Guangfu Jin

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/7300066/guangfu-jin-publications-by-year.pdf
Version: 2024-04-19

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

175 papers	4,816 citations	32 h-index	65 g-index
184 ext. papers	6,110 ext. citations	7.4 avg, IF	5.22 L-index

#	Paper	IF	Citations
175	Association of Maternal Dietary Patterns during Gestation and Offspring Neurodevelopment.. *Nutrients*, **2022**, 14,	6.7	2
174	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
173	Association Between Neuroticism and Risk of Lung Cancer: Results From Observational and Mendelian Randomization Analyses.. *Frontiers in Oncology*, **2022**, 12, 836159	5.3	
172	Association between Helicobacter pylori antibodies determined by multiplex serology and gastric cancer risk: A meta-analysis.. *Helicobacter*, **2022**, e12881	4.9	0
171	A polygenic risk score for nasopharyngeal carcinoma shows potential for risk stratification and personalized screening.. *Nature Communications*, **2022**, 13, 1966	17.4	0
170	Prevalence of Helicobacter pylori infection in China: A systematic review and meta-analysis. *Journal of Gastroenterology and Hepatology (Australia)*, **2021**,	4	7
169	Hypomethylation-activated cancer-testis gene LIN28B promotes cell proliferation and metastasis in gastric cancer.. *Gene*, **2021**, 813, 146115	3.8	0
168	Stress, anxiety, and depression in infertile couples are not associated with a first IVF or ICSI treatment outcome. *BMC Pregnancy and Childbirth*, **2021**, 21, 725	3.2	1
167	Relationships between sleep traits and lung cancer risk: a prospective cohort study in UK Biobank. *Sleep*, **2021**, 44,	1.1	4
166	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
165	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	
164	Sex-specific associations of circulating testosterone levels with all-cause and cause-specific mortality. *European Journal of Endocrinology*, **2021**, 184, 723-732	6.5	4
163	Identification of A-to-I RNA editing profiles and their clinical relevance in lung adenocarcinoma. *Science China Life Sciences*, **2021**, 1	8.5	2
162	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
161	Comprehensive functional annotation of susceptibility variants identifies genetic heterogeneity between lung adenocarcinoma and squamous cell carcinoma. *Frontiers of Medicine*, **2021**, 15, 275-291	12	6
160	Pre-diagnostic circulating concentrations of insulin-like growth factor-1 and risk of COVID-19 mortality: results from UK Biobank. *European Journal of Epidemiology*, **2021**, 36, 311-318	12.1	10
159	A nomogram for predicting lymph node metastasis in superficial esophageal squamous cell carcinoma. *Journal of Biomedical Research*, **2021**, 35, 361-370	1.5	

158	Prediction of live birth probability after in vitro fertilization and intracytoplasmic sperm injection treatment: A multi-center retrospective study in Chinese population. *Journal of Obstetrics and Gynaecology Research*, **2021**, 47, 1126-1133	1.9	0
157	Assisted reproductive technology and birth defects in a Chinese birth cohort study. *The Lancet Regional Health - Western Pacific*, **2021**, 7, 100090	5	5
156	Prediction and clinical utility of a liver cancer risk model in Chinese adults: A prospective cohort study of 0.5 million people. *International Journal of Cancer*, **2021**, 148, 2924-2934	7.5	1
155	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
154	Genetic Risk for Overall Cancer and the Benefit of Adherence to a Healthy Lifestyle. *Cancer Research*, **2021**, 81, 4618-4627	10.1	9
153	Whole-exome sequencing reveals common and rare variants in immunologic and neurological genes implicated in achalasia. *American Journal of Human Genetics*, **2021**, 108, 1478-1487	11	1
152	Diet and Risk of Incident Lung Cancer: A Large Prospective Cohort Study in UK Biobank. *American Journal of Clinical Nutrition*, **2021**,	7	2
151	LncPSCA in the 8q24.3 risk locus drives gastric cancer through destabilizing DDX5. *EMBO Reports*, **2021**, 22, e52707	6.5	2
150	The rates and medical necessity of cesarean delivery in China, 2012-2019: an inspiration from Jiangsu. *BMC Medicine*, **2021**, 19, 14	11.4	1
149	Remote modulation of lncRNA by risk variant at 16p13 underlying genetic susceptibility to gastric cancer. *Science Advances*, **2020**, 6, eaay5525	14.3	10
148	Functional genetic variants in centrosome-related genes CEP72 and YWHAG confer susceptibility to gastric cancer. *Archives of Toxicology*, **2020**, 94, 2861-2872	5.8	3
147	A nomogram for prediction of stage III/IV gastric cancer outcome after surgery: A multicenter population-based study. *Cancer Medicine*, **2020**, 9, 5490-5499	4.8	6
146	Transcriptome-wide association study for persistent hepatitis B virus infection and related hepatocellular carcinoma. *Liver International*, **2020**, 40, 2117-2127	7.9	1
145	Clinical characteristics of 24 asymptomatic infections with COVID-19 screened among close contacts in Nanjing, China. *Science China Life Sciences*, **2020**, 63, 706-711	8.5	815
144	Family-based whole-genome sequencing identifies compound heterozygous protein-coding and noncoding mutations in tetralogy of Fallot. *Gene*, **2020**, 741, 144555	3.8	4
143	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,	5.6	17
142	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
141	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

