Juncheng Dai

List of Publications by Citations

171 papers	3,921 citations	32 h-index	57 g-index
178 ext. papers	5,040 ext. citations	6.9 avg, IF	4.64 L-index

#	Paper	IF	Citations
171	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, 792-6	36.3	288
170	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. *Nature Genetics*, **2017**, 49, 1126-1132	36.3	246
169	A genome-wide association study identifies new susceptibility loci for non-cardia gastric cancer at 3q13.31 and 5p13.1. *Nature Genetics*, **2011**, 43, 1215-8	36.3	215
168	A five-microRNA panel in plasma was identified as potential biomarker for early detection of gastric cancer. *British Journal of Cancer*, **2014**, 110, 2291-9	8.7	171
167	Plasma miRNAs as early biomarkers for detecting hepatocellular carcinoma. *International Journal of Cancer*, **2015**, 137, 1679-90	7.5	152
166	GWAS identifies novel susceptibility loci on 6p21.32 and 21q21.3 for hepatocellular carcinoma in chronic hepatitis B virus carriers. *PLoS Genetics*, **2012**, 8, e1002791	6	142
165	A novel plasma circular RNA circFARSA is a potential biomarker for non-small cell lung cancer. *Cancer Medicine*, **2018**, 7, 2783-2791	4.8	131
164	Genome-wide association study in Chinese identifies novel loci for blood pressure and hypertension. *Human Molecular Genetics*, **2015**, 24, 865-74	5.6	129
163	Association analyses identify multiple new lung cancer susceptibility loci and their interactions with smoking in the Chinese population. *Nature Genetics*, **2012**, 44, 895-9	36.3	108
162	Epithelial-type systemic breast carcinoma cells with a restricted mesenchymal transition are a major source of metastasis. *Science Advances*, **2019**, 5, eaav4275	14.3	81
161	Systematic identification of genes with a cancer-testis expression pattern in 19 cancer types. *Nature Communications*, **2016**, 7, 10499	17.4	80
160	Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. *Human Molecular Genetics*, **2015**, 24, 1791-800	5.6	71
159	A genome-wide association study identifies two risk loci for congenital heart malformations in Han Chinese populations. *Nature Genetics*, **2013**, 45, 818-21	36.3	60
158	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, 928-34	11	59
157	Identification of risk loci and a polygenic risk score for lung cancer: a large-scale prospective cohort study in Chinese populations. *Lancet Respiratory Medicine,the*, **2019**, 7, 881-891	35.1	58
156	Associations Between Hepatitis B Virus Infection and Risk of All Cancer Types. *JAMA Network Open*, **2019**, 2, e195718	10.4	54
155	Identification of new susceptibility loci for gastric non-cardia adenocarcinoma: pooled results from two Chinese genome-wide association studies. *Gut*, **2017**, 66, 581-587	19.2	51

154	Association analysis identifies new risk loci for non-obstructive azoospermia in Chinese men. *Nature Communications*, **2014**, 5, 3857	17.4	50
153	Breast cancer risk assessment with five independent genetic variants and two risk factors in Chinese women. *Breast Cancer Research*, **2012**, 14, R17	8.3	50
152	Genome-wide association study identifies new susceptibility loci for epithelial ovarian cancer in Han Chinese women. *Nature Communications*, **2014**, 5, 4682	17.4	48
151	A cancer-testis non-coding RNA LIN28B-AS1 activates driver gene LIN28B by interacting with IGF2BP1 in lung adenocarcinoma. *Oncogene*, **2019**, 38, 1611-1624	9.2	45
150	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	7.5	43
149	Whole-genome sequencing reveals genomic signatures associated with the inflammatory microenvironments in Chinese NSCLC patients. *Nature Communications*, **2018**, 9, 2054	17.4	43
