

# Chen Wu

## List of Publications by Year in descending order

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134  
papers

10,046  
citations

31976

53  
h-index

38395

95  
g-index

139  
all docs

139  
docs citations

139  
times ranked

16942  
citing authors

#	ARTICLE	IF	CITATIONS
1	Multi-omic characterization of genome-wide abnormal DNA methylation reveals diagnostic and prognostic markers for esophageal squamous-cell carcinoma. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 53.	17.1	22
2	Efficacy and safety of camrelizumab plus apatinib during the perioperative period in resectable hepatocellular carcinoma: a single-arm, open label, phase II clinical trial. , 2022, 10, e004656.		59
3	Low-frequency somatic copy number alterations in normal human lymphocytes revealed by large-scale single-cell whole-genome profiling. <i>Genome Research</i> , 2022, 32, 44-54.	5.5	4
4	Computational Identification of Preneoplastic Cells Displaying High Stemness and Risk of Cancer Progression. <i>Cancer Research</i> , 2022, 82, 2520-2537.	0.9	9
5	Resolving mutational signatures in cancer development. <i>Cancer Cell</i> , 2022, 40, 711-713.	16.8	2
6	Metformin inhibits pancreatic cancer metastasis caused by SMAD4 deficiency and consequent HNF4G upregulation. <i>Protein and Cell</i> , 2021, 12, 128-144.	11.0	41
7	Sub-multiplicative interaction between polygenic risk score and household coal use in relation to lung adenocarcinoma among never-smoking women in Asia. <i>Environment International</i> , 2021, 147, 105975.	10.0	12
8	Genetic variants associated with expression of TCF19 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
9	LINC00842 inactivates transcription co-regulator PGC-1 $\beta$ to promote pancreatic cancer malignancy through metabolic remodelling. <i>Nature Communications</i> , 2021, 12, 3830.	12.8	34
10	VAV2 is required for DNA repair and implicated in cancer radiotherapy resistance. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 322.	17.1	14
11	A body map of somatic mutagenesis in morphologically normal human tissues. <i>Nature</i> , 2021, 597, 398-403.	27.8	107
12	Dissecting esophageal squamous-cell carcinoma ecosystem by single-cell transcriptomic analysis. <i>Nature Communications</i> , 2021, 12, 5291.	12.8	98
13	Analysis of the efficacy and prognostic factors of PD-1 inhibitors in advanced gallbladder cancer. <i>Annals of Translational Medicine</i> , 2021, 9, 1568-1568.	1.7	5
14	CstF64-Induced Shortening of the <i>BID</i> 3'UTR Promotes Esophageal Squamous Cell Carcinoma Progression by Disrupting ceRNA Cross-talk with <i>ZFP36L2</i> . <i>Cancer Research</i> , 2021, 81, 5638-5651.	0.9	13
15	Inflammatory cytokine-regulated tRNA-derived fragment tRF-21 suppresses pancreatic ductal adenocarcinoma progression. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	36
16	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
17	Genomic and transcriptomic alterations associated with drug vulnerabilities and prognosis in adenocarcinoma at the gastroesophageal junction. <i>Nature Communications</i> , 2020, 11, 6091.	12.8	21
18	Circulating circRNA predicting the occurrence of hepatocellular carcinoma in patients with HBV infection. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 10216-10222.	3.6	26

