

Guangfu Jin

List of Publications by Year in descending order

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Version: 2024-02-01

178
papers

7,133
citations

87888

38
h-index

74163

75
g-index

184
all docs

184
docs citations

184
times ranked

12749
citing authors

#	ARTICLE	IF	CITATIONS
1	Clinical characteristics of 24 asymptomatic infections with COVID-19 screened among close contacts in Nanjing, China. Science China Life Sciences, 2020, 63, 706-711.	4.9	1,090
2	A genome-wide association study identifies two new lung cancer susceptibility loci at 13q12.12 and 22q12.2 in Han Chinese. Nature Genetics, 2011, 43, 792-796.	21.4	340
3	Genome-wide association study identifies three new susceptibility loci for esophageal squamous-cell carcinoma in Chinese populations. Nature Genetics, 2011, 43, 679-684.	21.4	260
4	A genome-wide association study identifies new susceptibility loci for non-cardia gastric cancer at 3q13.31 and 5p13.1. Nature Genetics, 2011, 43, 1215-1218.	21.4	250
5	Genome-wide association analyses of esophageal squamous cell carcinoma in Chinese identify multiple susceptibility loci and gene-environment interactions. Nature Genetics, 2012, 44, 1090-1097.	21.4	238
6	Plasma miRNA's as early biomarkers for detecting hepatocellular carcinoma. International Journal of Cancer, 2015, 137, 1679-1690.	5.1	188
7	The 5p15.33 Locus Is Associated with Risk of Lung Adenocarcinoma in Never-Smoking Females in Asia. PLoS Genetics, 2010, 6, e1001051.	3.5	168
8	A novel plasma circular RNA circFARSA is a potential biomarker for non-small cell lung cancer. Cancer Medicine, 2018, 7, 2783-2791.	2.8	167
9	Identification of risk loci and a polygenic risk score for lung cancer: a large-scale prospective cohort study in Chinese populations. Lancet Respiratory Medicine, 2019, 7, 881-891.	10.7	167
10	Analysis of Heritability and Shared Heritability Based on Genome-Wide Association Studies for Thirteen Cancer Types. Journal of the National Cancer Institute, 2015, 107, djv279.	6.3	152
11	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
12	New loci associated with chronic hepatitis B virus infection in Han Chinese. Nature Genetics, 2013, 45, 1499-1503.	21.4	140
13	Association analyses identify multiple new lung cancer susceptibility loci and their interactions with smoking in the Chinese population. Nature Genetics, 2012, 44, 895-899.	21.4	129
14	Systematic identification of genes with a cancer-testis expression pattern in 19 cancer types. Nature Communications, 2016, 7, 10499.	12.8	124
15	Genetic risk, incident gastric cancer, and healthy lifestyle: a meta-analysis of genome-wide association studies and prospective cohort study. Lancet Oncology, 2020, 21, 1378-1386.	10.7	123
16	Associations Between Hepatitis B Virus Infection and Risk of All Cancer Types. JAMA Network Open, 2019, 2, e195718.	5.9	114
17	Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. Human Molecular Genetics, 2015, 24, 1791-1800.	2.9	105
18	The association between telomere length and cancer risk in population studies. Scientific Reports, 2016, 6, 22243.	3.3	101

