Dongxin Lin

List of Publications by Year
in descending order

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178	12,223	25034	29157
papers	citations	57 h-index	104 g-index

183	183	183	18800
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Association between gestational weight gain and perinatal outcomes among twin gestations based on the 2009 Institute of Medicine (IOM) guidelines: a systematic review. Journal of Maternal-Fetal and Neonatal Medicine, 2022, 35, 6527-6541.	1.5	3
2	Changes in lower uterine segment thickness during different gestational weeks in pregnant women qualified for trial of labor after cesarean section. International Journal of Gynecology and Obstetrics, 2022, 157, 710-718.	2.3	2
3	Assessment of different thresholds of birthweight discordance for early neonatal outcomes: retrospective analysis of 2348 twin pregnancies. BMC Pregnancy and Childbirth, 2022, 22, 93.	2.4	3
4	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.	2.8	8
5	Association Between Nausea and Vomiting During Pregnancy and Sleep Quality: Mediating Effect of Depressive Symptoms. International Journal of General Medicine, 2021, Volume 14, 41-49.	1.8	6
6	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.	6.0	17
7	The association of hypertensive disorders of pregnancy with small for gestational age and intertwin birthweight discordance. Journal of Clinical Hypertension, 2021, 23, 1354-1362.	2.0	4
8	Maternal and neonatal outcomes in transverse and vertical skin incision for placenta previa. BMC Pregnancy and Childbirth, 2021, 21, 441.	2.4	4
9	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.	2.7	8
10	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.	2.4	7
11	Mechanical Parameters and Trajectory of Two Chinese Cervical Manipulations Compared by a Motion Capture System. Frontiers in Bioengineering and Biotechnology, 2021, 9, 714292.	4.1	4
12	Maternal and Neonatal Outcomes of Placenta Previa with and without Coverage of a Uterine Scar: A Retrospective Cohort Study in a Tertiary Hospital. International Journal of Women's Health, 2021, Volume 13, 671-681.	2.6	6
13	Anesthetic management in cesarean delivery of women with placenta previa: a retrospective cohort study. BMC Anesthesiology, 2021, 21, 247.	1.8	3
14	Fasting Plasma Glucose Mediates the Prospective Effect of Maternal Metal Level on Birth Outcomes: A Retrospective and Longitudinal Population-Based Cohort Study. Frontiers in Endocrinology, 2021, 12, 763693.	3.5	2
15	Double-uterine-incision in the management of placenta previa complicated by placenta accreta spectrum.. American Journal of Translational Research (discontinued), 2021, 13, 13017-13023.	0.0	0
16	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.	1.5	7
17	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.	7.3	104
18	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.	2.9	15

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19	Feasibility of Transcatheter Closure of Secundum Atrial Septal Defect in Low Weight Infants Under 2-Year-Old from a 3-year Retrospective Cohort Study. American Journal of Cardiology, 2020, 132, 133-139.	1.6	3
20	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.	5.5	11
21	The effect of placental location identified before delivery on birthweight discordance among diamniotic-dichorionic twin pregnancies: a three-year retrospective cohort study. Scientific Reports, 2019, 9, 12099.	3.3	2
22	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.	10.7	167
23	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.	2.4	22
24	The gestational weight gain and perinatal outcomes among underweight women with twin pregnancies: Propensity score matched analysis from a three-year retrospective cohort. European Journal of Obstetrics, Gynecology and Reproductive Biology, 2019, 243, 97-102.	1.1	5
25	Genome landscapes of rectal cancer before and after preoperative chemoradiotherapy. Theranostics, 2019, 9, 6856-6866.	10.0	27
26	METTL3 facilitates tumor progression via an m6A-IGF2BP2-dependent mechanism in colorectal carcinoma. Molecular Cancer, 2019, 18, 112.	19.2	515
27	Excessive miR-25-3p maturation via N6-methyladenosine stimulated by cigarette smoke promotes pancreatic cancer progression. Nature Communications, 2019, 10, 1858.	12.8	242
28	PIWI-interacting RNA-36712 restrains breast cancer progression and chemoresistance by interaction with SEPW1 pseudogene SEPW1P RNA. Molecular Cancer, 2019, 18, 9.	19.2	139
29	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.	3.0	10
30	Trend and risk factors of low birth weight and macrosomia in south China, 2005â€“2017: a retrospective observational study. Scientific Reports, 2018, 8, 3393.	3.3	44
31	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.	21.4	75
32	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.	2.1	13
33	Associations of Genetic Variations in MicroRNA Seed Regions With Acute Adverse Events and Survival in Patients With Rectal Cancer Receiving Postoperative Chemoradiation Therapy. International Journal of Radiation Oncology Biology Physics, 2018, 100, 1026-1033.	0.8	3
34	Genetic variant repressing ADH1A expression confers susceptibility to esophageal squamous-cell carcinoma. Cancer Letters, 2018, 421, 43-50.	7.2	16
35	Functional role of PLCE1 intronic insertion variant associated with susceptibility to esophageal squamous cell carcinoma. Carcinogenesis, 2018, 39, 191-201.	2.8	5
36	Neonatal colonization of group B Streptococcus in China: Prevalence, antimicrobial resistance, serotypes, and molecular characterization. American Journal of Infection Control, 2018, 46, e19-e24.	2.3	20