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19	Serum piRNA-54265 is a New Biomarker for early detection and clinical surveillance of Human Colorectal Cancer. <i>Theranostics</i> , 2020, 10, 8468-8478.	10.0	58
20	Single-cell transcriptomic analysis in a mouse model deciphers cell transition states in the multistep development of esophageal cancer. <i>Nature Communications</i> , 2020, 11, 3715.	12.8	79
21	Metabolic remodeling by TIGAR overexpression is a therapeutic target in esophageal squamous-cell carcinoma. <i>Theranostics</i> , 2020, 10, 3488-3502.	10.0	27
22	Complete response to immunotherapy combined with an antiangiogenic agent in multiple hepatic metastases after radical surgery for advanced gallbladder cancer: a case report. <i>Annals of Translational Medicine</i> , 2020, 8, 1609-1609.	1.7	4
23	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.	10.7	167
24	Genome landscapes of rectal cancer before and after preoperative chemoradiotherapy. <i>Theranostics</i> , 2019, 9, 6856-6866.	10.0	27
25	Excessive miR-25-3p maturation via N6-methyladenosine stimulated by cigarette smoke promotes pancreatic cancer progression. <i>Nature Communications</i> , 2019, 10, 1858.	12.8	242
26	Liver Transplantation Using Right Lobe Graft With Focal Nodular Hyperplasia: Report of 2 Cases. <i>Transplantation Proceedings</i> , 2019, 51, 3347-3350.	0.6	0
27	Exome-wide analyses identify low-frequency variant in CYP26B1 and additional coding variants associated with esophageal squamous cell carcinoma. <i>Nature Genetics</i> , 2018, 50, 338-343.	21.4	75
28	Genetic variant repressing ADH1A expression confers susceptibility to esophageal squamous-cell carcinoma. <i>Cancer Letters</i> , 2018, 421, 43-50.	7.2	16
29	Functional role of PLCE1 intronic insertion variant associated with susceptibility to esophageal squamous cell carcinoma. <i>Carcinogenesis</i> , 2018, 39, 191-201.	2.8	5
30	Genomic alterations and precise medicine of esophageal squamous cell carcinoma. <i>Journal of Bio-X Research</i> , 2018, 1, 7-11.	0.2	1
31	PIWI-interacting RNA-54265 is oncogenic and a potential therapeutic target in colorectal adenocarcinoma. <i>Theranostics</i> , 2018, 8, 5213-5230.	10.0	115
32	Exome-wide analysis identifies three low-frequency missense variants associated with pancreatic cancer risk in Chinese populations. <i>Nature Communications</i> , 2018, 9, 3688.	12.8	32
33	CCGD-ESCC: A Comprehensive Database for Genetic Variants Associated with Esophageal Squamous Cell Carcinoma in Chinese Population. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 262-268.	6.9	17
34	Functional role of BTB and CNC Homology 1 gene in pancreatic cancer and its association with survival in patients treated with gemcitabine. <i>Theranostics</i> , 2018, 8, 3366-3379.	10.0	19
35	Integrative analysis of gene expression profiles reveals specific signaling pathways associated with pancreatic duct adenocarcinoma. <i>Cancer Communications</i> , 2018, 38, 1-12.	9.2	14
36	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.	12.1	68

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37	Solute Carrier Family 39 Member 6 Gene Promotes Aggressiveness of Esophageal Carcinoma Cells by Increasing Intracellular Levels of Zinc, Activating Phosphatidylinositol 3-Kinase Signaling, and Up-regulating Genes That Regulate Metastasis. <i>Gastroenterology</i> , 2017, 152, 1985-1997.e12.	1.3	40
38	Genomic analysis of oesophageal squamous-cell carcinoma identifies alcohol drinking-related mutation signature and genomic alterations. <i>Nature Communications</i> , 2017, 8, 15290.	12.8	195
39	Germline variation in the 3' untranslated region of the POU2AF1 gene is associated with susceptibility to lymphoma. <i>Molecular Carcinogenesis</i> , 2017, 56, 1945-1952.	2.7	9
40	BRCA1-Associated Protein Increases Invasiveness of Esophageal Squamous Cell Carcinoma. <i>Gastroenterology</i> , 2017, 153, 1304-1319.e5.	1.3	23
41	A cis-eQTL genetic variant of the cancer testis gene CCDC116 is associated with risk of multiple cancers. <i>Human Genetics</i> , 2017, 136, 987-997.	3.8	7
42	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.	5.1	66
43	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.	2.9	50
44	Pancreatic cancer risk variant in LINC00673 creates a miR-1231 binding site and interferes with PTPN11 degradation. <i>Nature Genetics</i> , 2016, 48, 747-757.	21.4	237
45	Whole exome sequencing identifies lncRNA GAS8-AS1 and LPAR4 as novel papillary thyroid carcinoma driver alternations. <i>Human Molecular Genetics</i> , 2016, 25, 1875-1884.	2.9	79
46	Genome-wide association studies in East Asians identify new loci for waist-hip ratio and waist circumference. <i>Scientific Reports</i> , 2016, 6, 17958.	3.3	58
47	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. <i>Nature Communications</i> , 2016, 7, 11843.	12.8	86
48	Circulating Metabolites and Survival Among Patients With Pancreatic Cancer. <i>Journal of the National Cancer Institute</i> , 2016, 108, djv409.	6.3	31
49	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.	2.9	50
50	Identification of Susceptibility Loci and Genes for Colorectal Cancer Risk. <i>Gastroenterology</i> , 2016, 150, 1633-1645.	1.3	97
51	Genome-wide association study of gastric adenocarcinoma in Asia: a comparison of associations between cardia and non-cardia tumours. <i>Gut</i> , 2016, 65, 1611-1618.	12.1	99
52	Genetic variants associated with longer telomere length are associated with increased lung cancer risk among never-smoking women in Asia: a report from the female lung cancer consortium in Asia. <i>International Journal of Cancer</i> , 2015, 137, 311-319.	5.1	72
53	Relatively Small Contribution of Methylation and Genomic Copy Number Aberration to the Aberrant Expression of Inflammation-Related Genes in HBV-Related Hepatocellular Carcinoma. <i>PLoS ONE</i> , 2015, 10, e0126836.	2.5	1
54	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. <i>American Journal of Human Genetics</i> , 2015, 96, 487-497.	6.2	101

