

# Guangfu Jin

## List of Publications by Year in descending order

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Version: 2024-02-01

178  
papers

7,133  
citations

87723

38  
h-index

74018

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. <i>Science China Life Sciences</i> , 2020, 63, 706-711.	2.3	1,090
2	A genome-wide association study identifies two new lung cancer susceptibility loci at 13q12.12 and 22q12.2 in Han Chinese. <i>Nature Genetics</i> , 2011, 43, 792-796.	9.4	340
3	Genome-wide association study identifies three new susceptibility loci for esophageal squamous-cell carcinoma in Chinese populations. <i>Nature Genetics</i> , 2011, 43, 679-684.	9.4	260
4	A genome-wide association study identifies new susceptibility loci for non-cardia gastric cancer at 3q13.31 and 5p13.1. <i>Nature Genetics</i> , 2011, 43, 1215-1218.	9.4	250
5	Genome-wide association analyses of esophageal squamous cell carcinoma in Chinese identify multiple susceptibility loci and gene-environment interactions. <i>Nature Genetics</i> , 2012, 44, 1090-1097.	9.4	238
6	Plasma miRNA as early biomarkers for detecting hepatocellular carcinoma. <i>International Journal of Cancer</i> , 2015, 137, 1679-1690.	2.3	188
7	The 5p15.33 Locus Is Associated with Risk of Lung Adenocarcinoma in Never-Smoking Females in Asia. <i>PLoS Genetics</i> , 2010, 6, e1001051.	1.5	168
8	A novel plasma circular RNA circFARSA is a potential biomarker for non-small cell lung cancer. <i>Cancer Medicine</i> , 2018, 7, 2783-2791.	1.3	167
9	Identification of risk loci and a polygenic risk score for lung cancer: a large-scale prospective cohort study in Chinese populations. <i>Lancet Respiratory Medicine</i> , 2019, 7, 881-891.	5.2	167
10	Analysis of Heritability and Shared Heritability Based on Genome-Wide Association Studies for Thirteen Cancer Types. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv279.	3.0	152
11	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
12	New loci associated with chronic hepatitis B virus infection in Han Chinese. <i>Nature Genetics</i> , 2013, 45, 1499-1503.	9.4	140
13	Association analyses identify multiple new lung cancer susceptibility loci and their interactions with smoking in the Chinese population. <i>Nature Genetics</i> , 2012, 44, 895-899.	9.4	129
14	Systematic identification of genes with a cancer-testis expression pattern in 19 cancer types. <i>Nature Communications</i> , 2016, 7, 10499.	5.8	124
15	Genetic risk, incident gastric cancer, and healthy lifestyle: a meta-analysis of genome-wide association studies and prospective cohort study. <i>Lancet Oncology</i> , 2020, 21, 1378-1386.	5.1	123
16	Associations Between Hepatitis B Virus Infection and Risk of All Cancer Types. <i>JAMA Network Open</i> , 2019, 2, e195718.	2.8	114
17	Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. <i>Human Molecular Genetics</i> , 2015, 24, 1791-1800.	1.4	105
18	The association between telomere length and cancer risk in population studies. <i>Scientific Reports</i> , 2016, 6, 22243.	1.6	101