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19	Prevalence of <i>Helicobacter pylori</i> infection in China: A systematic review and meta-analysis. Journal of Gastroenterology and Hepatology (Australia), 2022, 37, 464-470.	2.8	94
20	Genetic Variants at 6p21.1 and 7p15.3 Are Associated with Risk of Multiple Cancers in Han Chinese. American Journal of Human Genetics, 2012, 91, 928-934.	6.2	76
21	Genetic variants at 1q22 and 10q23 reproducibly associated with gastric cancer susceptibility in a Chinese population. Carcinogenesis, 2011, 32, 848-852.	2.8	73
22	Common genetic variants on 5p15.33 contribute to risk of lung adenocarcinoma in a Chinese population. Carcinogenesis, 2009, 30, 987-990.	2.8	72
23	Identification of new susceptibility loci for gastric non-cardia adenocarcinoma: pooled results from two Chinese genome-wide association studies. Gut, 2017, 66, 581-587.	12.1	68
24	Whole-genome sequencing reveals genomic signatures associated with the inflammatory microenvironments in Chinese NSCLC patients. Nature Communications, 2018, 9, 2054.	12.8	68
25	Estimation of heritability for nine common cancers using data from genome-wide association studies in Chinese population. International Journal of Cancer, 2017, 140, 329-336.	5.1	66
26	Association analysis identifies new risk loci for non-obstructive azoospermia in Chinese men. Nature Communications, 2014, 5, 3857.	12.8	64
27	A cancer-testis non-coding RNA LIN28B-AS1 activates driver gene LIN28B by interacting with IGF2BP1 in lung adenocarcinoma. Oncogene, 2019, 38, 1611-1624.	5.9	61
28	Identification of Novel T1D Risk Loci and Their Association With Age and Islet Function at Diagnosis in Autoantibody-Positive T1D Individuals: Based on a Two-Stage Genome-Wide Association Study. Diabetes Care, 2019, 42, 1414-1421.	8.6	60
29	Vitamin D Status and Risk of All-Cause and Cause-Specific Mortality in a Large Cohort: Results From the UK Biobank. Journal of Clinical Endocrinology and Metabolism, 2020, 105, e3606-e3619.	3.6	60
30	Exome Array Analysis Identifies Variants in SPOCD1 and BTN3A2 That Affect Risk for Gastric Cancer. Gastroenterology, 2017, 152, 2011-2021.	1.3	58
31	Role of <i>ATG10</i> expression quantitative trait loci in non-small cell lung cancer survival. International Journal of Cancer, 2016, 139, 1564-1573.	5.1	55
32	Association between GWAS-identified lung adenocarcinoma susceptibility loci and EGFR mutations in never-smoking Asian women, and comparison with findings from Western populations. Human Molecular Genetics, 2016, 26, ddw414.	2.9	50
33	Meta-analysis of genome-wide association studies identifies multiple lung cancer susceptibility loci in never-smoking Asian women. Human Molecular Genetics, 2016, 25, 620-629.	2.9	50
34	Genetic Risk for Overall Cancer and the Benefit of Adherence to a Healthy Lifestyle. Cancer Research, 2021, 81, 4618-4627.	0.9	48
35	A genome-wide gene-environment interaction analysis for tobacco smoke and lung cancer susceptibility. Carcinogenesis, 2014, 35, 1528-1535.	2.8	47
36	A functional variant in miR-155 regulation region contributes to lung cancer risk and survival. Oncotarget, 2015, 6, 42781-42792.	1.8	47

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37	Telomere length, genetic variants and gastric cancer risk in a Chinese population. <i>Carcinogenesis</i> , 2015, 36, 963-970.	2.8	46
38	A nomogram to predict the survival of stage IIIA-N2 non-small cell lung cancer after surgery. <i>Journal of Thoracic and Cardiovascular Surgery</i> , 2018, 155, 1784-1792.e3.	0.8	45
39	Independent prognostic role of human papillomavirus genotype in cervical cancer. <i>BMC Infectious Diseases</i> , 2017, 17, 391.	2.9	43
40	Low-Frequency Coding Variants at 6p21.33 and 20q11.21 Are Associated with Lung Cancer Risk in Chinese Populations. <i>American Journal of Human Genetics</i> , 2015, 96, 832-840.	6.2	41
41	Diet and Risk of Incident Lung Cancer: A Large Prospective Cohort Study in UK Biobank. <i>American Journal of Clinical Nutrition</i> , 2021, 114, 2043-2051.	4.7	38
42	Meta-analysis of genome-wide association studies and functional assays decipher susceptibility genes for gastric cancer in Chinese populations. <i>Gut</i> , 2020, 69, 641-651.	12.1	36
43	Genetic variants at 4q21, 4q23 and 12q24 are associated with esophageal squamous cell carcinoma risk in a Chinese population. <i>Human Genetics</i> , 2013, 132, 649-656.	3.8	34
44	Personal exposure to PM2.5, genetic variants and DNA damage: A multi-center population-based study in Chinese. <i>Toxicology Letters</i> , 2015, 235, 172-178.	0.8	34
45	Fine mapping the MHC region identified four independent variants modifying susceptibility to chronic hepatitis B in Han Chinese. <i>Human Molecular Genetics</i> , 2016, 25, 1225-1232.	2.9	33
46	Influencing factors of pregnancy loss and survival probability of clinical pregnancies conceived through assisted reproductive technology. <i>Reproductive Biology and Endocrinology</i> , 2018, 16, 74.	3.3	33
47	High mitochondrial DNA copy number was associated with an increased gastric cancer risk in a Chinese population. <i>Molecular Carcinogenesis</i> , 2017, 56, 2593-2600.	2.7	32
48	Blood groups A and AB are associated with increased gastric cancer risk: evidence from a large genetic study and systematic review. <i>BMC Cancer</i> , 2019, 19, 164.	2.6	30
49	Genetic variants in regulatory regions of microRNAs are associated with lung cancer risk. <i>Oncotarget</i> , 2016, 7, 47966-47974.	1.8	28
50	miR-486-5p expression pattern in esophageal squamous cell carcinoma, gastric cancer and its prognostic value. <i>Oncotarget</i> , 2016, 7, 15840-15853.	1.8	28
51	Tea consumption and risk of stroke in Chinese adults: a prospective cohort study of 0.5 million men and women. <i>American Journal of Clinical Nutrition</i> , 2020, 111, 197-206.	4.7	27
52	The inherited variations of a p53-responsive enhancer in 13q12.12 confer lung cancer risk by attenuating TNFRSF19 expression. <i>Genome Biology</i> , 2019, 20, 103.	8.8	27
53	Association analysis identifies new risk loci for congenital heart disease in Chinese populations. <i>Nature Communications</i> , 2015, 6, 8082.	12.8	26
54	A polymorphism in miR-1262 regulatory region confers the risk of lung cancer in Chinese population. <i>International Journal of Cancer</i> , 2017, 141, 958-966.	5.1	26