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55	Survival Among Patients With Pancreatic Cancer and Long-Standing or Recent-Onset Diabetes Mellitus. <i>Journal of Clinical Oncology</i> , 2015, 33, 29-35.	1.6	83
56	Interactions between household air pollution and GWAS-identified lung cancer susceptibility markers in the Female Lung Cancer Consortium in Asia (FLCCA). <i>Human Genetics</i> , 2015, 134, 333-341.	3.8	34
57	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
58	Two Novel Variants on 13q22.1 Are Associated with Risk of Esophageal Squamous Cell Carcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1774-1780.	2.5	12
59	Associations of ATM Polymorphisms With Survival in Advanced Esophageal Squamous Cell Carcinoma Patients Receiving Radiation Therapy. <i>International Journal of Radiation Oncology Biology Physics</i> , 2015, 93, 181-189.	0.8	4
60	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.	2.9	105
61	Exposure to airborne PM2.5 suppresses microRNA expression and deregulates target oncogenes that cause neoplastic transformation in NIH3T3 cells. <i>Oncotarget</i> , 2015, 6, 29428-29439.	1.8	46
62	Association of GWAS-Identified Lung Cancer Susceptibility Loci with Survival Length in Patients with Small-Cell Lung Cancer Treated with Platinum-Based Chemotherapy. <i>PLoS ONE</i> , 2014, 9, e113574.	2.5	8
63	A genome-wide gene-gene interaction analysis identifies an epistatic gene pair for lung cancer susceptibility in Han Chinese. <i>Carcinogenesis</i> , 2014, 35, 572-577.	2.8	29
64	Meta-analysis of genome-wide association studies in East Asian-ancestry populations identifies four new loci for body mass index. <i>Human Molecular Genetics</i> , 2014, 23, 5492-5504.	2.9	192
65	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. <i>Human Molecular Genetics</i> , 2014, 23, 6616-6633.	2.9	90
66	A genome wide association study of genetic loci that influence tumour biomarkers cancer antigen 19-9, carcinoembryonic antigen and $\alpha$ -fetoprotein and their associations with cancer risk. <i>Gut</i> , 2014, 63, 143-151.	12.1	67
67	Stability SCAD: a powerful approach to detect interactions in large-scale genomic study. <i>BMC Bioinformatics</i> , 2014, 15, 62.	2.6	1
68	Genome-wide association study of survival in patients with pancreatic adenocarcinoma. <i>Gut</i> , 2014, 63, 152-160.	12.1	59
69	A genome-wide association study identifies common variants influencing serum uric acid concentrations in a Chinese population. <i>BMC Medical Genomics</i> , 2014, 7, 10.	1.5	57
70	Joint analysis of three genome-wide association studies of esophageal squamous cell carcinoma in Chinese populations. <i>Nature Genetics</i> , 2014, 46, 1001-1006.	21.4	148
71	Genome-wide association study identifies three susceptibility loci for laryngeal squamous cell carcinoma in the Chinese population. <i>Nature Genetics</i> , 2014, 46, 1110-1114.	21.4	57
72	Genome-wide association study identifies new susceptibility loci for epithelial ovarian cancer in Han Chinese women. <i>Nature Communications</i> , 2014, 5, 4682.	12.8	59