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19	Prevalence of <i>Helicobacter pylori</i> infection in China: A systematic review and meta-analysis. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2022, 37, 464-470.	1.4	94
20	Genetic Variants at 6p21.1 and 7p15.3 Are Associated with Risk of Multiple Cancers in Han Chinese. <i>American Journal of Human Genetics</i> , 2012, 91, 928-934.	2.6	76
21	Genetic variants at 1q22 and 10q23 reproducibly associated with gastric cancer susceptibility in a Chinese population. <i>Carcinogenesis</i> , 2011, 32, 848-852.	1.3	73
22	Common genetic variants on 5p15.33 contribute to risk of lung adenocarcinoma in a Chinese population. <i>Carcinogenesis</i> , 2009, 30, 987-990.	1.3	72
23	Identification of new susceptibility loci for gastric non-cardia adenocarcinoma: pooled results from two Chinese genome-wide association studies. <i>Gut</i> , 2017, 66, 581-587.	6.1	68
24	Whole-genome sequencing reveals genomic signatures associated with the inflammatory microenvironments in Chinese NSCLC patients. <i>Nature Communications</i> , 2018, 9, 2054.	5.8	68
25	Estimation of heritability for nine common cancers using data from genome-wide association studies in Chinese population. <i>International Journal of Cancer</i> , 2017, 140, 329-336.	2.3	66
26	Association analysis identifies new risk loci for non-obstructive azoospermia in Chinese men. <i>Nature Communications</i> , 2014, 5, 3857.	5.8	64
27	A cancer-testis non-coding RNA LIN28B-AS1 activates driver gene LIN28B by interacting with IGF2BP1 in lung adenocarcinoma. <i>Oncogene</i> , 2019, 38, 1611-1624.	2.6	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. <i>Diabetes Care</i> , 2019, 42, 1414-1421.	4.3	60
29	Vitamin D Status and Risk of All-Cause and Cause-Specific Mortality in a Large Cohort: Results From the UK Biobank. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, e3606-e3619.	1.8	60
30	Exome Array Analysis Identifies Variants in SPOCD1 and BTN3A2 That Affect Risk for Gastric Cancer. <i>Gastroenterology</i> , 2017, 152, 2011-2021.	0.6	58
31	Role of <i>ATG10</i> expression quantitative trait loci in non-small cell lung cancer survival. <i>International Journal of Cancer</i> , 2016, 139, 1564-1573.	2.3	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. <i>Human Molecular Genetics</i> , 2016, 26, ddw414.	1.4	50
33	Meta-analysis of genome-wide association studies identifies multiple lung cancer susceptibility loci in never-smoking Asian women. <i>Human Molecular Genetics</i> , 2016, 25, 620-629.	1.4	50
34	Genetic Risk for Overall Cancer and the Benefit of Adherence to a Healthy Lifestyle. <i>Cancer Research</i> , 2021, 81, 4618-4627.	0.4	48
35	A genome-wide gene-environment interaction analysis for tobacco smoke and lung cancer susceptibility. <i>Carcinogenesis</i> , 2014, 35, 1528-1535.	1.3	47
36	A functional variant in miR-155 regulation region contributes to lung cancer risk and survival. <i>Oncotarget</i> , 2015, 6, 42781-42792.	0.8	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.	1.3	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.	0.4	45
39	Independent prognostic role of human papillomavirus genotype in cervical cancer. <i>BMC Infectious Diseases</i> , 2017, 17, 391.	1.3	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.	2.6	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.	2.2	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.	6.1	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.	1.8	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.	0.4	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.	1.4	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.	1.4	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.	1.3	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.	1.1	30
49	Genetic variants in regulatory regions of microRNAs are associated with lung cancer risk. <i>Oncotarget</i> , 2016, 7, 47966-47974.	0.8	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.	0.8	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.	2.2	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.	3.8	27
53	Association analysis identifies new risk loci for congenital heart disease in Chinese populations. <i>Nature Communications</i> , 2015, 6, 8082.	5.8	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.	2.3	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, .	0.6	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.	5.7	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.	2.0	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.	1.3	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.	4.7	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.	2.3	22
61	Comprehensive characterization of cancer-related testis genes in testicular germ cell tumor. <i>Cancer Medicine</i> , 2019, 8, 3511-3519.	1.3	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.	1.3	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.	0.9	21
64	Evaluation of genetic variants in autophagy pathway genes as prognostic biomarkers for breast cancer. <i>Gene</i> , 2017, 627, 549-555.	1.0	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.	1.5	21
66	Family History and Stroke Risk in China: Evidence from a Large Cohort Study. <i>Journal of Stroke</i> , 2017, 19, 188-195.	1.4	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.	1.4	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.	4.6	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.	1.1	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.	1.1	19
71	Germline genetic variants were interactively associated with somatic alterations in gastric cancer. <i>Cancer Medicine</i> , 2018, 7, 3912-3920.	1.3	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.	0.5	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.	2.3	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.	2.5	19
75	A polygenic risk score for nasopharyngeal carcinoma shows potential for risk stratification and personalized screening. <i>Nature Communications</i> , 2022, 13, 1966.	5.8	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.	1.2	18
77	The sex ratio of singleton and twin delivery offspring in assisted reproductive technology in China. <i>Scientific Reports</i> , 2017, 7, 7754.	1.6	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.	1.4	18
