## Dongxin Lin

List of Publications by Year in descending order

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178 papers 12,223 citations

24978 57 h-index 29081 104 g-index

183 all docs

183
docs citations

times ranked

183

18800 citing authors

#	Article	IF	CITATIONS
1	Identification of genomic alterations in oesophageal squamous cell cancer. Nature, 2014, 509, 91-95.	13.7	903
2	METTL3 facilitates tumor progression via an m6A-IGF2BP2-dependent mechanism in colorectal carcinoma. Molecular Cancer, 2019, 18, 112.	7.9	515
3	Circulating MicroRNAs, miR-21, miR-122, and miR-223, in patients with hepatocellular carcinoma or chronic hepatitis. Molecular Carcinogenesis, 2011, 50, 136-142.	1.3	494
4	A genome-wide association study identifies two new lung cancer susceptibility loci at 13q12.12 and 22q12.2 in Han Chinese. Nature Genetics, 2011, 43, 792-796.	9.4	340
5	Genome-wide association study identifies 1p36.22 as a new susceptibility locus for hepatocellular carcinoma in chronic hepatitis B virus carriers. Nature Genetics, 2010, 42, 755-758.	9.4	319
6	Genomic Analyses Reveal Mutational Signatures and Frequently Altered Genes in Esophageal Squamous Cell Carcinoma. American Journal of Human Genetics, 2015, 96, 597-611.	2.6	290
7	Genome-wide association analysis identifies new lung cancer susceptibility loci in never-smoking women in Asia. Nature Genetics, 2012, 44, 1330-1335.	9.4	286
8	Genome-wide association study identifies three new susceptibility loci for esophageal squamous-cell carcinoma in Chinese populations. Nature Genetics, 2011, 43, 679-684.	9.4	260
9	Genetic variants in STAT4 and HLA-DQ genes confer risk of hepatitis B virus–related hepatocellular carcinoma. Nature Genetics, 2013, 45, 72-75.	9.4	259
10	A genome-wide association study identifies new susceptibility loci for non-cardia gastric cancer at 3q13.31 and 5p13.1. Nature Genetics, 2011, 43, 1215-1218.	9.4	250
11	Excessive miR-25-3p maturation via N6-methyladenosine stimulated by cigarette smoke promotes pancreatic cancer progression. Nature Communications, 2019, 10, 1858.	5.8	242
12	Genome-wide association analyses of esophageal squamous cell carcinoma in Chinese identify multiple susceptibility loci and gene-environment interactions. Nature Genetics, 2012, 44, 1090-1097.	9.4	238
13	Pancreatic cancer risk variant in LINC00673 creates a miR-1231 binding site and interferes with PTPN11 degradation. Nature Genetics, 2016, 48, 747-757.	9.4	237
14	Genomic analysis of oesophageal squamous-cell carcinoma identifies alcohol drinking-related mutation signature and genomic alterations. Nature Communications, 2017, 8, 15290.	5.8	195
15	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.	1.5	177
16	The 5p15.33 Locus Is Associated with Risk of Lung Adenocarcinoma in Never-Smoking Females in Asia. PLoS Genetics, 2010, 6, e1001051.	1.5	168
17	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.	5.2	167
18	Genome-wide association study identifies five loci associated with susceptibility to pancreatic cancer in Chinese populations. Nature Genetics, 2012, 44, 62-66.	9.4	164