140	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
139	Tea consumption and risk of stroke in Chinese adults: a prospective cohort study of 0.5 million men and women. *American Journal of Clinical Nutrition*, **2020**, 111, 197-206	7	10
138	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
137	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
136	In vitro activity of new tetracycline analogues omadacycline and eravacycline against clinical isolates of Helicobacter pylori collected in China. *Diagnostic Microbiology and Infectious Disease*, **2020**, 98, 115129	2.9	3
135	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
134	Integration of GWAS and eQTL Analysis to Identify Risk Loci and Susceptibility Genes for Gastric Cancer. *Frontiers in Genetics*, **2020**, 11, 679	4.5	2
133	Alternations of gut microbiota composition in neonates conceived by assisted reproductive technology and its relation to infant growth. *Gut Microbes*, **2020**, 12, 1794466	8.8	1
132	Identification of Recurrent Variants in and across Multiple Cancers in the Chinese Population. *BioMed Research International*, **2020**, 2020, 6739823	3	1
131	Effect of endometrial thickness and embryo quality on live-birth rate of fresh IVF/ICSI cycles: a retrospective cohort study. *Reproductive Biology and Endocrinology*, **2020**, 18, 89	5	7
130	Cancer incidence in relation to body fatness among 0.5 million men and women: Findings from the China Kadoorie Biobank. *International Journal of Cancer*, **2020**, 146, 987-998	7.5	10
129	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
128	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
127	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
126	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
125	The inherited variations of a p53-responsive enhancer in 13q12.12 confer lung cancer risk by attenuating TNFRSF19 expression. *Genome Biology*, **2019**, 20, 103	18.3	14
124	Telomere length in cervical exfoliated cells, interaction with HPV genotype, and cervical cancer occurrence among high-risk HPV-positive women. *Cancer Medicine*, **2019**, 8, 4845-4851	4.8	4
123	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

122	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
121	Associations Between Hepatitis B Virus Infection and Risk of All Cancer Types. *JAMA Network Open*, **2019**, 2, e195718	10.4	54
120	Comprehensive characterization of cancer-testis genes in testicular germ cell tumor. *Cancer Medicine*, **2019**, 8, 3511-3519	4.8	12
119	Association of expression quantitative trait loci for long noncoding RNAs with lung cancer risk in Asians. *Molecular Carcinogenesis*, **2019**, 58, 1303-1313	5	5
118	A genetic variation in the CpG island of pseudogene GBAP1 promoter is associated with gastric cancer susceptibility. *Cancer*, **2019**, 125, 2465-2473	6.4	11
117	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
116	Cross-Cancer Pleiotropic Analysis Reveals Novel Susceptibility Loci for Lung Cancer. *Frontiers in Oncology*, **2019**, 9, 1492	5.3	3
115	Multi-marker analysis of genomic annotation on gastric cancer GWAS data from Chinese populations. *Gastric Cancer*, **2019**, 22, 60-68	7.6	6
114	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
113	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	
112	Mendelian randomization study of telomere length and lung cancer risk in East Asian population. *Cancer Medicine*, **2019**, 8, 7469-7476	4.8	8
111	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
110	A clinical, biologic and mechanistic analysis of the role of ZNF692 in cervical cancer. *Gynecologic Oncology*, **2019**, 152, 396-407	4.9	1
109	Association of Mosaic Loss of Chromosome Y with Lung Cancer Risk and Prognosis in a Chinese Population. *Journal of Thoracic Oncology*, **2019**, 14, 37-44	8.9	12
108	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
107	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
106	Interaction analysis between germline susceptibility loci and somatic alterations in lung cancer. *International Journal of Cancer*, **2018**, 143, 878-885	7.5	10
105	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