148	Genetic polymorphisms in the precursor MicroRNA flanking region and non-small cell lung cancer survival. *American Journal of Respiratory and Critical Care Medicine*, **2011**, 183, 641-8	10.2	41
147	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*, **2017**, 26, 454-465	5.6	40
146	Telomere length, genetic variants and gastric cancer risk in a Chinese population. *Carcinogenesis*, **2015**, 36, 963-70	4.6	39
145	Genetic risk, incident gastric cancer, and healthy lifestyle: a meta-analysis of genome-wide association studies and prospective cohort study. *Lancet Oncology, The*, **2020**, 21, 1378-1386	21.7	38
144	A functional variant in miR-155 regulation region contributes to lung cancer risk and survival. *Oncotarget*, **2015**, 6, 42781-92	3.3	36
143	A genome-wide gene-environment interaction analysis for tobacco smoke and lung cancer susceptibility. *Carcinogenesis*, **2014**, 35, 1528-35	4.6	35
142	Role of ATG10 expression quantitative trait loci in non-small cell lung cancer survival. *International Journal of Cancer*, **2016**, 139, 1564-73	7.5	34
141	Cancer-testis gene PIWIL1 promotes cell proliferation, migration, and invasion in lung adenocarcinoma. *Cancer Medicine*, **2018**, 7, 157-166	4.8	34
140	Exome Array Analysis Identifies Variants in SPOCD1 and BTN3A2 That Affect Risk for Gastric Cancer. *Gastroenterology*, **2017**, 152, 2011-2021	13.3	32
139	Meta-analysis of genome-wide association studies identifies multiple lung cancer susceptibility loci in never-smoking Asian women. *Human Molecular Genetics*, **2016**, 25, 620-9	5.6	32
138	Hepatitis B virus genotype, mutations, human leukocyte antigen polymorphisms and their interactions in hepatocellular carcinoma: a multi-centre case-control study. *Scientific Reports*, **2015**, 5, 16489	4.9	31
137	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	14.6	30

136	Low-frequency coding variants at 6p21.33 and 20q11.21 are associated with lung cancer risk in Chinese populations. *American Journal of Human Genetics*, **2015**, 96, 832-40	11	30
135	Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. *Nature Communications*, **2018**, 9, 3221	17.4	29
134	Personal exposure to PM2.5, genetic variants and DNA damage: a multi-center population-based study in Chinese. *Toxicology Letters*, **2015**, 235, 172-8	4.4	26
133	Genetic variants in regulatory regions of microRNAs are associated with lung cancer risk. *Oncotarget*, **2016**, 7, 47966-47974	3.3	26
132	Fine mapping the MHC region identified four independent variants modifying susceptibility to chronic hepatitis B in Han Chinese. *Human Molecular Genetics*, **2016**, 25, 1225-32	5.6	24
131	Fine mapping of MHC region in lung cancer highlights independent susceptibility loci by ethnicity. *Nature Communications*, **2018**, 9, 3927	17.4	24
130	Genome-wide association study of myelosuppression in non-small-cell lung cancer patients with platinum-based chemotherapy. *Pharmacogenomics Journal*, **2016**, 16, 41-6	3.5	23
129	Prediction models and risk assessment for silicosis using a retrospective cohort study among workers exposed to silica in China. *Scientific Reports*, **2015**, 5, 11059	4.9	22
128	Genetic variants on chromosome 6p21.1 and 6p22.3 are associated with type 2 diabetes risk: a case-control study in Han Chinese. *Journal of Human Genetics*, **2012**, 57, 320-5	4.3	22
127	Prognostic significance of survivin polymorphisms on non-small cell lung cancer survival. *Journal of Thoracic Oncology*, **2010**, 5, 1748-54	8.9	22
126	Genome-wide Association Study on Platinum-induced Hepatotoxicity in Non-Small Cell Lung Cancer Patients. *Scientific Reports*, **2015**, 5, 11556	4.9	20