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73	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. <i>Nature Genetics</i> , 2014, 46, 994-1000.	21.4	294
74	A genome-wide gene-environment interaction analysis for tobacco smoke and lung cancer susceptibility. <i>Carcinogenesis</i> , 2014, 35, 1528-1535.	2.8	47
75	Elevation of circulating branched-chain amino acids is an early event in human pancreatic adenocarcinoma development. <i>Nature Medicine</i> , 2014, 20, 1193-1198.	30.7	510
76	Multi-loci analysis reveals the importance of genetic variations in sensitivity of platinum-based chemotherapy in non-small-cell lung cancer. <i>Molecular Carcinogenesis</i> , 2013, 52, 923-931.	2.7	25
77	A Genome-Wide Association Study for Serum Bilirubin Levels and Gene-Environment Interaction in a Chinese Population. <i>Genetic Epidemiology</i> , 2013, 37, 293-300.	1.3	34
78	Genome-wide association study on serum alkaline phosphatase levels in a Chinese population. <i>BMC Genomics</i> , 2013, 14, 684.	2.8	11
79	Prediagnostic Body Mass Index and Pancreatic Cancer Survival. <i>Journal of Clinical Oncology</i> , 2013, 31, 4229-4234.	1.6	115
80	Evidence of associations of APOBEC3B gene deletion with susceptibility to persistent HBV infection and hepatocellular carcinoma. <i>Human Molecular Genetics</i> , 2013, 22, 1262-1269.	2.9	52
81	Identification of common variants in BRCA2 and MAP2K4 for susceptibility to sporadic pancreatic cancer. <i>Carcinogenesis</i> , 2013, 34, 1001-1005.	2.8	19
82	Genome-wide association study identifies common variants in SLC39A6 associated with length of survival in esophageal squamous-cell carcinoma. <i>Nature Genetics</i> , 2013, 45, 632-638.	21.4	97
83	Genetic variants in STAT4 and HLA-DQ genes confer risk of hepatitis B virus-related hepatocellular carcinoma. <i>Nature Genetics</i> , 2013, 45, 72-75.	21.4	259
84	A genome-wide association study identifies two new cervical cancer susceptibility loci at 4q12 and 17q12. <i>Nature Genetics</i> , 2013, 45, 918-922.	21.4	108
85	Risk prediction of esophageal squamous-cell carcinoma with common genetic variants and lifestyle factors in Chinese population. <i>Carcinogenesis</i> , 2013, 34, 1782-1786.	2.8	37
86	Hyperglycemia, Insulin Resistance, Impaired Pancreatic Î²-Cell Function, and Risk of Pancreatic Cancer. <i>Journal of the National Cancer Institute</i> , 2013, 105, 1027-1035.	6.3	146
87	Risk of genome-wide association study-identified genetic variants for non-Hodgkin lymphoma in a Chinese population. <i>Carcinogenesis</i> , 2013, 34, 1516-1519.	2.8	11
88	Genome-Wide Association Study Identifies a Novel Susceptibility Locus at 12q23.1 for Lung Squamous Cell Carcinoma in Han Chinese. <i>PLoS Genetics</i> , 2013, 9, e1003190.	3.5	41
89	Imputation-based association analyses identify new lung cancer susceptibility variants in CDK6 and SH3RF1 and their interactions with smoking in Chinese populations. <i>Carcinogenesis</i> , 2013, 34, 2010-2016.	2.8	7
90	Reproducibility of Metabolomic Profiles among Men and Women in 2 Large Cohort Studies. <i>Clinical Chemistry</i> , 2013, 59, 1657-1667.	3.2	189