104	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
103	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
102	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
101	Evaluation of CpG-SNPs in miRNA promoters and risk of breast cancer. *Gene*, **2018**, 651, 1-8	3.8	10
100	A nomogram to predict the survival of stage IIIA-N2 non-small cell lung cancer after surgery. *Journal of Thoracic and Cardiovascular Surgery*, **2018**, 155, 1784-1792.e3	1.5	29
99	The functional polymorphisms of ARID5B and IKZF1 are associated with acute myeloid leukemia risk in a Han Chinese population. *Gene*, **2018**, 647, 115-120	3.8	4
98	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
97	Genome-wide association studies identified loci contribute to phenotypic variance of gastric cancer. *Gut*, **2018**, 67, 1366-1368	19.2	3
96	Genetic variants within 17q12 are associated with the risk of cervical cancer in the Han Chinese population. *Gene*, **2018**, 678, 124-128	3.8	1
95	Influencing factors of pregnancy loss and survival probability of clinical pregnancies conceived through assisted reproductive technology. *Reproductive Biology and Endocrinology*, **2018**, 16, 74	5	13
94	Germline genetic variants were interactively associated with somatic alterations in gastric cancer. *Cancer Medicine*, **2018**, 7, 3912-3920	4.8	2
93	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
92	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
91	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
90	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
89	Whole-genome sequencing reveals genomic signatures associated with the inflammatory microenvironments in Chinese NSCLC patients. *Nature Communications*, **2018**, 9, 2054	17.4	43
88	Genetically determined height was associated with lung cancer risk in East Asian population. *Cancer Medicine*, **2018**, 7, 3445	4.8	5
87	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

86	Exome-Wide Association Study Identified New Risk Loci for Hirschsprung's Disease. *Molecular Neurobiology*, **2017**, 54, 1777-1785	6.2	7
85	The functional polymorphisms of LIS1 are associated with acute myeloid leukemia risk in a Han Chinese population. *Leukemia Research*, **2017**, 54, 7-11	2.7	4
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	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
82	Exome Array Analysis Identifies Variants in SPOCD1 and BTN3A2 That Affect Risk for Gastric Cancer. *Gastroenterology*, **2017**, 152, 2011-2021	13.3	32
81	Potentially functional variants in lncRNAs are associated with breast cancer risk in a Chinese population. *Molecular Carcinogenesis*, **2017**, 56, 2048-2057	5	8
80	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
79	Genetic variants in autophagy associated genes are associated with DNA damage levels in Chinese population. *Gene*, **2017**, 626, 414-419	3.8	
78	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
77	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
76	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
75	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
74	Genetic Variants in the Promoter Region of and the Risk of Breast Cancer. *BioMed Research International*, **2017**, 2017, 2352874	3	2
73	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
72	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
71	The sex ratio of singleton and twin delivery offspring in assisted reproductive technology in China. *Scientific Reports*, **2017**, 7, 7754	4.9	12
70	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
69	Genetic association of telomere length with hepatocellular carcinoma risk: A Mendelian randomization analysis. *Cancer Epidemiology*, **2017**, 50, 39-45	2.8	10

68	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
67	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
66	Evaluation of genetic variants in autophagy pathway genes as prognostic biomarkers for breast cancer. *Gene*, **2017**, 627, 549-555	3.8	18
65	Independent prognostic role of human papillomavirus genotype in cervical cancer. *BMC Infectious Diseases*, **2017**, 17, 391	4	24
64	Short leukocyte telomere length, alone and in combination with smoking, contributes to increased risk of gastric cancer or esophageal squamous cell carcinoma. *Carcinogenesis*, **2017**, 38, 12-18	4.6	10
63	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
62	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
61	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
60	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
59	Systematic identification of long non-coding RNAs with cancer-testis expression patterns in 14 cancer types. *Oncotarget*, **2017**, 8, 94769-94779	3.3	9
58	Functional polymorphisms in are associated with gastric cancer risk in Chinese population. *Oncotarget*, **2017**, 8, 105312-105319	3.3	4
57	Family History and Stroke Risk in China: Evidence from a Large Cohort Study. *Journal of Stroke*, **2017**, 19, 188-195	5.6	20
56	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
55	The association between telomere length and cancer risk in population studies. *Scientific Reports*, **2016**, 6, 22243	4.9	83
54	Genetic variants in chromatin-remodeling pathway associated with lung cancer risk in a Chinese population. *Gene*, **2016**, 587, 178-82	3.8	6
53	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
52	Systematic identification of genes with a cancer-testis expression pattern in 19 cancer types. *Nature Communications*, **2016**, 7, 10499	17.4	80
51	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

