

# Kai Yu

## List of Publications by Year in descending order

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Version: 2024-02-01

133  
papers

12,272  
citations

57631

44  
h-index

26548

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. <i>Biometrics</i> , 2022, 78, 1080-1091.	0.8	2
2	Prediagnostic Serum Vitamin D, Vitamin D Binding Protein Isoforms, and Cancer Survival. <i>JNCI Cancer Spectrum</i> , 2022, 6, .	1.4	9
3	Abstract P3-01-26: Mammographic density in relation to breast cancer risk factors among Chinese women. <i>Cancer Research</i> , 2022, 82, P3-01-26-P3-01-26.	0.4	0
4	Comprehensive analysis based in silico study of organophosphate flame retardants - environmental explanation of bladder cancer progression. <i>Environmental Toxicology and Pharmacology</i> , 2022, 92, 103851.	2.0	7
5	Relationship between chocolate consumption and overall and cause-specific mortality, systematic review and updated meta-analysis. <i>European Journal of Epidemiology</i> , 2022, 37, 321-333.	2.5	7
6	Retrospective versus prospective score tests for genetic association with caseâ€control data. <i>Biometrics</i> , 2021, 77, 102-112.	0.8	3
7	ABO genotypes and the risk of esophageal and gastric cancers. <i>BMC Cancer</i> , 2021, 21, 589.	1.1	8
8	Hepcidin-regulating iron metabolism genes and pancreatic ductal adenocarcinoma: a pathway analysis of genome-wide association studies. <i>American Journal of Clinical Nutrition</i> , 2021, 114, 1408-1417.	2.2	9
9	Altered regulation of DPF3, a member of the SWI/SNF complexes, underlies the 14q24 renal cancer susceptibility locus. <i>American Journal of Human Genetics</i> , 2021, 108, 1590-1610.	2.6	9
10	Phylogenomic Analysis of Human Papillomavirus Type 31 and Cervical Carcinogenesis: A Study of 2093 Viral Genomes. <i>Viruses</i> , 2021, 13, 1948.	1.5	7
11	Association between serum retinol and overall and cause-specific mortality in a 30-year prospective cohort study. <i>Nature Communications</i> , 2021, 12, 6418.	5.8	15
12	A Prospective Study of Serum Vitamin E and 28-Year Risk of Lung Cancer. <i>Journal of the National Cancer Institute</i> , 2020, 112, 191-199.	3.0	18
13	Tuberculosis infection and lung adenocarcinoma: Mendelian randomization and pathway analysis of genome-wide association study data from never-smoking Asian women. <i>Genomics</i> , 2020, 112, 1223-1232.	1.3	15
14	On Mendelian randomization analysis of caseâ€control study. <i>Biometrics</i> , 2020, 76, 380-391.	0.8	7
15	Approximation of bias and meanâ€squared error in twoâ€sample Mendelian randomization analyses. <i>Biometrics</i> , 2020, 76, 369-379.	0.8	7
16	A Transcriptome-Wide Association Study Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer. <i>Journal of the National Cancer Institute</i> , 2020, 112, 1003-1012.	3.0	59
17	Pathway Analysis of Renal Cell Carcinoma Genome-Wide Association Studies Identifies Novel Associations. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 2065-2069.	1.1	6
18	Mendelian Randomization Analysis of n-6 Polyunsaturated Fatty Acid Levels and Pancreatic Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 2735-2739.	1.1	6