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19	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.	3.0	152
20	Functional Genetic Variations in <i>Cytotoxic T-Lymphocyte Antigen 4</i> and Susceptibility to Multiple Types of Cancer. Cancer Research, 2008, 68, 7025-7034.	0.4	151
21	An estrogen receptor α suppressor, microRNAâ€22, is downregulated in estrogen receptor αâ€positive human breast cancer cell lines and clinical samples. FEBS Journal, 2010, 277, 1684-1694.	2.2	148
22	Joint analysis of three genome-wide association studies of esophageal squamous cell carcinoma in Chinese populations. Nature Genetics, 2014, 46, 1001-1006.	9.4	148
23	PIWI-interacting RNA-36712 restrains breast cancer progression and chemoresistance by interaction with SEPW1 pseudogene SEPW1P RNA. Molecular Cancer, 2019, 18, 9.	7.9	139
24	Genetic Variants on Chromosome 15q25 Associated with Lung Cancer Risk in Chinese Populations. Cancer Research, 2009, 69, 5065-5072.	0.4	138
25	Association analyses identify multiple new lung cancer susceptibility loci and their interactions with smoking in the Chinese population. Nature Genetics, 2012, 44, 895-899.	9.4	129
26	Genomic Characterization of Esophageal Squamous Cell Carcinoma Reveals Critical Genes Underlying Tumorigenesis and Poor Prognosis. American Journal of Human Genetics, 2016, 98, 709-727.	2.6	129
27	Overexpression and Hypomethylation of (i) Flap Endonuclease $1 < l$ i) Gene in Breast and Other Cancers. Molecular Cancer Research, 2008, 6, 1710-1717.	1.5	117
28	PIWI-interacting RNA-54265 is oncogenic and a potential therapeutic target in colorectal adenocarcinoma. Theranostics, 2018, 8, 5213-5230.	4.6	115
29	A genome-wide association study identifies two new cervical cancer susceptibility loci at 4q12 and 17q12. Nature Genetics, 2013, 45, 918-922.	9.4	108
30	Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. Human Molecular Genetics, 2015, 24, 1791-1800.	1.4	105
31	The MDM2 Promoter SNP285C/309G Haplotype Diminishes Sp1 Transcription Factor Binding and Reduces Risk for Breast and Ovarian Cancer in Caucasians. Cancer Cell, 2011, 19, 273-282.	7.7	104
32	Long Noncoding RNA p53â€Stabilizing and Activating RNA Promotes p53 Signaling by Inhibiting Heterogeneous Nuclear Ribonucleoprotein K deSUMOylation and Suppresses Hepatocellular Carcinoma. Hepatology, 2020, 71, 112-129.	3.6	104
33	Meta- and Pooled Analyses of the Methylenetetrahydrofolate Reductase C677T and A1298C Polymorphisms and Gastric Cancer Risk: A Huge-GSEC Review. American Journal of Epidemiology, 2007, 167, 505-516.	1.6	103
34	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	2.6	101
35	Genome-wide association study of gastric adenocarcinoma in Asia: a comparison of associations between cardia and non-cardia tumours. Gut, 2016, 65, 1611-1618.	6.1	99
36	Winner's Curse Correction and Variable Thresholding Improve Performance of Polygenic Risk Modeling Based on Genome-Wide Association Study Summary-Level Data. PLoS Genetics, 2016, 12, e1006493.	1.5	98

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37	Genome-wide association study identifies common variants in SLC39A6 associated with length of survival in esophageal squamous-cell carcinoma. Nature Genetics, 2013, 45, 632-638.	9.4	97
38	Identification of Susceptibility Loci and Genes for Colorectal Cancer Risk. Gastroenterology, 2016, 150, 1633-1645.	0.6	97
39	Suppression of CYP2C9 by MicroRNA hsa-miR-128-3p in Human Liver Cells and Association with Hepatocellular Carcinoma. Scientific Reports, 2015, 5, 8534.	1.6	92
40	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. Human Molecular Genetics, 2014, 23, 6616-6633.	1.4	90
41	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	5.8	86
42	Functional Variants in Cell Death Pathway Genes and Risk of Pancreatic Cancer. Clinical Cancer Research, 2008, 14, 3230-3236.	3.2	82
43	Whole exome sequencing identifies lncRNA <i>GAS8-AS1</i> and <i>LPAR4</i> as novel papillary thyroid carcinoma driver alternations. Human Molecular Genetics, 2016, 25, 1875-1884.	1.4	79
44	Functional <i>FEN1 </i>  i>polymorphisms are associated with DNA damage levels and lung cancer risk. Human Mutation, 2009, 30, 1320-1328.	1.1	77
45	ATM Polymorphisms Are Associated With Risk of Radiation-Induced Pneumonitis. International Journal of Radiation Oncology Biology Physics, 2010, 77, 1360-1368.	0.4	77
46	Genetic Variants at 6p21.1 and 7p15.3 Are Associated with Risk of Multiple Cancers in Han Chinese. American Journal of Human Genetics, 2012, 91, 928-934.	2.6	76
47	Exome-wide analyses identify low-frequency variant in CYP26B1 and additional coding variants associated with esophageal squamous cell carcinoma. Nature Genetics, 2018, 50, 338-343.	9.4	75
48	Genetic Variation in an miRNA-1827 Binding Site in <i>MYCL1</i> Alters Susceptibility to Small-Cell Lung Cancer. Cancer Research, 2011, 71, 5175-5181.	0.4	73
49	<scp>G</scp> enetic variants associated with longer telomere length are associated with increased lung cancer risk among neverâ€smoking women in Asia: a report from the female lung cancer consortium in Asia. International Journal of Cancer, 2015, 137, 311-319.	2.3	72
50	OTUB1 promotes esophageal squamous cell carcinoma metastasis through modulating Snail stability. Oncogene, 2018, 37, 3356-3368.	2.6	72
51	Smoking and Genetic Risk Variation Across Populations of <scp>E</scp> uropean, <scp>A</scp> sian, and <scp>A</scp> frican <scp>A</scp> merican Ancestryâ€"A Metaâ€Analysis of Chromosome 15q25. Genetic Epidemiology, 2012, 36, 340-351.	0.6	69
52	Interaction of P53 Arg72Pro and MDM2 T309G polymorphisms and their associations with risk of gastric cardia cancer. Carcinogenesis, 2007, 28, 1996-2001.	1.3	68
53	Identification of new susceptibility loci for gastric non-cardia adenocarcinoma: pooled results from two Chinese genome-wide association studies. Gut, 2017, 66, 581-587.	6.1	68
54	A genome wide association study of genetic loci that influence tumour biomarkers cancer antigen 19-9, carcinoembryonic antigen and $l_{\pm}$ fetoprotein and their associations with cancer risk. Gut, 2014, 63, 143-151.	6.1	67