125	Association analysis identifies new risk loci for congenital heart disease in Chinese populations. *Nature Communications*, **2015**, 6, 8082	17.4	19
124	Systematic analysis reveals long noncoding RNAs regulating neighboring transcription factors in human cancers. *Biochimica Et Biophysica Acta - Molecular Basis of Disease*, **2018**, 1864, 2785-2792	6.9	19
123	A polymorphism in miR-1262 regulatory region confers the risk of lung cancer in Chinese population. *International Journal of Cancer*, **2017**, 141, 958-966	7.5	18
122	Genome-wide copy number variation analysis identified ANO1 as a novel oncogene and prognostic biomarker in esophageal squamous cell cancer. *Carcinogenesis*, **2019**, 40, 1198-1208	4.6	18
121	A Screen for Genomic Disorders of Infertility Identifies MAST2 Duplications Associated with Nonobstructive Azoospermia in Humans. *Biology of Reproduction*, **2015**, 93, 61	3.9	18
120	High mitochondrial DNA copy number was associated with an increased gastric cancer risk in a Chinese population. *Molecular Carcinogenesis*, **2017**, 56, 2593-2600	5	18
119	Evaluation of genetic variants in autophagy pathway genes as prognostic biomarkers for breast cancer. *Gene*, **2017**, 627, 549-555	3.8	18

118	Genetic variations in the flanking regions of miR-101-2 are associated with increased risk of breast cancer. *PLoS ONE*, **2014**, 9, e86319	3.7	18
117	Meta-analysis of genome-wide association studies and functional assays decipher susceptibility genes for gastric cancer in Chinese populations. *Gut*, **2020**, 69, 641-651	19.2	18
116	Systematic cancer-testis gene expression analysis identified CDCA5 as a potential therapeutic target in esophageal squamous cell carcinoma. *EBioMedicine*, **2019**, 46, 54-65	8.8	17
115	Circulating Tumor Cells Enriched by the Depletion of Leukocytes with Bi-Antibodies in Non-Small Cell Lung Cancer: Potential Clinical Application. *PLoS ONE*, **2015**, 10, e0137076	3.7	16
114	Genetically predicted high body mass index is associated with increased gastric cancer risk. *European Journal of Human Genetics*, **2017**, 25, 1061-1066	5.3	15
113	Metabolome-wide association study identified the association between a circulating polyunsaturated fatty acids variant rs174548 and lung cancer. *Carcinogenesis*, **2017**, 38, 1147-1154	4.6	14
112	Cumulative effect and predictive value of genetic variants associated with type 2 diabetes in Han Chinese: a case-control study. *PLoS ONE*, **2015**, 10, e0116537	3.7	14
111	Blood groups A and AB are associated with increased gastric cancer risk: evidence from a large genetic study and systematic review. *BMC Cancer*, **2019**, 19, 164	4.8	13
110	Systematical analyses of variants in CTCF-binding sites identified a novel lung cancer susceptibility locus among Chinese population. *Scientific Reports*, **2015**, 5, 7833	4.9	13
109	Elevated Platelet Count Appears to Be Causally Associated with Increased Risk of Lung Cancer: A Mendelian Randomization Analysis. *Cancer Epidemiology Biomarkers and Prevention*, **2019**, 28, 935-942	4	12
108	Comprehensive characterization of cancer-testis genes in testicular germ cell tumor. *Cancer Medicine*, **2019**, 8, 3511-3519	4.8	12
107	HLA-DP is the cervical cancer susceptibility loci among women infected by high-risk human papillomavirus: potential implication for triage of human papillomavirus-positive women. *Tumor Biology*, **2016**, 37, 8019-25	2.9	11
106	Host immune gene polymorphisms were associated with the prognosis of non-small-cell lung cancer in Chinese. *International Journal of Cancer*, **2012**, 130, 671-6	7.5	11
