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	Identification of Genetic Susceptibility Loci for Colorectal Tumors in a Genome-Wide Meta-analysis. Gastroenterology, 2013, 144, 799-807.e24.	1.3	292
2	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
3	Meta-analysis of new genome-wide association studies of colorectal cancer risk. Human Genetics, 2012, 131, 217-234.	3.8	183
4	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
5	Characterization of Geneâ€"Environment Interactions for Colorectal Cancer Susceptibility Loci. Cancer Research, 2012, 72, 2036-2044.	0.9	140
6	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. Nature Communications, 2015, 6, 7138.	12.8	138
7	Estimating the heritability of colorectal cancer. Human Molecular Genetics, 2014, 23, 3898-3905.	2.9	114
8	Genome-Wide Diet-Gene Interaction Analyses for Risk of Colorectal Cancer. PLoS Genetics, 2014, 10, e1004228.	3.5	81
9	Powerful Cocktail Methods for Detecting Genomeâ€Wide Geneâ€Environment Interaction. Genetic Epidemiology, 2012, 36, 183-194.	1.3	80
10	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
11	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
12	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
13	Geneâ€"Environment Interaction Involving Recently Identified Colorectal Cancer Susceptibility Loci. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1824-1833.	2.5	48
14	SBERIA: Setâ€Based Geneâ€Environment Interaction Test for Rare and Common Variants in Complex Diseases. Genetic Epidemiology, 2013, 37, 452-464.	1.3	39
15	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
16	Imputation of coding variants in African Americans: better performance using data from the exome sequencing project. Bioinformatics, 2013, 29, 2744-2749.	4.1	36
17	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
18	Genome-Wide Search for Gene-Gene Interactions in Colorectal Cancer. PLoS ONE, 2012, 7, e52535.	2.5	35

#	Article	IF	Citations
19	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
20	The use of imputed values in the meta-analysis of genome-wide association studies. Genetic Epidemiology, 2011, 35, 597-605.	1.3	27
21	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
22	Genetic variants of adiponectin and risk of colorectal cancer. International Journal of Cancer, 2015, 137, 154-164.	5.1	16
23	Powerful Setâ€Based Geneâ€Environment Interaction Testing Framework for Complex Diseases. Genetic Epidemiology, 2015, 39, 609-618.	1.3	15
24	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
25	A Variational Bayes Discrete Mixture Test for Rare Variant Association. Genetic Epidemiology, 2014, 38, 21-30.	1.3	12
26	Evaluation of the colorectal cancer risk conferred by rareUNC5Calleles. World Journal of Gastroenterology, 2014, 20, 204.	3.3	11
27	The t-mixture model approach for detecting differentially expressed genes in microarrays. Functional and Integrative Genomics, 2008, 8, 181-186.	3.5	10
28	On correcting the overestimation of the permutation-based false discovery rate estimator. Bioinformatics, 2008, 24, 1655-1661.	4.1	10
29	No Evidence of Geneâ€“Calcium Interactions from Genome-Wide Analysis of Colorectal Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2971-2976.	2.5	9
30	Fine-Mapping of Common Genetic Variants Associated with Colorectal Tumor Risk Identified Potential Functional Variants. PLoS ONE, 2016, 11, e0157521.	2.5	8
31	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