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55	Estimation of heritability for nine common cancers using data from genomeâ€wide association studies in Chinese population. International Journal of Cancer, 2017, 140, 329-336.	2.3	66
56	Polymorphisms of EGFR predict clinical outcome in advanced non-small-cell lung cancer patients treated with Gefitinib. Lung Cancer, 2009, 66, 114-119.	0.9	65
57	Genome-wide association study of survival in patients with pancreatic adenocarcinoma. Gut, 2014, 63, 152-160.	6.1	59
58	Genome-wide association study identifies new susceptibility loci for epithelial ovarian cancer in Han Chinese women. Nature Communications, 2014, 5, 4682.	5.8	59
59	Genetic Polymorphisms in <i>Cytotoxic T-Lymphocyte Antigen 4</i> and Cancer: The Dialectical Nature of Subtle Human Immune Dysregulation. Cancer Research, 2009, 69, 6011-6014.	0.4	58
60	Risk of Genome-Wide Association Study–Identified Genetic Variants for Colorectal Cancer in a Chinese Population. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 1855-1861.	1.1	58
61	Genome-wide association studies in East Asians identify new loci for waist-hip ratio and waist circumference. Scientific Reports, 2016, 6, 17958.	1.6	58
62	A Genome Wide Association Study Identifies Common Variants Associated with Lipid Levels in the Chinese Population. PLoS ONE, 2013, 8, e82420.	1.1	57
63	A genome-wide association study identifies common variants influencing serum uric acid concentrations in a Chinese population. BMC Medical Genomics, 2014, 7, 10.	0.7	57
64	Genome-wide association study identifies three susceptibility loci for laryngeal squamous cell carcinoma in the Chinese population. Nature Genetics, 2014, 46, 1110-1114.	9.4	57
65	Genome-Wide Association Study of Prognosis in Advanced Non–Small Cell Lung Cancer Patients Receiving Platinum-Based Chemotherapy. Clinical Cancer Research, 2012, 18, 5507-5514.	3.2	56
66	A functional BRCA1 coding sequence genetic variant contributes to risk of esophageal squamous cell carcinoma. Carcinogenesis, 2013, 34, 2309-2313.	1.3	54
67	Genome-Wide Interrogation Identifies <i>YAP1</i> Variants Associated with Survival of Small-Cell Lung Cancer Patients. Cancer Research, 2010, 70, 9721-9729.	0.4	53
68	Association of P53 and ATM Polymorphisms With Risk of Radiation-Induced Pneumonitis in Lung Cancer Patients Treated With Radiotherapy. International Journal of Radiation Oncology Biology Physics, 2011, 79, 1402-1407.	0.4	53
69	Characterization of Functional Excision Repair Cross-Complementation Group 1 Variants and Their Association with Lung Cancer Risk and Prognosis. Clinical Cancer Research, 2008, 14, 2878-2886.	3.2	52
70	Evidence of associations of APOBEC3B gene deletion with susceptibility to persistent HBV infection and hepatocellular carcinoma. Human Molecular Genetics, 2013, 22, 1262-1269.	1.4	52
71	XRCC1 polymorphisms and severe toxicity in lung cancer patients treated with cisplatin-based chemotherapy in Chinese population. Lung Cancer, 2008, 62, 99-104.	0.9	51
72	Two genetic variants in prostate stem cell antigen and gastric cancer susceptibility in a chinese population. Molecular Carcinogenesis, 2009, 48, 1131-1138.	1.3	50