105	Transcriptome-wide association study revealed two novel genes associated with nonobstructive azoospermia in a Chinese population. *Fertility and Sterility*, **2017**, 108, 1056-1062.e4	4.8	11
104	The eQTL-missense polymorphisms of APOBEC3H are associated with lung cancer risk in a Han Chinese population. *Scientific Reports*, **2015**, 5, 14969	4.9	11
103	Association of KCTD10, MVK, and MMAB polymorphisms with dyslipidemia and coronary heart disease in Han Chinese population. *Lipids in Health and Disease*, **2016**, 15, 171	4.4	11
102	Telomere length, genetic variants and risk of squamous cell carcinoma of the head and neck in Southeast Chinese. *Scientific Reports*, **2016**, 6, 20675	4.9	11
101	Genetic variants, PM exposure level and global DNA methylation level: A multi-center population-based study in Chinese. *Toxicology Letters*, **2017**, 269, 77-82	4.4	10

100	Interaction analysis between germline susceptibility loci and somatic alterations in lung cancer. *International Journal of Cancer*, **2018**, 143, 878-885	7.5	10
99	ATG12 expression quantitative trait loci associated with head and neck squamous cell carcinoma risk in a Chinese Han population. *Molecular Carcinogenesis*, **2018**, 57, 1030-1037	5	10
98	Evaluation of CpG-SNPs in miRNA promoters and risk of breast cancer. *Gene*, **2018**, 651, 1-8	3.8	10
97	Genetic association of telomere length with hepatocellular carcinoma risk: A Mendelian randomization analysis. *Cancer Epidemiology*, **2017**, 50, 39-45	2.8	10
96	Whole-exome sequencing identifies SGCD and ACVRL1 mutations associated with total anomalous pulmonary venous return (TAPVR) in Chinese population. *Oncotarget*, **2017**, 8, 27812-27819	3.3	10
95	Genetic variants at 9p21.3 are associated with risk of esophageal squamous cell carcinoma in a Chinese population. *Cancer Science*, **2017**, 108, 250-255	6.9	9
94	Fine mapping of chromosome 5p15.33 identifies novel lung cancer susceptibility loci in Han Chinese. *International Journal of Cancer*, **2017**, 141, 447-456	7.5	9
93	An esophageal adenocarcinoma susceptibility locus at 9q22 also confers risk to esophageal squamous cell carcinoma by regulating the function of BARX1. *Cancer Letters*, **2018**, 421, 103-111	9.9	9
92	Low-frequency nonsynonymous variants in FKBPL and ARPC1B genes are associated with breast cancer risk in Chinese women. *Molecular Carcinogenesis*, **2017**, 56, 774-780	5	9
91	Systematic identification of long non-coding RNAs with cancer-testis expression patterns in 14 cancer types. *Oncotarget*, **2017**, 8, 94769-94779	3.3	9
90	MicroRNA-210 promotes spinal cord injury recovery by inhibiting inflammation via the JAK-STAT pathway. *European Review for Medical and Pharmacological Sciences*, **2018**, 22, 6609-6615	2.9	9
89	Comprehensive characterization of functional eRNAs in lung adenocarcinoma reveals novel regulators and a prognosis-related molecular subtype. *Theranostics*, **2020**, 10, 11264-11277	12.1	9
88	A nomogram to predict overall survival of patients with early stage non-small cell lung cancer. *Journal of Thoracic Disease*, **2019**, 11, 5407-5416	2.6	9
87	Spontaneous Seroclearance of Hepatitis B Surface Antigen and Risk of Hepatocellular Carcinoma. *Clinical Gastroenterology and Hepatology*, **2019**, 17, 1204-1206	6.9	9
86	Integrating expression-related SNPs into genome-wide gene- and pathway-based analyses identified novel lung cancer susceptibility genes. *International Journal of Cancer*, **2018**, 142, 1602-1610	7.5	9
85	Genetic Risk for Overall Cancer and the Benefit of Adherence to a Healthy Lifestyle. *Cancer Research*, **2021**, 81, 4618-4627	10.1	9
