Shuo Jiao

List of Publications by Year
in descending order

31 papers	1,991 citations	361413 20 h-index	434195 31 g-index
31 all docs	31 docs citations	31 times ranked	5082 citing authors

#	ARTICLE	IF	CITATIONS
1	Fine-Mapping of Common Genetic Variants Associated with Colorectal Tumor Risk Identified Potential Functional Variants. PLoS ONE, 2016, 11, e0157521.	2.5	8
2	CYP24A1 variant modifies the association between use of oestrogen plus progestogen therapy and colorectal cancer risk. British Journal of Cancer, 2016, 114, 221-229.	6.4	18
3	Genome-Wide Interaction Analyses between Genetic Variants and Alcohol Consumption and Smoking for Risk of Colorectal Cancer. PLoS Genetics, 2016, 12, e1006296.	3.5	38
4	Powerful Set‑Based Gene‑Environment Interaction Testing Framework for Complex Diseases. Genetic Epidemiology, 2015, 39, 609-618.	1.3	15
5	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. Nature Communications, 2015, 6, 7138.	12.8	138
6	Association of Aspirin and NSAID Use With Risk of Colorectal Cancer According to Genetic Variants. JAMA - Journal of the American Medical Association, 2015, 313, 1133.	7.4	171
7	Identification of a common variant with potential pleiotropic effect on risk of inflammatory bowel disease and colorectal cancer. Carcinogenesis, 2015, 36, 999-1007.	2.8	28
8	Genetic variants of adiponectin and risk of colorectal cancer. International Journal of Cancer, 2015, 137, 154-164.	5.1	16
9	Gene‑Environment Interaction Involving Recently Identified Colorectal Cancer Susceptibility Loci. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1824-1833.	2.5	48
10	No Evidence of Gene‑Calcium Interactions from Genome-Wide Analysis of Colorectal Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2971-2976.	2.5	9
11	Pleiotropic effects of genetic risk variants for other cancers on colorectal cancer risk: PAGE, GECCO and CCFR consortia. Gut, 2014, 63, 800-807.	12.1	35
12	Whole-exome imputation of sequence variants identified two novel alleles associated with adult body height in African Americans. Human Molecular Genetics, 2014, 23, 6607-6615.	2.9	14
13	Genome-Wide Diet-Gene Interaction Analyses for Risk of Colorectal Cancer. PLoS Genetics, 2014, 10, e1004228.	3.5	81
14	Estimating the heritability of colorectal cancer. Human Molecular Genetics, 2014, 23, 3898-3905.	2.9	114
15	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
16	A Variational Bayes Discrete Mixture Test for Rare Variant Association. Genetic Epidemiology, 2014, 38, 21-30.	1.3	12
17	Evaluation of the colorectal cancer risk conferred by rare *UNC5C* alleles. World Journal of Gastroenterology, 2014, 20, 204.	3.3	11
18	Identification of Genetic Susceptibility Loci for Colorectal Tumors in a Genome-Wide Meta-analysis. Gastroenterology, 2013, 144, 799-807.e24.	1.3	292

#	ARTICLE	IF	CITATIONS
19	A Systematic Mapping Approach of 16q12.2/FTO and BMI in More Than 20,000 African Americans Narrows in on the Underlying Functional Variation: Results from the Population Architecture using Genomics and Epidemiology (PAGE) Study. PLoS Genetics, 2013, 9, e1003171.	3.5	63
20	Imputation of coding variants in African Americans: better performance using data from the exome sequencing project. Bioinformatics, 2013, 29, 2744-2749.	4.1	36
21	SBERIA: Set‐Based Gene‐Environment Interaction Test for Rare and Common Variants in Complex Diseases. Genetic Epidemiology, 2013, 37, 452-464.	1.3	39
22	Common and rare von Willebrand factor (VWF) coding variants, VWF levels, and factor VIII levels in African Americans: the NHLBI Exome Sequencing Project. Blood, 2013, 122, 590-597.	1.4	70
23	A Pooled Analysis of Smoking and Colorectal Cancer: Timing of Exposure and Interactions with Environmental Factors. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 1974-1985.	2.5	54
24	Characterization of Gene–Environment Interactions for Colorectal Cancer Susceptibility Loci. Cancer Research, 2012, 72, 2036-2044.	0.9	140
25	Powerful Cocktail Methods for Detecting Genome‐Wide Gene‐Environment Interaction. Genetic Epidemiology, 2012, 36, 183-194.	1.3	80
26	Meta-analysis of new genome-wide association studies of colorectal cancer risk. Human Genetics, 2012, 131, 217-234.	3.8	183
27	Genome-Wide Search for Gene-Gene Interactions in Colorectal Cancer. PLoS ONE, 2012, 7, e52535.	2.5	35
28	The use of imputed values in the meta-analysis of genome-wide association studies. Genetic Epidemiology, 2011, 35, 597-605.	1.3	27
29	Estimating the Proportion of Equivalently Expressed Genes in Microarray Data Based on Transformed Test Statistics. Journal of Computational Biology, 2010, 17, 177-187.	1.6	3
30	The t-mixture model approach for detecting differentially expressed genes in microarrays. Functional and Integrative Genomics, 2008, 8, 181-186.	3.5	10
31	On correcting the overestimation of the permutation-based false discovery rate estimator. Bioinformatics, 2008, 24, 1655-1661.	4.1	10