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73	Interaction of Cyclooxygenase-2 Variants and Smoking in Pancreatic Cancer: A Possible Role of Nucleophosmin. Gastroenterology, 2009, 136, 1659-1668.	0.6	50
74	Association between GWAS-identified lung adenocarcinoma susceptibility loci andEGFRmutations in never-smoking Asian women, and comparison with findings from Western populations. Human Molecular Genetics, 2016, 26, ddw414.	1.4	50
75	Meta-analysis of genome-wide association studies identifies multiple lung cancer susceptibility loci in never-smoking Asian women. Human Molecular Genetics, 2016, 25, 620-629.	1.4	50
76	Association of TGF- $\hat{1}^21$ and XPD polymorphisms with severe acute radiation-induced esophageal toxicity in locally advanced lung cancer patients treated with radiotherapy. Radiotherapy and Oncology, 2010, 97, 19-25.	0.3	47
77	A genome-wide gene-environment interaction analysis for tobacco smoke and lung cancer susceptibility. Carcinogenesis, 2014, 35, 1528-1535.	1.3	47
78	Exposure to airborne PM2.5 suppresses microRNA expression and deregulates target oncogenes that cause neoplastic transformation in NIH3T3 cells. Oncotarget, 2015, 6, 29428-29439.	0.8	46
79	Association of candidate genetic variations with gastric cardia adenocarcinoma in Chinese population: a multiple interaction analysis. Carcinogenesis, 2011, 32, 336-342.	1.3	45
80	Trend and risk factors of low birth weight and macrosomia in south China, 2005–2017: a retrospective observational study. Scientific Reports, 2018, 8, 3393.	1.6	44
81	Genome-wide association study of B cell non-Hodgkin lymphoma identifies 3q27 as a susceptibility locus in the Chinese population. Nature Genetics, 2013, 45, 804-807.	9.4	43
82	Functional evaluation of missense variations in the human MAD1L1 and MAD2L1 genes and their impact on susceptibility to lung cancer. Journal of Medical Genetics, 2010, 47, 616-622.	1.5	42
83	Increased risk of lung cancer associated with a functionally impaired polymorphic variant of the human DNA glycosylase NEIL2. DNA Repair, 2012, 11, 570-578.	1.3	42
84	Genome-Wide Association Study Identifies a Novel Susceptibility Locus at 12q23.1 for Lung Squamous Cell Carcinoma in Han Chinese. PLoS Genetics, 2013, 9, e1003190.	1.5	41
85	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, 832-840.	2.6	41
86	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 RegulateÂMetastasis. Gastroenterology, 2017, 152, 1985-1997.e12.	0.6	40
87	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. Cancer Genetics and Cytogenetics, 2010, 196, 76-82.	1.0	39
88	Genetic variant in TP63 on locus 3q28 is associated with risk of lung adenocarcinoma among never-smoking females in Asia. Human Genetics, 2012, 131, 1197-1203.	1.8	39
89	Functional Role of <i>\$100A14</i> Genetic Variants and Their Association with Esophageal Squamous Cell Carcinoma. Cancer Research, 2009, 69, 3451-3457.	0.4	38
90	Combined Effect of Genetic Polymorphisms in P53, P73, and MDM2 on Non-small Cell Lung Cancer Survival. Journal of Thoracic Oncology, 2011, 6, 1793-1800.	0.5	38