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19	Generalized integration model for improved statistical inference by leveraging external summary data. <i>Biometrika</i> , 2020, 107, 689-703.	1.3	26
20	Massively parallel reporter assays of melanoma risk variants identify MX2 as a gene promoting melanoma. <i>Nature Communications</i> , 2020, 11, 2718.	5.8	53
21	Association of <scp>HPV35</scp> with cervical carcinogenesis among women of African ancestry: Evidence of viral-host interaction with implications for disease intervention. <i>International Journal of Cancer</i> , 2020, 147, 2677-2686.	2.3	44
22	Genome-Wide Association Study Data Reveal Genetic Susceptibility to Chronic Inflammatory Intestinal Diseases and Pancreatic Ductal Adenocarcinoma Risk. <i>Cancer Research</i> , 2020, 80, 4004-4013.	0.4	5
23	Mutations in the HPV16 genome induced by APOBEC3 are associated with viral clearance. <i>Nature Communications</i> , 2020, 11, 886.	5.8	52
24	Power calculation for the general two-sample Mendelian randomization analysis. <i>Genetic Epidemiology</i> , 2020, 44, 290-299.	0.6	25
25	A Pathway Analysis of Hereditary Hemochromatosis-related Genes and Pancreatic Ductal Adenocarcinoma Risk (FS11-05-19). <i>Current Developments in Nutrition</i> , 2019, 3, nzz037.FS11-05-19.	0.1	0
26	Evaluation of Rare and Common Variants from Suspected Familial or Sporadic Nasopharyngeal Carcinoma (NPC) Susceptibility Genes in Sporadic NPC. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 1682-1686.	1.1	5
27	Relationship Between Serum Alpha-Tocopherol and Overall and Cause-Specific Mortality. <i>Circulation Research</i> , 2019, 125, 29-40.	2.0	44
28	Diurnal variation of metabolites in three individual participants. <i>Chronobiology International</i> , 2019, 36, 332-342.	0.9	10
29	Agnostic Pathway/Gene Set Analysis of Genome-Wide Association Data Identifies Associations for Pancreatic Cancer. <i>Journal of the National Cancer Institute</i> , 2019, 111, 557-567.	3.0	21
30	Automated Cervical Screening and Triage, Based on HPV Testing and Computer-Interpreted Cytology. <i>Journal of the National Cancer Institute</i> , 2018, 110, 1222-1228.	3.0	12
31	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. <i>Nature Communications</i> , 2018, 9, 556.	5.8	188
32	A multi-locus genetic association test for a dichotomous trait and its secondary phenotype. <i>Statistical Methods in Medical Research</i> , 2018, 27, 1464-1475.	0.7	0
33	Proper joint analysis of summary association statistics requires the adjustment of heterogeneity in SNP coverage pattern. <i>Briefings in Bioinformatics</i> , 2018, 19, 1337-1343.	3.2	2
34	Serum Beta Carotene and Overall and Cause-Specific Mortality. <i>Circulation Research</i> , 2018, 123, 1339-1349.	2.0	67
35	Association of Coffee Drinking With Mortality by Genetic Variation in Caffeine Metabolism. <i>JAMA Internal Medicine</i> , 2018, 178, 1086.	2.6	120
36	Circulating 25-hydroxyvitamin D up to 3 decades prior to diagnosis in relation to overall and organ-specific cancer survival. <i>European Journal of Epidemiology</i> , 2018, 33, 1087-1099.	2.5	32