84	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. *Journal of Thoracic Oncology*, **2017**, 12, 644-656	8.9	8
83	Potentially functional variants in lncRNAs are associated with breast cancer risk in a Chinese population. *Molecular Carcinogenesis*, **2017**, 56, 2048-2057	5	8

82	HBV mutations in EnhII/BCP/PC region contribute to the prognosis of hepatocellular carcinoma. *Cancer Medicine*, **2019**, 8, 3086-3093	4.8	8
81	Identification of lung cancer histology-specific variants applying Bayesian framework variant prioritization approaches within the TRICL and ILCCO consortia. *Carcinogenesis*, **2015**, 36, 1314-26	4.6	8
80	Polymorphisms in alternative splicing associated genes are associated with lung cancer risk in a Chinese population. *Lung Cancer*, **2015**, 89, 238-42	5.9	8
79	U-shaped association between telomere length and esophageal squamous cell carcinoma risk: a case-control study in Chinese population. *Frontiers of Medicine*, **2015**, 9, 478-86	12	8
78	Genome-wide compound heterozygosity analysis highlighted 4 novel susceptibility loci for congenital heart disease in Chinese population. *Clinical Genetics*, **2018**, 94, 296-302	4	8
77	Mendelian randomization study of telomere length and lung cancer risk in East Asian population. *Cancer Medicine*, **2019**, 8, 7469-7476	4.8	8
76	Fine-mapping the MHC region in Asian populations identified novel variants modifying susceptibility to lung cancer. *Lung Cancer*, **2017**, 112, 169-175	5.9	8
75	Risk assessment models for genetic risk predictors of lung cancer using two-stage replication for Asian and European populations. *Oncotarget*, **2017**, 8, 53959-53967	3.3	8
74	Association Between Levels of Sex Hormones and Risk of Esophageal Adenocarcinoma and Barrett's Esophagus. *Clinical Gastroenterology and Hepatology*, **2020**, 18, 2701-2709.e3	6.9	8
73	Tuberculosis infection and lung adenocarcinoma: Mendelian randomization and pathway analysis of genome-wide association study data from never-smoking Asian women. *Genomics*, **2020**, 112, 1223-1232	4.3	8
72	Targeted sequencing of chromosome 15q25 identified novel variants associated with risk of lung cancer and smoking behavior in Chinese. *Carcinogenesis*, **2017**, 38, 552-558	4.6	7
71	Genetic variants in Ser-Arg protein-coding genes are associated with the risk of nonobstructive azoospermia in Chinese men. *Fertility and Sterility*, **2014**, 101, 1711-7.e1-2	4.8	7
70	Association of assisted reproductive technology, germline de novo mutations and congenital heart defects in a prospective birth cohort study. *Cell Research*, **2021**, 31, 919-928	24.7	7
69	Dataset for regulation between lncRNAs and their nearby protein-coding genes in human cancers. *Data in Brief*, **2018**, 19, 1902-1906	1.2	7
68	Pathway analysis for a genome-wide association study of pneumoconiosis. *Toxicology Letters*, **2015**, 232, 284-92	4.4	6
67	Systematic analyses of genetic variants in chromatin interaction regions identified four novel lung cancer susceptibility loci. *Journal of Cancer*, **2020**, 11, 1075-1081	4.5	6
66	Mitochondrial DNA copy number is associated with risk of head and neck squamous cell carcinoma in Chinese population. *Cancer Medicine*, **2018**, 7, 2776-2782	4.8	6
65	Genetic variants in chromatin-remodeling pathway associated with lung cancer risk in a Chinese population. *Gene*, **2016**, 587, 178-82	3.8	6

64	Genetic variants in multisynthetase complex genes are associated with DNA damage levels in Chinese populations. *Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis*, **2016**, 786, 8-13	3.3	6