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91	Cyclooxygenase-2 Genetic Variants Are Associated with Survival in Unresectable Locally Advanced Nonâ€"Small Cell Lung Cancer. Clinical Cancer Research, 2010, 16, 2383-2390.	3.2	37
92	Risk prediction of esophageal squamous-cell carcinoma with common genetic variants and lifestyle factors in Chinese population. Carcinogenesis, 2013, 34, 1782-1786.	1.3	37
93	A functional polymorphism (â^1607 1Gâ†'2G) in the matrix metalloproteinaseâ€1 promoter is associated with development and progression of lung cancer. Cancer, 2011, 117, 5172-5181.	2.0	35
94	Copy number variation at 6q13 functions as a long-range regulator and is associated with pancreatic cancer risk. Carcinogenesis, 2012, 33, 94-100.	1.3	34
95	A Genomeâ€Wide Association Study for Serum Bilirubin Levels and Geneâ€Environment Interaction in a Chinese Population. Genetic Epidemiology, 2013, 37, 293-300.	0.6	34
96	Interactions between household air pollution and GWAS-identified lung cancer susceptibility markers in the Female Lung Cancer Consortium in Asia (FLCCA). Human Genetics, 2015, 134, 333-341.	1.8	34
97	A functional â^777T>C polymorphism in XRCC1 is associated with risk of breast cancer. Breast Cancer Research and Treatment, 2011, 125, 479-487.	1.1	32
98	Exome-wide analysis identifies three low-frequency missense variants associated with pancreatic cancer risk in Chinese populations. Nature Communications, 2018, 9, 3688.	5.8	32
99	Assessment of XPD Lys751Gln and XRCC1 T–77C polymorphisms in advanced non-small-cell lung cancer patients treated with platinum-based chemotherapy. Lung Cancer, 2011, 73, 110-115.	0.9	31
100	A variant of the Cockayne syndrome B geneERCC6 confers risk of lung cancer. Human Mutation, 2008, 29, 113-122.	1.1	30
101	Variations in <i>HSPA1B</i> at 6p21.3 Are Associated with Lung Cancer Risk and Prognosis in Chinese Populations. Cancer Research, 2011, 71, 7576-7586.	0.4	30
102	A genome-wide gene–gene interaction analysis identifies an epistatic gene pair for lung cancer susceptibility in Han Chinese. Carcinogenesis, 2014, 35, 572-577.	1.3	29
103	Genome landscapes of rectal cancer before and after preoperative chemoradiotherapy. Theranostics, 2019, 9, 6856-6866.	4.6	27
104	A polymorphism in mi <scp>R</scp> â€1262 regulatory region confers the risk of lung cancer in <scp>C</scp> hinese population. International Journal of Cancer, 2017, 141, 958-966.	2.3	26
105	Genome-wide examination of genetic variants associated with response to platinum-based chemotherapy in patients with small-cell lung cancer. Pharmacogenetics and Genomics, 2010, 20, 389-395.	0.7	26
106	Multiâ€loci analysis reveals the importance of genetic variations in sensitivity of platinumâ€based chemotherapy in nonâ€smallâ€cell lung cancer. Molecular Carcinogenesis, 2013, 52, 923-931.	1.3	25
107	Non-hospital environment contamination with Staphylococcus aureus and methicillin-resistant Staphylococcus aureus: proportion meta-analysis and features of antibiotic resistance and molecular genetics. Environmental Research, 2016, 150, 528-540.	3.7	25
108	A Meta-Analysis of the Global Prevalence Rates of Staphylococcus aureus and Methicillin-Resistant S. aureus Contamination of Different Raw Meat Products. Journal of Food Protection, 2017, 80, 763-774.	0.8	25