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37	Measuring serum melatonin in postmenopausal women: Implications for epidemiologic studies and breast cancer studies. <i>PLoS ONE</i> , 2018, 13, e0195666.	1.1	5
38	Landscape of Combination Immunotherapy and Targeted Therapy to Improve Cancer Management. <i>Cancer Research</i> , 2017, 77, 3666-3671.	0.4	93
39	HPV16 E7 Genetic Conservation Is Critical to Carcinogenesis. <i>Cell</i> , 2017, 170, 1164-1174.e6.	13.5	221
40	Inherited variation in circadian rhythm genes and risks of prostate cancer and three other cancer sites in combined cancer consortia. <i>International Journal of Cancer</i> , 2017, 141, 1794-1802.	2.3	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 CIN2. <i>International Journal of Cancer</i> , 2017, 140, 718-725.	2.3	19
42	Three new pancreatic cancer susceptibility signals identified on chromosomes 1q32.1, 5p15.33 and 8q24.21. <i>Oncotarget</i> , 2016, 7, 66328-66343.	0.8	88
43	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. <i>PLoS ONE</i> , 2016, 11, e0160316.	1.1	12
44	Calibration and seasonal adjustment for matched case-control studies of vitamin D and cancer. <i>Statistics in Medicine</i> , 2016, 35, 2133-2148.	0.8	28
45	Endogenous Estrogens, Estrogen Metabolites, and Breast Cancer Risk in Postmenopausal Chinese Women. <i>Journal of the National Cancer Institute</i> , 2016, 108, djw103.	3.0	67
46	Burden of Nonsynonymous Mutations among TCGA Cancers and Candidate Immune Checkpoint Inhibitor Responses. <i>Cancer Research</i> , 2016, 76, 3767-3772.	0.4	124
47	HPV16 Sublineage Associations With Histology-Specific Cancer Risk Using HPV Whole-Genome Sequences in 3200 Women. <i>Journal of the National Cancer Institute</i> , 2016, 108, djw100.	3.0	147
48	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. <i>Nature Communications</i> , 2016, 7, 11843.	5.8	86
49	Pathway, <i>in silico</i> and tissue-specific expression quantitative analyses of oesophageal squamous cell carcinoma genome-wide association studies data. <i>International Journal of Epidemiology</i> , 2016, 45, 206-220.	0.9	19
50	A GWAS Meta-analysis and Replication Study Identifies a Novel Locus within <i>CLPTM1L/TERT</i> Associated with Nasopharyngeal Carcinoma in Individuals of Chinese Ancestry. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 188-192.	1.1	45
51	A Powerful Procedure for Pathway-Based Meta-analysis Using Summary Statistics Identifies 43 Pathways Associated with Type II Diabetes in European Populations. <i>PLoS Genetics</i> , 2016, 12, e1006122.	1.5	34
52	Winner's Curse Correction and Variable Thresholding Improve Performance of Polygenic Risk Modeling Based on Genome-Wide Association Study Summary-Level Data. <i>PLoS Genetics</i> , 2016, 12, e1006493.	1.5	98
53	Sleep Duration and Cancer in the NIH-AARP Diet and Health Study Cohort. <i>PLoS ONE</i> , 2016, 11, e0161561.	1.1	67
54	A hybrid parametric and empirical likelihood model for evaluating interactions in case-control studies. <i>Statistics and Its Interface</i> , 2016, 9, 147-158.	0.2	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. <i>Annals of Occupational Hygiene</i> , 2015, 59, 455-66.	1.9	9
56	Vitamin D Metabolic Pathway Genes and Pancreatic Cancer Risk. <i>PLoS ONE</i> , 2015, 10, e0117574.	1.1	29
57	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. <i>American Journal of Human Genetics</i> , 2015, 96, 487-497.	2.6	101
58	Vitamin D-Associated Genetic Variation and Risk of Breast Cancer in the Breast and Prostate Cancer Cohort Consortium (BPC3). <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 627-630.	1.1	20
59	Using covariate-specific disease prevalence information to increase the power of case-control studies. <i>Biometrika</i> , 2015, 102, 169-180.	1.3	36
60	Deep sequencing of HPV16 genomes: A new high-throughput tool for exploring the carcinogenicity and natural history of HPV16 infection. <i>Papillomavirus Research (Amsterdam, Netherlands)</i> , 2015, 1, 3-11.	4.5	75
61	A robust association test for detecting genetic variants with heterogeneous effects. <i>Biostatistics</i> , 2015, 16, 5-16.	0.9	1
62	Integration of multiethnic fine-mapping and genomic annotation to prioritize candidate functional SNPs at prostate cancer susceptibility regions. <i>Human Molecular Genetics</i> , 2015, 24, 5603-5618.	1.4	50
63	Prospective study of <i>Helicobacter pylori</i> antigens and gastric noncardia cancer risk in the nutrition intervention trial cohort. <i>International Journal of Cancer</i> , 2015, 137, 1938-1946.	2.3	16
64	Two susceptibility loci identified for prostate cancer aggressiveness. <i>Nature Communications</i> , 2015, 6, 6889.	5.8	88
65	Common genetic variants in epigenetic machinery genes and risk of upper gastrointestinal cancers. <i>International Journal of Epidemiology</i> , 2015, 44, 1341-1352.	0.9	13
66	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015, 20, 647-656.	4.1	235
67	Human Leukocyte Antigen Class I and II Alleles and Cervical Adenocarcinoma. <i>Frontiers in Oncology</i> , 2014, 4, 119.	1.3	23
68	A fast and powerful tree-based association test for detecting complex joint effects in case-control studies. <i>Bioinformatics</i> , 2014, 30, 2171-2178.	1.8	4
69	Variants Associated with Susceptibility to Pancreatic Cancer and Melanoma Do Not Reciprocally Affect Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 1121-1124.	1.1	14
70	Comparison of Ordinal and Nominal Classification Trees to Predict Ordinal Expert-Based Occupational Exposure Estimates in a Case-Control Study. <i>Annals of Occupational Hygiene</i> , 2014, 59, 324-35.	1.9	7
71	A fast multilocus test with adaptive SNP selection for large-scale genetic-association studies. <i>European Journal of Human Genetics</i> , 2014, 22, 696-702.	1.4	19
72	Stochastic approximation Monte Carlo importance sampling for approximating exact conditional probabilities. <i>Statistics and Computing</i> , 2014, 24, 505-520.	0.8	3