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55	Relationships between sleep traits and lung cancer risk: a prospective cohort study in UK Biobank. <i>Sleep</i> , 2021, 44, .	1.1	26
56	Association of assisted reproductive technology, germline de novo mutations and congenital heart defects in a prospective birth cohort study. <i>Cell Research</i> , 2021, 31, 919-928.	12.0	26
57	A genetic variation in the CpG island of pseudogene <i>GBAP1</i> promoter is associated with gastric cancer susceptibility. <i>Cancer</i> , 2019, 125, 2465-2473.	4.1	25
58	Assisted reproductive technology and birth defects in a Chinese birth cohort study. <i>The Lancet Regional Health - Western Pacific</i> , 2021, 7, 100090.	2.9	24
59	Remote modulation of lncRNA <i>GCLET</i> by risk variant at 16p13 underlying genetic susceptibility to gastric cancer. <i>Science Advances</i> , 2020, 6, eaay5525.	10.3	23
60	Putative functional polymorphisms of <i>MMP9</i> predict survival of NSCLC in a Chinese population. <i>International Journal of Cancer</i> , 2009, 124, 2172-2178.	5.1	22
61	Comprehensive characterization of cancer-related testis genes in testicular germ cell tumor. <i>Cancer Medicine</i> , 2019, 8, 3511-3519.	2.8	22
62	Metabolome-wide association study identified the association between a circulating polyunsaturated fatty acids variant rs174548 and lung cancer. <i>Carcinogenesis</i> , 2017, 38, 1147-1154.	2.8	21
63	Fine-mapping the MHC region in Asian populations identified novel variants modifying susceptibility to lung cancer. <i>Lung Cancer</i> , 2017, 112, 169-175.	2.0	21
64	Evaluation of genetic variants in autophagy pathway genes as prognostic biomarkers for breast cancer. <i>Gene</i> , 2017, 627, 549-555.	2.2	21
65	Comprehensive functional annotation of susceptibility variants identifies genetic heterogeneity between lung adenocarcinoma and squamous cell carcinoma. <i>Frontiers of Medicine</i> , 2021, 15, 275-291.	3.4	21
66	Family History and Stroke Risk in China: Evidence from a Large Cohort Study. <i>Journal of Stroke</i> , 2017, 19, 188-195.	3.2	21
67	Genetically predicted high body mass index is associated with increased gastric cancer risk. <i>European Journal of Human Genetics</i> , 2017, 25, 1061-1066.	2.8	20
68	Comprehensive characterization of functional eRNAs in lung adenocarcinoma reveals novel regulators and a prognosis-related molecular subtype. <i>Theranostics</i> , 2020, 10, 11264-11277.	10.0	20
69	Genetic Variations in the Flanking Regions of miR-101-2 Are Associated with Increased Risk of Breast Cancer. <i>PLoS ONE</i> , 2014, 9, e86319.	2.5	19
70	Cumulative Effect and Predictive Value of Genetic Variants Associated with Type 2 Diabetes in Han Chinese: A Case-Control Study. <i>PLoS ONE</i> , 2015, 10, e0116537.	2.5	19
71	Germline genetic variants were interactively associated with somatic alterations in gastric cancer. <i>Cancer Medicine</i> , 2018, 7, 3912-3920.	2.8	19
72	Association of Mosaic Loss of Chromosome Y with Lung Cancer Risk and Prognosis in a Chinese Population. <i>Journal of Thoracic Oncology</i> , 2019, 14, 37-44.	1.1	19