63	Multi-marker analysis of genomic annotation on gastric cancer GWAS data from Chinese populations. *Gastric Cancer*, **2019**, 22, 60-68	7.6	6
62	Genetic variants at 10p11 confer risk of Tetralogy of Fallot in Chinese of Nanjing. *PLoS ONE*, **2014**, 9, e89636	3.7	6
61	Genetic Variation in the 3′ Untranslated Region of NBN Gene Is Associated with Gastric Cancer Risk in a Chinese Population. *PLoS ONE*, **2015**, 10, e0139059	3.7	6
60	Comprehensive functional annotation of susceptibility variants identifies genetic heterogeneity between lung adenocarcinoma and squamous cell carcinoma. *Frontiers of Medicine*, **2021**, 15, 275-291	1.2	6
59	Genetic variants in nuclear DNA along with environmental factors modify mitochondrial DNA copy number: a population-based exome-wide association study. *BMC Genomics*, **2018**, 19, 752	4.5	6
58	A potentially functional polymorphism in ABCG2 predicts clinical outcome of non-small cell lung cancer in a Chinese population. *Pharmacogenomics Journal*, **2017**, 17, 280-285	3.5	5
57	A functional SNP rs1892901 in FOSL1 is associated with gastric cancer in Chinese population. *Scientific Reports*, **2017**, 7, 41737	4.9	5
56	Leukocyte telomere length, lipid parameters and gestational diabetes risk: a case-control study in a Chinese population. *Scientific Reports*, **2019**, 9, 8483	4.9	5
55	Association of expression quantitative trait loci for long noncoding RNAs with lung cancer risk in Asians. *Molecular Carcinogenesis*, **2019**, 58, 1303-1313	5	5
54	Genetic variations in miR-125 family and the survival of non-small cell lung cancer in Chinese population. *Cancer Medicine*, **2019**, 8, 2636-2645	4.8	5
53	Genetic variants in SMARC genes are associated with DNA damage levels in Chinese population. *Toxicology Letters*, **2014**, 229, 327-32	4.4	5
52	Potentially functional polymorphisms in PAK1 are associated with risk of lung cancer in a Chinese population. *Cancer Medicine*, **2015**, 4, 1781-7	4.8	5
51	Family-based whole-exome sequencing identifies novel loss-of-function mutations of for Marfan syndrome. *PeerJ*, **2018**, 6, e5927	3.1	5
50	KIT polymorphisms were associated with the risk for head and neck squamous carcinoma in Chinese population. *Molecular Carcinogenesis*, **2017**, 56, 232-237	5	4
49	Effects of potentially functional polymorphisms in suppressor of cytokine signaling 3 (SOCS3) on the risk of head and neck squamous cancer. *Journal of Oral Pathology and Medicine*, **2017**, 46, 598-602	3.3	4
48	Polymorphisms in CARS are associated with gastric cancer risk: a two-stage case-control study in the Chinese population. *Gastric Cancer*, **2017**, 20, 940-947	7.6	4
47	Family-based whole-genome sequencing identifies compound heterozygous protein-coding and noncoding mutations in tetralogy of Fallot. *Gene*, **2020**, 741, 144555	3.8	4

46	Association of 48 type 2 diabetes susceptibility loci with fasting plasma glucose and lipid levels in Chinese Hans. *Diabetes Research and Clinical Practice*, **2018**, 139, 114-121	7.4	4
45	A genetic variant at KIF1B predicts clinical outcome of HBV-related hepatocellular carcinoma in Chinese. *Cancer Epidemiology*, **2014**, 38, 608-12	2.8	4
44	A cis-eQTL genetic variant of the cancer-testis gene CCDC116 is associated with risk of multiple cancers. *Human Genetics*, **2017**, 136, 987-997	6.3	4
43	Relationships between sleep traits and lung cancer risk: a prospective cohort study in UK Biobank. *Sleep*, **2021**, 44,	1.1	4
42	Associations Between Sleep Quality and Health Span: A Prospective Cohort Study Based on 328,850 UK Biobank Participants. *Frontiers in Genetics*, **2021**, 12, 663449	4.5	4