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73	Genetic variants in fas signaling pathway genes and risk of gastric cancer. <i>International Journal of Cancer</i> , 2014, 134, 822-831.	2.3	26
74	Genome-wide association study of circulating vitamin D-binding protein. <i>American Journal of Clinical Nutrition</i> , 2014, 99, 1424-1431.	2.2	49
75	Joint analysis of three genome-wide association studies of esophageal squamous cell carcinoma in Chinese populations. <i>Nature Genetics</i> , 2014, 46, 1001-1006.	9.4	148
76	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. <i>Nature Genetics</i> , 2014, 46, 994-1000.	9.4	294
77	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. <i>Nature Genetics</i> , 2014, 46, 1103-1109.	9.4	408
78	High Prevalence of Screen Detected Prostate Cancer in West Africans: Implications for Racial Disparity of Prostate Cancer. <i>Journal of Urology</i> , 2014, 192, 730-736.	0.2	46
79	Genetic variants in DNA repair pathway genes and risk of esophageal squamous cell carcinoma and gastric adenocarcinoma in a Chinese population. <i>Carcinogenesis</i> , 2013, 34, 1536-1542.	1.3	68
80	Semiparametric inference on the penetrances of rare genetic mutations based on a case-family design. <i>Journal of Statistical Planning and Inference</i> , 2013, 143, 368-377.	0.4	0
81	Bayesian Subset Modeling for High-Dimensional Generalized Linear Models. <i>Journal of the American Statistical Association</i> , 2013, 108, 589-606.	1.8	49
82	Polymorphisms in genes related to one-carbon metabolism are not related to pancreatic cancer in PanScan and PanC4. <i>Cancer Causes and Control</i> , 2013, 24, 595-602.	0.8	4
83	Genetic variants in sex hormone metabolic pathway genes and risk of esophageal squamous cell carcinoma. <i>Carcinogenesis</i> , 2013, 34, 1062-1068.	1.3	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. <i>PLoS ONE</i> , 2013, 8, e68999.	1.1	17
85	Individual Variations in Serum Melatonin Levels through Time: Implications for Epidemiologic Studies. <i>PLoS ONE</i> , 2013, 8, e83208.	1.1	32
86	A Flexible Bayesian Model for Studying Gene-Environment Interaction. <i>PLoS Genetics</i> , 2012, 8, e1002482.	1.5	20
87	Pathway analysis of genome-wide association study data highlights pancreatic development genes as susceptibility factors for pancreatic cancer. <i>Carcinogenesis</i> , 2012, 33, 1384-1390.	1.3	102
88	The association between inflammation-related genes and serum androgen levels in men: The prostate, lung, colorectal, and ovarian study. <i>Prostate</i> , 2012, 72, 65-71.	1.2	8
89	Single Nucleotide Polymorphisms in the PRDX3 and RPS19 and Risk of HPV Persistence and Cervical Precancer/Cancer. <i>PLoS ONE</i> , 2012, 7, e33619.	1.1	37
90	A comprehensive candidate gene approach identifies genetic variation associated with osteosarcoma. <i>BMC Cancer</i> , 2011, 11, 209.	1.1	69

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91	Robust joint analysis allowing for model uncertainty in two-stage genetic association studies. BMC Bioinformatics, 2011, 12, 9.	1.2	16
92	Improved genetic association tests for an ordinal outcome representing the disease progression process. Genetic Epidemiology, 2011, 35, n/a-n/a.	0.6	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.	1.4	43
94	Large-scale fine mapping of the HNF1B locus and prostate cancer risk. Human Molecular Genetics, 2011, 20, 3322-3329.	1.4	28
95	Efficient p-value evaluation for resampling-based tests. Biostatistics, 2011, 12, 582-593.	0.9	16
96	Serum 25-hydroxyvitamin D and lung cancer risk. FASEB Journal, 2011, 25, 214.7.	0.2	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.	2.6	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.	0.4	2
100	Approximating probabilities of correlated events. Science China Mathematics, 2010, 53, 2937-2948.	0.8	1
101	The association of telomere length and genetic variation in telomere biology genes. Human Mutation, 2010, 31, 1050-1058.	1.1	93
102	A Partially Linear Tree-based Regression Model for Multivariate Outcomes. Biometrics, 2010, 66, 89-96.	0.8	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.	9.4	539
104	A shared susceptibility locus in PLCE1 at 10q23 for gastric adenocarcinoma and esophageal squamous cell carcinoma. Nature Genetics, 2010, 42, 764-767.	9.4	453
105	Common Genetic Variants and Risk for HPV Persistence and Progression to Cervical Cancer. PLoS ONE, 2010, 5, e8667.	1.1	104
106	Genome-wide association study of circulating vitamin D levels. Human Molecular Genetics, 2010, 19, 2739-2745.	1.4	700
107	Pesticide Use Modifies the Association Between Genetic Variants on Chromosome 8q24 and Prostate Cancer. Cancer Research, 2010, 70, 9224-9233.	0.4	41
108	Statistical inference on the penetrances of rare genetic mutations based on a case-family design. Biostatistics, 2010, 11, 519-532.	0.9	5