79	LncPSCA in the 8q24.3 risk locus drives gastric cancer through destabilizing DDX5. <i>EMBO Reports</i> , 2021, 22, e52707.	2.0	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.	1.1	18
81	Human genome epidemiology, progress and future. <i>Journal of Biomedical Research</i> , 2013, 27, 167-169.	0.7	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.	1.6	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.	2.3	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.	1.9	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.	1.6	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.	1.2	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.	0.6	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.	1.2	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.	1.6	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.	1.3	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.	0.5	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.	1.3	15
93	Evaluation of CpG-SNPs in miRNA promoters and risk of breast cancer. <i>Gene</i> , 2018, 651, 1-8.	1.0	15
94	Mendelian randomization study of telomere length and lung cancer risk in East Asian population. <i>Cancer Medicine</i> , 2019, 8, 7469-7476.	1.3	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.	1.3	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.	2.3	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.	2.9	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.	2.0	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.	1.7	14
100	Genetic association of telomere length with hepatocellular carcinoma risk: A Mendelian randomization analysis. <i>Cancer Epidemiology</i> , 2017, 50, 39-45.	0.8	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.	1.3	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.	2.3	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.	1.6	13
104	Interaction analysis between germline susceptibility loci and somatic alterations in lung cancer. <i>International Journal of Cancer</i> , 2018, 143, 878-885.	2.3	13
105	<i>ATG12</i> 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.	1.3	13
106	An esophageal adenocarcinoma susceptibility locus at 9q22 also confers risk to esophageal squamous cell carcinoma by regulating the function of <i>BARX1</i> . <i>Cancer Letters</i> , 2018, 421, 103-111.	3.2	13
107	Functional genetic variants in centrosome-related genes <i>CEP72</i> and <i>YWHAG</i> confer susceptibility to gastric cancer. <i>Archives of Toxicology</i> , 2020, 94, 2861-2872.	1.9	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.	1.3	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.	1.6	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.	1.6	12
111	Exome-Wide Association Study Identified New Risk Loci for Hirschsprung's Disease. <i>Molecular Neurobiology</i> , 2017, 54, 1777-1785.	1.9	12
112	Low-frequency nonsynonymous variants in <i>FKBPL</i> and <i>ARPC1B</i> genes are associated with breast cancer risk in Chinese women. <i>Molecular Carcinogenesis</i> , 2017, 56, 774-780.	1.3	12
113	Association of Maternal Dietary Patterns during Gestation and Offspring Neurodevelopment. <i>Nutrients</i> , 2022, 14, 730.	1.7	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.	1.3	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.	0.8	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.	1.5	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.	0.5	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.	0.4	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.	1.3	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.	1.6	10
121	A clinical, biologic and mechanistic analysis of the role of ZNF692 in cervical cancer. <i>Gynecologic Oncology</i> , 2019, 152, 396-407.	0.6	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.	1.1	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.	0.8	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.	0.9	9
125	Genetic variants in chromatin-remodeling pathway associated with lung cancer risk in a Chinese population. <i>Gene</i> , 2016, 587, 178-182.	1.0	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.	4.3	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.	1.4	9
128	Functional polymorphisms in <i>NR3C1</i> are associated with gastric cancer risk in Chinese population. <i>Oncotarget</i> , 2017, 8, 105312-105319.	0.8	9
129	Pathway analysis for a genome-wide association study of pneumoconiosis. <i>Toxicology Letters</i> , 2015, 232, 284-292.	0.4	8
130	Multi-marker analysis of genomic annotation on gastric cancer GWAS data from Chinese populations. <i>Gastric Cancer</i> , 2019, 22, 60-68.	2.7	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.	1.0	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.	2.3	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.	1.8	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.	1.3	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.	0.9	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.	0.5	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.	1.5	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.	1.1	7
139	Genetic Variants at 10p11 Confer Risk of Tetralogy of Fallot in Chinese of Nanjing. <i>PLoS ONE</i> , 2014, 9, e89636.	1.1	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.	0.4	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.	1.3	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.	0.4	6
143	Genetically determined height was associated with lung cancer risk in East Asian population. <i>Cancer Medicine</i> , 2018, 7, 3445-3452.	1.3	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.	1.3	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.	1.3	6
146	Transcriptome-wide association study for persistent hepatitis B virus infection and related hepatocellular carcinoma. <i>Liver International</i> , 2020, 40, 2117-2127.	1.9	6
147	Cross-Cancer Pleiotropic Analysis Reveals Novel Susceptibility Loci for Lung Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 1492.	1.3	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.	1.1	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.	2.3	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.	2.3	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.	2.6	6
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