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91	The Caseâ€œOnly Test for Geneâ€œEnvironment Interaction is Not Uniformly Powerful: An Empirical Example. <i>Genetic Epidemiology</i> , 2013, 37, 402-407.	1.3	8
92	Pathway Analysis for Genome-Wide Association Study of Lung Cancer in Han Chinese Population. <i>PLoS ONE</i> , 2013, 8, e57763.	2.5	9
93	Functional Polymorphisms in FAS/FASL System Increase the Risk of Neuroblastoma in Chinese Population. <i>PLoS ONE</i> , 2013, 8, e71656.	2.5	30
94	A Genome Wide Association Study Identifies Common Variants Associated with Lipid Levels in the Chinese Population. <i>PLoS ONE</i> , 2013, 8, e82420.	2.5	57
95	Copy number variation at 6q13 functions as a long-range regulator and is associated with pancreatic cancer risk. <i>Carcinogenesis</i> , 2012, 33, 94-100.	2.8	34
96	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.	21.4	129
97	Cytokine <i>BAFF</i> Gene Variation Is Associated with Survival of Patients with T-cell Lymphomas. <i>Clinical Cancer Research</i> , 2012, 18, 2250-2256.	7.0	13
98	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.	6.2	76
99	Genome-wide association analysis identifies new lung cancer susceptibility loci in never-smoking women in Asia. <i>Nature Genetics</i> , 2012, 44, 1330-1335.	21.4	286
100	Genome-Wide Association Study of Prognosis in Advanced Nonâ€œSmall Cell Lung Cancer Patients Receiving Platinum-Based Chemotherapy. <i>Clinical Cancer Research</i> , 2012, 18, 5507-5514.	7.0	56
101	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.	21.4	238
102	Genome-wide association study identifies five loci associated with susceptibility to pancreatic cancer in Chinese populations. <i>Nature Genetics</i> , 2012, 44, 62-66.	21.4	164
103	Smoking and Genetic Risk Variation Across Populations of <i>European</i> , <i>Asian</i> , and <i>African American</i> Ancestryâ€œA Metaâ€œAnalysis of Chromosome 15q25. <i>Genetic Epidemiology</i> , 2012, 36, 340-351.	1.3	69
104	Genetic variant in TP63 on locus 3q28 is associated with risk of lung adenocarcinoma among never-smoking females in Asia. <i>Human Genetics</i> , 2012, 131, 1197-1203.	3.8	39
105	Increased risk of lung cancer associated with a functionally impaired polymorphic variant of the human DNA glycosylase NEIL2. <i>DNA Repair</i> , 2012, 11, 570-578.	2.8	42
106	Association between genetic variations in tumor necrosis factor receptor genes and survival of patients with T-cell lymphoma. <i>Chinese Journal of Cancer</i> , 2012, 31, 335-341.	4.9	3
107	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.	21.4	340
108	Association of candidate genetic variations with gastric cardia adenocarcinoma in Chinese population: a multiple interaction analysis. <i>Carcinogenesis</i> , 2011, 32, 336-342.	2.8	45