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109	Genetic Admixture and Population Substructure in Guanacaste Costa Rica. <i>PLoS ONE</i> , 2010, 5, e13336.	1.1	16
110	Genome-Wide and Candidate Gene Association Study of Cigarette Smoking Behaviors. <i>PLoS ONE</i> , 2009, 4, e4653.	1.1	226
111	Age-Dependent Cancer Risk Is Not Different in between <i>MSH2</i> and <i>MLH1</i> Mutation Carriers. <i>Journal of Cancer Epidemiology</i> , 2009, 2009, 1-6.	0.5	4
112	Genetic background comparison using distance-based regression, with applications in population stratification evaluation and adjustment. <i>Genetic Epidemiology</i> , 2009, 33, 432-441.	0.6	19
113	Pathway analysis by adaptive combination of <i>P</i> -values. <i>Genetic Epidemiology</i> , 2009, 33, 700-709.	0.6	248
114	A multistage genome-wide association study in breast cancer identifies two new risk alleles at 1p11.2 and 14q24.1 ( <i>RAD51L1</i> ). <i>Nature Genetics</i> , 2009, 41, 579-584.	9.4	487
115	Genome-wide association study identifies variants in the ABO locus associated with susceptibility to pancreatic cancer. <i>Nature Genetics</i> , 2009, 41, 986-990.	9.4	597
116	Robust Tests for Single-marker Analysis in Case-Control Genetic Association Studies. <i>Annals of Human Genetics</i> , 2009, 73, 245-252.	0.3	21
117	Inference of non-centrality parameter of a truncated non-central chi-squared distribution. <i>Journal of Statistical Planning and Inference</i> , 2009, 139, 2431-2444.	0.4	3
118	A Genome-wide Association Study of Lung Cancer Identifies a Region of Chromosome 5p15 Associated with Risk for Adenocarcinoma. <i>American Journal of Human Genetics</i> , 2009, 85, 679-691.	2.6	489
119	MAX-rank: a simple and robust genome-wide scan for case-control association studies. <i>Human Genetics</i> , 2008, 123, 617-623.	1.8	36
120	Improved correction for population stratification in genome-wide association studies by identifying hidden population structures. <i>Genetic Epidemiology</i> , 2008, 32, 215-226.	0.6	123
121	Multiple loci identified in a genome-wide association study of prostate cancer. <i>Nature Genetics</i> , 2008, 40, 310-315.	9.4	871
122	Efficient Approximation of <i>P</i> -value of the Maximum of Correlated Tests, with Applications to Genome-Wide Association Studies. <i>Annals of Human Genetics</i> , 2008, 72, 397-406.	0.3	71
123	Population Substructure and Control Selection in Genome-Wide Association Studies. <i>PLoS ONE</i> , 2008, 3, e2551.	1.1	111
124	Flexible Design for Following Up Positive Findings. <i>American Journal of Human Genetics</i> , 2007, 81, 540-551.	2.6	47
125	A partially linear tree-based regression model for assessing complex joint gene-gene and gene-environment effects. <i>Genetic Epidemiology</i> , 2007, 31, 238-251.	0.6	22
126	Genome-wide association study of prostate cancer identifies a second risk locus at 8q24. <i>Nature Genetics</i> , 2007, 39, 645-649.	9.4	1,059



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127	A genome-wide association study identifies alleles in FCGR2 associated with risk of sporadic postmenopausal breast cancer. <i>Nature Genetics</i> , 2007, 39, 870-874.	9.4	1,370
128	Two-sample Comparison Based on Prediction Error, with Applications to Candidate Gene Association Studies. <i>Annals of Human Genetics</i> , 2007, 71, 107-118.	0.3	8
129	Using Tree-Based Recursive Partitioning Methods to Group Haplotypes for Increased Power in Association Studies. <i>Annals of Human Genetics</i> , 2005, 69, 577-589.	0.3	24
130	Global transmission/disequilibrium tests based on haplotype sharing in multiple candidate genes. <i>Genetic Epidemiology</i> , 2005, 29, 323-335.	0.6	7
131	A Haplotype Similarity Based Transmission/Disequilibrium Test under Founder Heterogeneity. <i>Annals of Human Genetics</i> , 2005, 69, 455-467.	0.3	11
132	Adolescent age at first pregnancy and subsequent obesity. <i>Paediatric and Perinatal Epidemiology</i> , 1997, 11, 130-141.	0.8	34
133	Does changing paternity contribute to the risk of intrauterine growth retardation?. <i>Paediatric and Perinatal Epidemiology</i> , 1997, 11, 41-47.	0.8	11