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73	Cancer incidence in relation to body fatness among 0.5 million men and women: Findings from the China Kadoorie Biobank. <i>International Journal of Cancer</i> , 2020, 146, 987-998.	5.1	19
74	Pre-diagnostic circulating concentrations of insulin-like growth factor-1 and risk of COVID-19 mortality: results from UK Biobank. <i>European Journal of Epidemiology</i> , 2021, 36, 311-318.	5.7	19
75	A polygenic risk score for nasopharyngeal carcinoma shows potential for risk stratification and personalized screening. <i>Nature Communications</i> , 2022, 13, 1966.	12.8	19
76	Association of KCTD10, MVK, and MMAB polymorphisms with dyslipidemia and coronary heart disease in Han Chinese population. <i>Lipids in Health and Disease</i> , 2016, 15, 171.	3.0	18
77	The sex ratio of singleton and twin delivery offspring in assisted reproductive technology in China. <i>Scientific Reports</i> , 2017, 7, 7754.	3.3	18
78	Effect of endometrial thickness and embryo quality on live-birth rate of fresh IVF/ICSI cycles: a retrospective cohort study. <i>Reproductive Biology and Endocrinology</i> , 2020, 18, 89.	3.3	18
79	LncPSCA in the 8q24.3 risk locus drives gastric cancer through destabilizing DDX5. <i>EMBO Reports</i> , 2021, 22, e52707.	4.5	18
80	Circulating Tumor Cells Enriched by the Depletion of Leukocytes with Bi-Antibodies in Non-Small Cell Lung Cancer: Potential Clinical Application. <i>PLoS ONE</i> , 2015, 10, e0137076.	2.5	18
81	Human genome epidemiology, progress and future. <i>Journal of Biomedical Research</i> , 2013, 27, 167-169.	1.6	17
82	The known genetic loci for telomere length may be involved in the modification of telomeres length after birth. <i>Scientific Reports</i> , 2016, 6, 38729.	3.3	17
83	Fine mapping of chromosome 5p15.33 identifies novel lung cancer susceptibility loci in Han Chinese. <i>International Journal of Cancer</i> , 2017, 141, 447-456.	5.1	17
84	Sex-specific associations of circulating testosterone levels with all-cause and cause-specific mortality. <i>European Journal of Endocrinology</i> , 2021, 184, 723-732.	3.7	17
85	Systematical analyses of variants in CTCF-binding sites identified a novel lung cancer susceptibility locus among Chinese population. <i>Scientific Reports</i> , 2015, 5, 7833.	3.3	16
86	Genetic variants in nuclear DNA along with environmental factors modify mitochondrial DNA copy number: a population-based exome-wide association study. <i>BMC Genomics</i> , 2018, 19, 752.	2.8	16
87	A nomogram to predict overall survival of patients with early stage non-small cell lung cancer. <i>Journal of Thoracic Disease</i> , 2019, 11, 5407-5416.	1.4	16
88	Systematic analyses of genetic variants in chromatin interaction regions identified four novel lung cancer susceptibility loci. <i>Journal of Cancer</i> , 2020, 11, 1075-1081.	2.5	16
89	The eQTL-missense polymorphisms of APOBEC3H are associated with lung cancer risk in a Han Chinese population. <i>Scientific Reports</i> , 2015, 5, 14969.	3.3	15
90	Potentially functional polymorphisms in aminoacyl-tRNA synthetases genes are associated with breast cancer risk in a Chinese population. <i>Molecular Carcinogenesis</i> , 2015, 54, 577-583.	2.7	15