41	Single-cell RNA-Seq reveals a highly coordinated transcriptional program in mouse germ cells during primordial follicle formation. *Aging Cell*, **2021**, 20, e13424	9.9	4
40	Fine mapping the MHC region identified rs4997052 as a new variant associated with nonobstructive azoospermia in Han Chinese males. *Fertility and Sterility*, **2019**, 111, 61-68	4.8	4
39	Integrated gene-based and pathway analyses using UK Biobank data identify novel genes for chronic respiratory diseases. *Gene*, **2021**, 767, 145287	3.8	4
38	Genome-wide analysis of expression quantitative trait loci identified potential lung cancer susceptibility variants among Asian populations. *Carcinogenesis*, **2019**, 40, 263-268	4.6	3
37	Integrating of genomic and transcriptomic profiles for the prognostic assessment of breast cancer. *Breast Cancer Research and Treatment*, **2019**, 175, 691-699	4.4	3
36	Genetic variants of H2AX gene were associated with PM2.5-modulated DNA damage levels in Chinese Han populations. *Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis*, **2015**, 778, 41-5	3.3	3
35	Genomic Signature of Mismatch Repair Deficiency in Areca Nut-Related Oral Cancer. *Journal of Dental Research*, **2020**, 99, 1252-1261	8.1	3
34	Cross-Cancer Pleiotropic Analysis Reveals Novel Susceptibility Loci for Lung Cancer. *Frontiers in Oncology*, **2019**, 9, 1492	5.3	3
33	Functional Polymorphisms in Are Related to Hepatocellular Carcinoma Risk in Chinese Population. *BioMed Research International*, **2018**, 2018, 1252849	3	3
32	Genetic variants affecting telomere length are associated with the prognosis of esophageal squamous cell carcinoma in a Chinese population. *Molecular Carcinogenesis*, **2017**, 56, 1021-1029	5	3
31	Genetic variants at 10q23.33 are associated with plasma lipid levels in a Chinese population. *Journal of Biomedical Research*, **2014**, 28, 53-8	1.5	3
30	Systematic analyses of regulatory variants in DNase I hypersensitive sites identified two novel lung cancer susceptibility loci. *Carcinogenesis*, **2019**, 40, 432-440	4.6	3
29	Gastric cancer may share genetic predisposition with esophageal squamous cell carcinoma in Chinese populations. *Journal of Human Genetics*, **2018**, 63, 1159-1168	4.3	3

28	Systematical analyses of variants in DNase I hypersensitive sites to identify hepatocellular carcinoma susceptibility loci in a Chinese population. *Journal of Gastroenterology and Hepatology (Australia)*, **2017**, 32, 1887-1894	4	2
27	Genetic Association of Plasma Homocysteine Levels with Gastric Cancer Risk: A Two-Sample Mendelian Randomization Study. *Cancer Epidemiology Biomarkers and Prevention*, **2020**, 29, 487-492	4	2
26	Genetic Variants in the Promoter Region of and the Risk of Breast Cancer. *BioMed Research International*, **2017**, 2017, 2352874	3	2
25	Predictors of Hypertension in Mauritians with Normotension and Prehypertension at Baseline: A Cohort Study. *International Journal of Environmental Research and Public Health*, **2018**, 15,	4.6	2
24	Potentially Functional Polymorphisms in POU5F1 Gene Are Associated with the Risk of Lung Cancer in Han Chinese. *BioMed Research International*, **2015**, 2015, 851320	3	2
23	Some tips about statistics on medical research. *Journal of Thoracic Disease*, **2015**, 7, E177-8	2.6	2
22	Genome-wide association study of INDELs identified four novel susceptibility loci associated with lung cancer risk. *International Journal of Cancer*, **2020**, 146, 2855-2864	7.5	2
21	Investigation of the relationships between sleep behaviors and risk of healthspan termination: a prospective cohort study based on 323,373 UK-Biobank participants. *Sleep and Breathing*, **2021**, 1	3.1	2
