105	Common Genetic Variants and Risk for HPV Persistence and Progression to Cervical Cancer. PLoS ONE, 2010, 5, e8667.	2.5	104
106	Genome-wide association study of circulating vitamin D levels. Human Molecular Genetics, 2010, 19, 2739-2745.	2.9	700
107	Pesticide Use Modifies the Association Between Genetic Variants on Chromosome 8q24 and Prostate Cancer. Cancer Research, 2010, 70, 9224-9233.	0.9	41
108	Statistical inference on the penetrances of rare genetic mutations based on a case-family design. Biostatistics, 2010, 11, 519-532.	1.5	5

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109	Genetic Admixture and Population Substructure in Guanacaste Costa Rica. PLoS ONE, 2010, 5, e13336.	2.5	16
110	Genome-Wide and Candidate Gene Association Study of Cigarette Smoking Behaviors. PLoS ONE, 2009, 4, e4653.	2.5	226
111	Age-Dependent Cancer Risk Is Not Different in betweenMSH2andMLH1Mutation Carriers. Journal of Cancer Epidemiology, 2009, 2009, 1-6.	1.1	4
112	Genetic background comparison using distanceâ€based regression, with applications in population stratification evaluation and adjustment. Genetic Epidemiology, 2009, 33, 432-441.	1.3	19
113	Pathway analysis by adaptive combination of Pâ€values. Genetic Epidemiology, 2009, 33, 700-709.	1.3	248
114	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.	21.4	487
115	Genome-wide association study identifies variants in the ABO locus associated with susceptibility to pancreatic cancer. Nature Genetics, 2009, 41, 986-990.	21.4	597
116	Robust Tests for Singleâ€marker Analysis in Caseâ€Control Genetic Association Studies. Annals of Human Genetics, 2009, 73, 245-252.	0.8	21
117	Inference of non-centrality parameter of a truncated non-central chi-squared distribution. Journal of Statistical Planning and Inference, 2009, 139, 2431-2444.	0.6	3
118	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.	6.2	489
119	MAX-rank: a simple and robust genome-wide scan for case-control association studies. Human Genetics, 2008, 123, 617-623.	3.8	36
120	Improved correction for population stratification in genomeâ€wide association studies by identifying hidden population structures. Genetic Epidemiology, 2008, 32, 215-226.	1.3	123
121	Multiple loci identified in a genome-wide association study of prostate cancer. Nature Genetics, 2008, 40, 310-315.	21.4	871
122	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.	0.8	71
123	Population Substructure and Control Selection in Genome-Wide Association Studies. PLoS ONE, 2008, 3, e2551.	2.5	111
124	Flexible Design for Following Up Positive Findings. American Journal of Human Genetics, 2007, 81, 540-551.	6.2	47
125	A partially linear tree-based regression model for assessing complex joint geneâ€"gene and geneâ€"environment effects. Genetic Epidemiology, 2007, 31, 238-251.	1.3	22
126	Genome-wide association study of prostate cancer identifies a second risk locus at 8q24. Nature Genetics, 2007, 39, 645-649.	21.4	1,059

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127	A genome-wide association study identifies alleles in FGFR2 associated with risk of sporadic postmenopausal breast cancer. Nature Genetics, 2007, 39, 870-874.	21.4	1,370
128	Two-sample Comparison Based on Prediction Error, with Applications to Candidate Gene Association Studies. Annals of Human Genetics, 2007, 71, 107-118.	0.8	8
129	Using Tree-Based Recursive Partitioning Methods to Group Haplotypes for Increased Power in Association Studies. Annals of Human Genetics, 2005, 69, 577-589.	0.8	24
130	Global transmission/disequilibrium tests based on haplotype sharing in multiple candidate genes. Genetic Epidemiology, 2005, 29, 323-335.	1.3	7
131	A Haplotype Similarity Based Transmission/Disequilibrium Test under Founder Heterogeneity. Annals of Human Genetics, 2005, 69, 455-467.	0.8	11
132	Adolescent age at first pregnancy and subsequent obesity. Paediatric and Perinatal Epidemiology, 1997, 11, 130-141.	1.7	34
133	Does changing paternity contribute to the risk of intrauterine growth retardation?. Paediatric and Perinatal Epidemiology, 1997, 11, 41-47.	1.7	11