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109	There Is No Association between MicroRNA Gene Polymorphisms and Risk of Triple Negative Breast Cancer in a Chinese Han Population. PLoS ONE, 2013, 8, e60195.	1.1	25
110	Metro system in Guangzhou as a hazardous reservoir of methicillin-resistant Staphylococci: findings from a point-prevalence molecular epidemiologic study. Scientific Reports, 2015, 5, 16087.	1.6	24
111	Association of the variable number of tandem repeats polymorphism in the promoter region of the SMYD3 gene with risk of esophageal squamous cell carcinoma in relation to tobacco smoking. Cancer Science, 2008, 99, 787-791.	1.7	23
112	BRCA1-Associated Protein Increases Invasiveness of Esophageal Squamous Cell Carcinoma. Gastroenterology, 2017, 153, 1304-1319.e5.	0.6	23
113	The effect of gestational weight gain on perinatal outcomes among Chinese twin gestations based on Institute of Medicine guidelines. BMC Pregnancy and Childbirth, 2019, 19, 262.	0.9	22
114	Population distribution and ancestry of the cancer protective MDM2 SNP285 (rs117039649). Oncotarget, 2014, 5, 8223-8234.	0.8	22
115	Metabolome-wide association study identified the association between a circulating polyunsaturated fatty acids variant rs174548 and lung cancer. Carcinogenesis, 2017, 38, 1147-1154.	1.3	21
116	Methicillin-Resistant Staphylococcus aureus Nasal Colonization in Chinese Children: A Prevalence Meta-Analysis and Review of Influencing Factors. PLoS ONE, 2016, 11, e0159728.	1.1	20
117	Neonatal colonization of group B Streptococcus in China: Prevalence, antimicrobial resistance, serotypes, and molecular characterization. American Journal of Infection Control, 2018, 46, e19-e24.	1.1	20
118	Identification of common variants in BRCA2 and MAP2K4 for susceptibility to sporadic pancreatic cancer. Carcinogenesis, 2013, 34, 1001-1005.	1.3	19
119	Functional role of BTB and CNC Homology 1 gene in pancreatic cancer and its association with survival in patients treated with gemcitabine. Theranostics, $2018$ , $8$ , $3366$ - $3379$ .	4.6	19
120	CCGD-ESCC: A Comprehensive Database for Genetic Variants Associated with Esophageal Squamous Cell Carcinoma in Chinese Population. Genomics, Proteomics and Bioinformatics, 2018, 16, 262-268.	3.0	17
121	Prospective association of metal levels with gestational diabetes mellitus and glucose: A retrospective cohort study from South China. Ecotoxicology and Environmental Safety, 2021, 210, 111854.	2.9	17
122	Systematical analyses of variants in CTCF-binding sites identified a novel lung cancer susceptibility locus among Chinese population. Scientific Reports, 2015, 5, 7833.	1.6	16
123	A meta-analysis of the rates of Staphylococcus aureus and methicillin-resistant S aureus contamination on the surfaces of environmental objects that health care workers frequently touch. American Journal of Infection Control, 2017, 45, 421-429.	1.1	16
124	Genetic variant repressing ADH1A expression confers susceptibility to esophageal squamous-cell carcinoma. Cancer Letters, 2018, 421, 43-50.	3.2	16
125	A large meta-analysis of the global prevalence rates of <i>S. aureus</i> and MRSA contamination of milk. Critical Reviews in Food Science and Nutrition, 2018, 58, 2213-2228.	5.4	16
126	A prospective cohort study of <em>Staphylococcus aureus </em> and methicillin-resistant <em>Staphylococcus aureus </em> carriage in neonates: the role of maternal carriage and phenotypic and molecular characteristics. Infection and Drug Resistance, 2018, Volume 11, 555-565.	1.1	16

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127	Genetic polymorphism in chemokine CCL22 and susceptibility to ⟨i⟩Helicobacter pylori⟨ i⟩ infectionâ€related gastric carcinoma. Cancer, 2009, 115, 2430-2437.	2.0	15
128	Pulmonary expression of <i>CYP2A13</i> and <i>ABCB1</i> is regulated by FOXA2, and their genetic interaction is associated with lung cancer. FASEB Journal, 2015, 29, 1986-1998.	0.2	15
129	Genotype imputation for Han Chinese population using Haplotype Reference Consortium as reference. Human Genetics, 2018, 137, 431-436.	1.8	15
130	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.	1.3	15
131	Reply to â€A promoter polymorphism in the CASP8 gene is not associated with cancer risk― Nature Genetics, 2008, 40, 260-261.	9.4	14
132	Integrative analysis of gene expression profiles reveals specific signaling pathways associated with pancreatic duct adenocarcinoma. Cancer Communications, 2018, 38, 1-12.	3.7	14
133	Cytokine <i>BAFF</i> Gene Variation Is Associated with Survival of Patients with T-cell Lymphomas. Clinical Cancer Research, 2012, 18, 2250-2256.	3.2	13
134	Genetic variants at $5p15$ are associated with risk and early onset of gastric cancer in Chinese populations. Carcinogenesis, 2013, 34, 2539-2542.	1.3	13
135	Phenotypic and molecular characterization of Streptococcus agalactiae colonized in Chinese pregnant women: predominance of ST19/III and ST17/III. Research in Microbiology, 2018, 169, 101-107.	1.0	13
136	A single-nucleotide polymorphism in the 3′-UTR region of the adipocyte fatty acid binding protein 4 gene is associated with prognosis of triple-negative breast cancer. Oncotarget, 2016, 7, 18984-18998.	0.8	13
137	Genetic variants of <i>Clorf10 </i> and risk of esophageal squamous cell carcinoma in a Chinese population. Cancer Science, 2009, 100, 1695-1700.	1.7	12
138	No association between XRCC1 polymorphisms and survival in non-small-cell lung cancer patients treated with platinum-based chemotherapy. Cancer Biology and Therapy, 2010, 10, 854-859.	1.5	12
139	Two Novel Variants on 13q22.1 Are Associated with Risk of Esophageal Squamous Cell Carcinoma. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1774-1780.	1.1	12
140	Prevalence and characteristics of <i>Staphylococcus aureus</i> and methicillinâ€resistant <i>Staphylococcus aureus</i> nasal colonization among a communityâ€based diabetes population in Foshan, China. Journal of Diabetes Investigation, 2017, 8, 383-391.	1.1	12
141	<i>Cyclooxygenaseâ€2</i> Gly587Arg variant is associated with differential enzymatic activity and risk of esophageal squamousâ€cell carcinoma. Molecular Carcinogenesis, 2009, 48, 934-941.	1.3	11
142	Genome-wide association study on serum alkaline phosphatase levels in a Chinese population. BMC Genomics, 2013, 14, 684.	1.2	11
143	Risk of genome-wide association study-identified genetic variants for non-Hodgkin lymphoma in a Chinese population. Carcinogenesis, 2013, 34, 1516-1519.	1.3	11
144	Efficacy and safety of umbilical cord mesenchymal stem cells in treatment of cesarean section skin scars: a randomized clinical trial. Stem Cell Research and Therapy, 2020, 11, 244.	2.4	11