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91	Transcriptome-wide association study revealed two novel genes associated with nonobstructive azoospermia in a Chinese population. <i>Fertility and Sterility</i> , 2017, 108, 1056-1062.e4.	1.0	15
92	Mitochondrial DNA copy number is associated with risk of head and neck squamous cell carcinoma in Chinese population. <i>Cancer Medicine</i> , 2018, 7, 2776-2782.	2.8	15
93	Evaluation of CpG-SNPs in miRNA promoters and risk of breast cancer. <i>Gene</i> , 2018, 651, 1-8.	2.2	15
94	Mendelian randomization study of telomere length and lung cancer risk in East Asian population. <i>Cancer Medicine</i> , 2019, 8, 7469-7476.	2.8	15
95	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.	2.9	15
96	Circulating C-reactive protein increases lung cancer risk: Results from a prospective cohort of UK Biobank. <i>International Journal of Cancer</i> , 2022, 150, 47-55.	5.1	15
97	Adherence to Healthy Lifestyle and Liver cancer in Chinese: a prospective cohort study of 0.5 million people. <i>British Journal of Cancer</i> , 2022, 126, 815-821.	6.4	15
98	Genetic variants in one-carbon metabolism-related genes contribute to NSCLC prognosis in a Chinese population. <i>Cancer</i> , 2010, 116, 5700-5709.	4.1	14
99	Genetic variants at 9p21.3 are associated with risk of esophageal squamous cell carcinoma in a Chinese population. <i>Cancer Science</i> , 2017, 108, 250-255.	3.9	14
100	Genetic association of telomere length with hepatocellular carcinoma risk: A Mendelian randomization analysis. <i>Cancer Epidemiology</i> , 2017, 50, 39-45.	1.9	14
101	Short leukocyte telomere length, alone and in combination with smoking, contributes to increased risk of gastric cancer or esophageal squamous cell carcinoma. <i>Carcinogenesis</i> , 2017, 38, 12-18.	2.8	14
102	Integrating expression-related SNPs into genome-wide gene and pathway-based analyses identified novel lung cancer susceptibility genes. <i>International Journal of Cancer</i> , 2018, 142, 1602-1610.	5.1	14
103	Telomere length, genetic variants and risk of squamous cell carcinoma of the head and neck in Southeast Chinese. <i>Scientific Reports</i> , 2016, 6, 20675.	3.3	13
104	Interaction analysis between germline susceptibility loci and somatic alterations in lung cancer. <i>International Journal of Cancer</i> , 2018, 143, 878-885.	5.1	13
105	ATG12 expression quantitative trait loci associated with head and neck squamous cell carcinoma risk in a Chinese Han population. <i>Molecular Carcinogenesis</i> , 2018, 57, 1030-1037.	2.7	13
106	An esophageal adenocarcinoma susceptibility locus at 9q22 also confers risk to esophageal squamous cell carcinoma by regulating the function of BARX1. <i>Cancer Letters</i> , 2018, 421, 103-111.	7.2	13
107	Functional genetic variants in centrosome-related genes CEP72 and YWHAG confer susceptibility to gastric cancer. <i>Archives of Toxicology</i> , 2020, 94, 2861-2872.	4.2	13
108	A nomogram for prediction of stage III/IV gastric cancer outcome after surgery: A multicenter population-based study. <i>Cancer Medicine</i> , 2020, 9, 5490-5499.	2.8	13