50	Commentary: Post-GWAS era: What can we do beyond cancer genetic association studies?. *International Journal of Epidemiology*, **2016**, 45, 221-2	7.8	1
49	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
48	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
47	Genetic variants in regulatory regions of microRNAs are associated with lung cancer risk. *Oncotarget*, **2016**, 7, 47966-47974	3.3	26
46	miR-486-5p expression pattern in esophageal squamous cell carcinoma, gastric cancer and its prognostic value. *Oncotarget*, **2016**, 7, 15840-53	3.3	25
45	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
44	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
43	The known genetic loci for telomere length may be involved in the modification of telomeres length after birth. *Scientific Reports*, **2016**, 6, 38729	4.9	11
42	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
41	Joint effect of CENTD2 and KCNQ1 polymorphisms on the risk of type 2 diabetes mellitus among Chinese Han population. *Molecular and Cellular Endocrinology*, **2015**, 407, 46-51	4.4	9
40	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
39	Plasma miRNAs as early biomarkers for detecting hepatocellular carcinoma. *International Journal of Cancer*, **2015**, 137, 1679-90	7.5	152
38	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
37	Association analysis identifies new risk loci for congenital heart disease in Chinese populations. *Nature Communications*, **2015**, 6, 8082	17.4	19
36	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
35	Telomere length, genetic variants and gastric cancer risk in a Chinese population. *Carcinogenesis*, **2015**, 36, 963-70	4.6	39
34	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
33	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

32	Potentially functional polymorphisms in aminoacyl-tRNA synthetases genes are associated with breast cancer risk in a Chinese population. *Molecular Carcinogenesis*, **2015**, 54, 577-83	5	7
31	Pathway analysis for a genome-wide association study of pneumoconiosis. *Toxicology Letters*, **2015**, 232, 284-92	4.4	6
30	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
29	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
28	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	9.7	107
27	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
26	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
25	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
24	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
23	Genetic Variation in the 3ɄUntranslated Region of NBN Gene Is Associated with Gastric Cancer Risk in a Chinese Population. *PLoS ONE*, **2015**, 10, e0139059	3.7	6
22	A functional variant in miR-155 regulation region contributes to lung cancer risk and survival. *Oncotarget*, **2015**, 6, 42781-92	3.3	36
21	Joint analysis of three genome-wide association studies of esophageal squamous cell carcinoma in Chinese populations. *Nature Genetics*, **2014**, 46, 1001-1006	36.3	112
20	A genome-wide gene-environment interaction analysis for tobacco smoke and lung cancer susceptibility. *Carcinogenesis*, **2014**, 35, 1528-35	4.6	35
19	Genetic variants in SMARC genes are associated with DNA damage levels in Chinese population. *Toxicology Letters*, **2014**, 229, 327-32	4.4	5
18	Association analysis identifies new risk loci for non-obstructive azoospermia in Chinese men. *Nature Communications*, **2014**, 5, 3857	17.4	50
17	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
16	Genetic variants at 10p11 confer risk of Tetralogy of Fallot in Chinese of Nanjing. *PLoS ONE*, **2014**, 9, e89636	3.7	6
15	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

14	Genetic variants at 4q21, 4q23 and 12q24 are associated with esophageal squamous cell carcinoma risk in a Chinese population. *Human Genetics*, **2013**, 132, 649-56	6.3	30
13	New loci associated with chronic hepatitis B virus infection in Han Chinese. *Nature Genetics*, **2013**, 45, 1499-503	36.3	108
12	Human genome epidemiology, progress and future. *Journal of Biomedical Research*, **2013**, 27, 167-9	1.5	17
11	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
10	Genome-wide association analyses of esophageal squamous cell carcinoma in Chinese identify multiple susceptibility loci and gene-environment interactions. *Nature Genetics*, **2012**, 44, 1090-7	36.3	196
9	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
8	Genome-wide association study identifies three new susceptibility loci for esophageal squamous-cell carcinoma in Chinese populations. *Nature Genetics*, **2011**, 43, 679-84	36.3	233
7	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
6	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
5	Genetic variants at 1q22 and 10q23 reproducibly associated with gastric cancer susceptibility in a Chinese population. *Carcinogenesis*, **2011**, 32, 848-52	4.6	67
4	The 5p15.33 locus is associated with risk of lung adenocarcinoma in never-smoking females in Asia. *PLoS Genetics*, **2010**, 6, e1001051	6	141
3	Genetic variants in one-carbon metabolism-related genes contribute to NSCLC prognosis in a Chinese population. *Cancer*, **2010**, 116, 5700-9	6.4	13
2	Common genetic variants on 5p15.33 contribute to risk of lung adenocarcinoma in a Chinese population. *Carcinogenesis*, **2009**, 30, 987-90	4.6	63
1	Putative functional polymorphisms of MMP9 predict survival of NSCLC in a Chinese population. *International Journal of Cancer*, **2009**, 124, 2172-8	7.5	21