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109	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.	21.4	260
110	Assessment of XPD Lys751Gln and XRCC1 T477C polymorphisms in advanced non-small-cell lung cancer patients treated with platinum-based chemotherapy. <i>Lung Cancer</i> , 2011, 73, 110-115.	2.0	31
111	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.	21.4	250
112	Combined Effect of Genetic Polymorphisms in P53, P73, and MDM2 on Non-small Cell Lung Cancer Survival. <i>Journal of Thoracic Oncology</i> , 2011, 6, 1793-1800.	1.1	38
113	A functional A77T polymorphism in XRCC1 is associated with risk of breast cancer. <i>Breast Cancer Research and Treatment</i> , 2011, 125, 479-487.	2.5	32
114	Circulating MicroRNAs, miR-21, miR-122, and miR-223, in patients with hepatocellular carcinoma or chronic hepatitis. <i>Molecular Carcinogenesis</i> , 2011, 50, 136-142.	2.7	494
115	A functional polymorphism (A1607 G>2G) in the matrix metalloproteinase-1 promoter is associated with development and progression of lung cancer. <i>Cancer</i> , 2011, 117, 5172-5181.	4.1	35
116	Association of P53 and ATM Polymorphisms With Risk of Radiation-Induced Pneumonitis in Lung Cancer Patients Treated With Radiotherapy. <i>International Journal of Radiation Oncology Biology Physics</i> , 2011, 79, 1402-1407.	0.8	53
117	Genetic Variation in an miRNA-1827 Binding Site in MYCL1 Alters Susceptibility to Small-Cell Lung Cancer. <i>Cancer Research</i> , 2011, 71, 5175-5181.	0.9	73
118	Variations in HSPA1B at 6p21.3 Are Associated with Lung Cancer Risk and Prognosis in Chinese Populations. <i>Cancer Research</i> , 2011, 71, 7576-7586.	0.9	30
119	Genetic polymorphism of PSCA and risk of advanced precancerous gastric lesions in a Chinese population. <i>Chinese Journal of Cancer Research: Official Journal of China Anti-Cancer Association</i> , Beijing Institute for Cancer Research, 2010, 22, 99-105.	2.2	0
120	Functional XPF polymorphisms associated with lung cancer susceptibility in a Chinese population. <i>Frontiers of Medicine in China</i> , 2010, 4, 82-89.	0.1	4
121	Genetic polymorphisms in cytochrome P450 genes are associated with an increased risk of squamous cell carcinoma of the larynx and hypopharynx in a Chinese population. <i>Cancer Genetics and Cytogenetics</i> , 2010, 196, 76-82.	1.0	39
122	An estrogen receptor $\beta$ suppressor, microRNA-22, is downregulated in estrogen receptor $\beta$ -positive human breast cancer cell lines and clinical samples. <i>FEBS Journal</i> , 2010, 277, 1684-1694.	4.7	148
123	Genome-wide association study identifies 1p36.22 as a new susceptibility locus for hepatocellular carcinoma in chronic hepatitis B virus carriers. <i>Nature Genetics</i> , 2010, 42, 755-758.	21.4	319
124	Risk of Genome-Wide Association Study-Identified Genetic Variants for Colorectal Cancer in a Chinese Population. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 1855-1861.	2.5	58
125	The 5p15.33 Locus Is Associated with Risk of Lung Adenocarcinoma in Never-Smoking Females in Asia. <i>PLoS Genetics</i> , 2010, 6, e1001051.	3.5	168
126	Genome-Wide Interrogation Identifies YAP1 Variants Associated with Survival of Small-Cell Lung Cancer Patients. <i>Cancer Research</i> , 2010, 70, 9721-9729.	0.9	53

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127	No association betweenXRCC1 polymorphisms and survival in non-small-cell lung cancer patients treated with platinum-based chemotherapy. <i>Cancer Biology and Therapy</i> , 2010, 10, 854-859.	3.4	12
128	Association of TGF- $\beta$ 1 and XPD polymorphisms with severe acute radiation-induced esophageal toxicity in locally advanced lung cancer patients treated with radiotherapy. <i>Radiotherapy and Oncology</i> , 2010, 97, 19-25.	0.6	47
129	Genome-wide examination of genetic variants associated with response to platinum-based chemotherapy in patients with small-cell lung cancer. <i>Pharmacogenetics and Genomics</i> , 2010, 20, 389-395.	1.5	26
130	Genetic Variants on Chromosome 15q25 Associated with Lung Cancer Risk in Chinese Populations. <i>Cancer Research</i> , 2009, 69, 5065-5072.	0.9	138
131	Functional FEN1 polymorphisms are associated with DNA damage levels and lung cancer risk. <i>Human Mutation</i> , 2009, 30, 1320-1328.	2.5	77
132	Genetic polymorphism in chemokine CCL22 and susceptibility to <i>Helicobacter pylori</i> infection-related gastric carcinoma. <i>Cancer</i> , 2009, 115, 2430-2437.	4.1	15
133	Two genetic variants in prostate stem cell antigen and gastric cancer susceptibility in a chinese population. <i>Molecular Carcinogenesis</i> , 2009, 48, 1131-1138.	2.7	50
134	Polymorphisms of EGFR predict clinical outcome in advanced non-small-cell lung cancer patients treated with Gefitinib. <i>Lung Cancer</i> , 2009, 66, 114-119.	2.0	65