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109	Association between <i>Helicobacter pylori</i> antibodies determined by multiplex serology and gastric cancer risk: A meta-analysis. <i>Helicobacter</i> , 2022, 27, e12881.	3.5	13
110	Joint effect of CENTD2 and KCNQ1 polymorphisms on the risk of type 2 diabetes mellitus among Chinese Han population. <i>Molecular and Cellular Endocrinology</i> , 2015, 407, 46-51.	3.2	12
111	Exome-Wide Association Study Identified New Risk Loci for Hirschsprung's Disease. <i>Molecular Neurobiology</i> , 2017, 54, 1777-1785.	4.0	12
112	Low-frequency nonsynonymous variants in <i>FKBP1</i> and <i>ARPC1B</i> genes are associated with breast cancer risk in Chinese women. <i>Molecular Carcinogenesis</i> , 2017, 56, 774-780.	2.7	12
113	Association of Maternal Dietary Patterns during Gestation and Offspring Neurodevelopment. <i>Nutrients</i> , 2022, 14, 730.	4.1	12
114	Potentially functional variants in lncRNAs are associated with breast cancer risk in a Chinese population. <i>Molecular Carcinogenesis</i> , 2017, 56, 2048-2057.	2.7	11
115	Risk assessment models for genetic risk predictors of lung cancer using two-stage replication for Asian and European populations. <i>Oncotarget</i> , 2017, 8, 53959-53967.	1.8	11
116	U-shaped association between telomere length and esophageal squamous cell carcinoma risk: a case-control study in Chinese population. <i>Frontiers of Medicine</i> , 2015, 9, 478-486.	3.4	10
117	Exome-Wide Association Study Identifies Low-Frequency Coding Variants in 2p23.2 and 7p11.2 Associated with Survival of Non-Small Cell Lung Cancer Patients. <i>Journal of Thoracic Oncology</i> , 2017, 12, 644-656.	1.1	10
118	Genetic variants, PM2.5 exposure level and global DNA methylation level: A multi-center population-based study in Chinese. <i>Toxicology Letters</i> , 2017, 269, 77-82.	0.8	10
119	Targeted sequencing of chromosome 15q25 identified novel variants associated with risk of lung cancer and smoking behavior in Chinese. <i>Carcinogenesis</i> , 2017, 38, 552-558.	2.8	10
120	Leukocyte telomere length, lipid parameters and gestational diabetes risk: a case-control study in a Chinese population. <i>Scientific Reports</i> , 2019, 9, 8483.	3.3	10
121	A clinical, biologic and mechanistic analysis of the role of ZNF692 in cervical cancer. <i>Gynecologic Oncology</i> , 2019, 152, 396-407.	1.4	10
122	Integration of GWAS and eQTL Analysis to Identify Risk Loci and Susceptibility Genes for Gastric Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 679.	2.3	10
123	Systematic identification of long non-coding RNAs with cancer-testis expression patterns in 14 cancer types. <i>Oncotarget</i> , 2017, 8, 94769-94779.	1.8	10
124	Polymorphisms in alternative splicing associated genes are associated with lung cancer risk in a Chinese population. <i>Lung Cancer</i> , 2015, 89, 238-242.	2.0	9
125	Genetic variants in chromatin-remodeling pathway associated with lung cancer risk in a Chinese population. <i>Gene</i> , 2016, 587, 178-182.	2.2	9
126	Alterations of gut microbiota composition in neonates conceived by assisted reproductive technology and its relation to infant growth. <i>Gut Microbes</i> , 2020, 12, 1794466.	9.8	9