20	Identification of A-to-I RNA editing profiles and their clinical relevance in lung adenocarcinoma. *Science China Life Sciences*, **2021**, 1	8.5	2
19	Association Analysis of Driver Gene-Related Genetic Variants Identified Novel Lung Cancer Susceptibility Loci with 20,871 Lung Cancer Cases and 15,971 Controls. *Cancer Epidemiology Biomarkers and Prevention*, **2020**, 29, 1423-1429	4	2
18	Fine mapping in TERT-CLPTM1L region identified three independent lung cancer susceptibility signals: A large-scale multi-ethnic population study. *Molecular Carcinogenesis*, **2018**, 57, 1289-1299	5	2
17	Circulating C-reactive protein increases lung cancer risk: Results from a prospective cohort of UK Biobank. *International Journal of Cancer*, **2022**, 150, 47-55	7.5	2
16	Diet and Risk of Incident Lung Cancer: A Large Prospective Cohort Study in UK Biobank. *American Journal of Clinical Nutrition*, **2021**,	7	2
15	Transcriptome-wide association study for persistent hepatitis B virus infection and related hepatocellular carcinoma. *Liver International*, **2020**, 40, 2117-2127	7.9	1
14	Genetic Variations in miR-30 Family Member Regulatory Regions Are Associated with Breast Cancer Risk in a Chinese Population. *BioMed Research International*, **2020**, 2020, 8781348	3	1
13	Sex-Specific Associations of Testosterone and Genetic Factors With Health Span.. *Frontiers in Endocrinology*, **2021**, 12, 773464	5.7	1
12	Using structural analysis to explore the role of hepatitis B virus mutations in immune escape from liver cancer in Chinese, European and American populations. *Journal of Biomolecular Structure and Dynamics*, **2020**, 1-11	3.6	1
11	Analysis of the interaction effect of 48 SNPs and obesity on type 2 diabetes in Chinese Hans. *BMJ Open Diabetes Research and Care*, **2020**, 8,	4.5	1

List of Publications

10	Identification of Recurrent Variants in and across Multiple Cancers in the Chinese Population. *BioMed Research International*, **2020**, 2020, 6739823	3	1
9	Investigation of Causal Effect of Type 2 Diabetes Mellitus on Lung Cancer: A Mendelian Randomization Study. *Frontiers in Genetics*, **2021**, 12, 673687	4.5	1
8	Identification of genetic features associated with fine particulate matter (PM2.5) modulated DNA damage using improved random forest analysis. *Gene*, **2020**, 740, 144570	3.8	0
7	A cross-tissue transcriptome-wide association study identifies novel susceptibility genes for lung cancer in Chinese populations. *Human Molecular Genetics*, **2021**, 30, 1666-1676	5.6	0
6	Genome-wide gene-smoking interaction study identified novel susceptibility loci for non-small cell lung cancer in Chinese populations. *Carcinogenesis*, **2021**, 42, 1154-1161	4.6	0
5	Genetic variants in autophagy associated genes are associated with DNA damage levels in Chinese population. *Gene*, **2017**, 626, 414-419	3.8	
4	Fine Mapping in Chromosome 3q28 Identified Two Variants Associated with Lung Cancer Risk in Asian Population. *Journal of Cancer*, **2019**, 10, 1862-1869	4.5	
3	Potential functional variants of KIAA genes are associated with breast cancer risk in a case control study. *Annals of Translational Medicine*, **2021**, 9, 549	3.2	
2	Coding variants in the PCNT and CEP295 genes contribute to breast cancer risk in Chinese women. *Pathology Research and Practice*, **2021**, 225, 153581	3.4	
1	Association Between Neuroticism and Risk of Lung Cancer: Results From Observational and Mendelian Randomization Analyses.. *Frontiers in Oncology*, **2022**, 12, 836159	5.3	