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145	Targeted sequencing of chromosome 15q25 identified novel variants associated with risk of lung cancer and smoking behavior in Chinese. Carcinogenesis, 2017, 38, 552-558.	1.3	10
146	Associations of Genetic Variations in Mismatch Repair Genes MSH3 and PMS1 with Acute Adverse Events and Survival in Patients with Rectal Cancer Receiving Postoperative Chemoradiotherapy. Cancer Research and Treatment, 2019, 51, 1198-1206.	1.3	10
147	Pathway Analysis for Genome-Wide Association Study of Lung Cancer in Han Chinese Population. PLoS ONE, 2013, 8, e57763.	1.1	9
148	Germline variation in the 3′â€untranslated region of the POU2AF1 gene is associated with susceptibility to lymphoma. Molecular Carcinogenesis, 2017, 56, 1945-1952.	1.3	9
149	Comparison of dimension reduction-based logistic regression models forcase-control genome-wide association study: principal components analysis vs. partial least squares. Journal of Biomedical Research, 2015, 29, 298.	0.7	9
150	The Caseâ€Only Test for Gene–Environment Interaction is Not Uniformly Powerful: An Empirical Example. Genetic Epidemiology, 2013, 37, 402-407.	0.6	8
151	Association of GWAS-Identified Lung Cancer Susceptibility Loci with Survival Length in Patients with Small-Cell Lung Cancer Treated with Platinum-Based Chemotherapy. PLoS ONE, 2014, 9, e113574.	1.1	8
152	Association between IVF/ICSI treatment and preterm birth and major perinatal outcomes among dichorionicâ€diamnionic twin pregnancies: A sevenâ€year retrospective cohort study. Acta Obstetricia Et Gynecologica Scandinavica, 2021, 100, 162-169.	1.3	8
153	Prevalence of and Risk Factors for Poor Sleep During Different Trimesters of Pregnancy Among Women in China: A Cross-Sectional Study. Nature and Science of Sleep, 2021, Volume 13, 811-820.	1.4	8
154	Imputation-based association analyses identify new lung cancer susceptibility variants in CDK6 and SH3RF1 and their interactions with smoking in Chinese populations. Carcinogenesis, 2013, 34, 2010-2016.	1.3	7
155	A cis-eQTL genetic variant of the cancer–testis gene CCDC116 is associated with risk of multiple cancers. Human Genetics, 2017, 136, 987-997.	1.8	7
156	Role of velamentous cord insertion in monochorionic twin pregnancies: a PRISMA-compliant systematic review and meta-analysis of observational studies. Journal of Maternal-Fetal and Neonatal Medicine, 2020, 33, 2377-2386.	0.7	7
157	Should singleton birth weight standards be applied to identify small-for-gestational age twins?: analysis of a retrospective cohort study. BMC Pregnancy and Childbirth, 2021, 21, 446.	0.9	7
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