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127	A cross-tissue transcriptome-wide association study identifies novel susceptibility genes for lung cancer in Chinese populations. <i>Human Molecular Genetics</i> , 2021, 30, 1666-1676.	2.9	9
128	Functional polymorphisms in <i>NR3C1</i> are associated with gastric cancer risk in Chinese population. <i>Oncotarget</i> , 2017, 8, 105312-105319.	1.8	9
129	Pathway analysis for a genome-wide association study of pneumoconiosis. <i>Toxicology Letters</i> , 2015, 232, 284-292.	0.8	8
130	Multi-marker analysis of genomic annotation on gastric cancer GWAS data from Chinese populations. <i>Gastric Cancer</i> , 2019, 22, 60-68.	5.3	8
131	Family-based whole-genome sequencing identifies compound heterozygous protein-coding and noncoding mutations in tetralogy of Fallot. <i>Gene</i> , 2020, 741, 144555.	2.2	8
132	The rates and medical necessity of cesarean delivery in China, 2012–2019: an inspiration from Jiangsu. <i>BMC Medicine</i> , 2021, 19, 14.	5.5	8
133	A cis-eQTL genetic variant of the cancer-testis gene <i>CCDC116</i> is associated with risk of multiple cancers. <i>Human Genetics</i> , 2017, 136, 987-997.	3.8	7
134	Genetic variants affecting telomere length are associated with the prognosis of esophageal squamous cell carcinoma in a Chinese population. <i>Molecular Carcinogenesis</i> , 2017, 56, 1021-1029.	2.7	7
135	Genetic Variants in the Promoter Region of <i>miR-10b</i> and the Risk of Breast Cancer. <i>BioMed Research International</i> , 2017, 2017, 1-7.	1.9	7
136	Fine mapping the MHC region identified rs4997052 as a new variant associated with nonobstructive azoospermia in Han Chinese males. <i>Fertility and Sterility</i> , 2019, 111, 61-68.	1.0	7
137	Genetic variants associated with expression of <i>TCF19</i> contribute to the risk of head and neck cancer in Chinese population. <i>Journal of Medical Genetics</i> , 2021, , jmedgenet-2020-107410.	3.2	7
138	Genetic Variation in the 3'-Untranslated Region of <i>NBN</i> Gene Is Associated with Gastric Cancer Risk in a Chinese Population. <i>PLoS ONE</i> , 2015, 10, e0139059.	2.5	7
139	Genetic Variants at 10p11 Confer Risk of Tetralogy of Fallot in Chinese of Nanjing. <i>PLoS ONE</i> , 2014, 9, e89636.	2.5	6
140	Genetic variants in <i>SMARC</i> genes are associated with DNA damage levels in Chinese population. <i>Toxicology Letters</i> , 2014, 229, 327-332.	0.8	6
141	Potentially functional polymorphisms in <i>PAK 1</i> are associated with risk of lung cancer in a Chinese population. <i>Cancer Medicine</i> , 2015, 4, 1781-1787.	2.8	6
142	Genetic variants in multisynthetase complex genes are associated with DNA damage levels in Chinese populations. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2016, 786, 8-13.	1.0	6
143	Genetically determined height was associated with lung cancer risk in East Asian population. <i>Cancer Medicine</i> , 2018, 7, 3445-3452.	2.8	6
144	Telomere length in cervical exfoliated cells, interaction with HPV genotype, and cervical cancer occurrence among high-risk HPV-positive women. <i>Cancer Medicine</i> , 2019, 8, 4845-4851.	2.8	6

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145	Association of expression quantitative trait loci for long noncoding RNAs with lung cancer risk in Asians. <i>Molecular Carcinogenesis</i> , 2019, 58, 1303-1313.	2.7	6
146	Transcriptome-wide association study for persistent hepatitis B virus infection and related hepatocellular carcinoma. <i>Liver International</i> , 2020, 40, 2117-2127.	3.9	6
147	Cross-Cancer Pleiotropic Analysis Reveals Novel Susceptibility Loci for Lung Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 1492.	2.8	6
148	Association Analysis of Driver Gene-Related Genetic Variants Identified Novel Lung Cancer Susceptibility Loci with 20,871 Lung Cancer Cases and 15,971 Controls. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 1423-1429.	2.5	6
149	Prediction and clinical utility of a liver cancer risk model in Chinese adults: A prospective cohort study of 0.5 million people. <i>International Journal of Cancer</i> , 2021, 148, 2924-2934.	5.1	6
150	Identification of A-to-I RNA editing profiles and their clinical relevance in lung adenocarcinoma. <i>Science China Life Sciences</i> , 2022, 65, 19-32.	4.9	6
151	Whole-exome sequencing reveals common and rare variants in immunologic and neurological genes implicated in achalasia. <i>American Journal of Human Genetics</i> , 2021, 108, 1478-1487.	6.2	6
152	Stress, anxiety, and depression in infertile couples are not associated with a first IVF or ICSI treatment outcome. <i>BMC Pregnancy and Childbirth</i> , 2021, 21, 725.	2.4	6
153	Hypomethylation-activated cancer-testis gene LIN28B promotes cell proliferation and metastasis in gastric cancer. <i>Gene</i> , 2022, 813, 146115.	2.2	6
154	Genetic risk, metabolic syndrome, and gastrointestinal cancer risk: A prospective cohort study. <i>Cancer Medicine</i> , 2023, 12, 597-605.	2.8	6
155	The functional polymorphisms of LIS1 are associated with acute myeloid leukemia risk in a Han Chinese population. <i>Leukemia Research</i> , 2017, 54, 7-11.	0.8	5
156	Gastric cancer may share genetic predisposition with esophageal squamous cell carcinoma in Chinese populations. <i>Journal of Human Genetics</i> , 2018, 63, 1159-1168.	2.3	5
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