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37	OTUB1 promotes esophageal squamous cell carcinoma metastasis through modulating Snail stability. Oncogene, 2018, 37, 3356-3368.	5.9	72
38	A large meta-analysis of the global prevalence rates of S. aureus and MRSA contamination of milk. Critical Reviews in Food Science and Nutrition, 2018, 58, 2213-2228.	10.3	16
39	A prospective cohort study of Staphylococcus aureus and methicillin-resistant Staphylococcus aureus carriage in neonates: the role of maternal carriage and phenotypic and molecular characteristics. Infection and Drug Resistance, 2018, Volume 11, 555-565.	2.7	16
40	PIWI-interacting RNA-54265 is oncogenic and a potential therapeutic target in colorectal adenocarcinoma. Theranostics, 2018, 8, 5213-5230.	10.0	115
41	Exome-wide analysis identifies three low-frequency missense variants associated with pancreatic cancer risk in Chinese populations. Nature Communications, 2018, 9, 3688.	12.8	32
42	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.	6.9	17
43	Genotype imputation for Han Chinese population using Haplotype Reference Consortium as reference. Human Genetics, 2018, 137, 431-436.	3.8	15
44	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.	10.0	19
45	Integrative analysis of gene expression profiles reveals specific signaling pathways associated with pancreatic duct adenocarcinoma. Cancer Communications, 2018, 38, 1-12.	9.2	14
46	Identification of new susceptibility loci for gastric non-cardia adenocarcinoma: pooled results from two Chinese genome-wide association studies. Gut, 2017, 66, 581-587.	12.1	68
47	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.	1.3	40
48	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.	5.1	26
49	Genomic analysis of oesophageal squamous-cell carcinoma identifies alcohol drinking-related mutation signature and genomic alterations. Nature Communications, 2017, 8, 15290.	12.8	195
50	Targeted sequencing of chromosome 15q25 identified novel variants associated with risk of lung cancer and smoking behavior in Chinese. Carcinogenesis, 2017, 38, 552-558.	2.8	10
51	Germline variation in the 3â€²â€untranslated region of the POU2AF1 gene is associated with susceptibility to lymphoma. Molecular Carcinogenesis, 2017, 56, 1945-1952.	2.7	9
52	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.	2.3	16
53	Metabolome-wide association study identified the association between a circulating polyunsaturated fatty acids variant rs174548 and lung cancer. Carcinogenesis, 2017, 38, 1147-1154.	2.8	21
54	BRCA1-Associated Protein Increases Invasiveness of Esophageal Squamous Cell Carcinoma. Gastroenterology, 2017, 153, 1304-1319.e5.	1.3	23

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55	Prevalence and characteristics of Staphylococcus aureus and methicillinâ€resistant Staphylococcus aureus nasal colonization among a communityâ€based diabetes population in Foshan, China. Journal of Diabetes Investigation, 2017, 8, 383-391.	2.4	12
56	A cis-eQTL genetic variant of the cancerâ€“testis gene CCDC116 is associated with risk of multiple cancers. Human Genetics, 2017, 136, 987-997.	3.8	7
57	Nasal colonization of Staphylococcus aureus colonal complex 5: Prevalence, influencing factors, and phenotypic and molecular characteristics in pregnant Chinese women. American Journal of Infection Control, 2017, 45, 1106-1110.	2.3	4
58	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.	5.1	66
59	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.	1.7	25
60	Methicillin-Resistant Staphylococcus aureus Nasal Colonization in Chinese Children: A Prevalence Meta-Analysis and Review of Influencing Factors. PLoS ONE, 2016, 11, e0159728.	2.5	20
61	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.	2.9	50
62	Pancreatic cancer risk variant in LINC00673 creates a miR-1231 binding site and interferes with PTPN11 degradation. Nature Genetics, 2016, 48, 747-757.	21.4	237
63	Genomic Characterization of Esophageal Squamous Cell Carcinoma Reveals Critical Genes Underlying Tumorigenesis and Poor Prognosis. American Journal of Human Genetics, 2016, 98, 709-727.	6.2	129
64	Whole exome sequencing identifies lncRNAGAS8-AS1andLPAR4as novel papillary thyroid carcinoma driver alternations. Human Molecular Genetics, 2016, 25, 1875-1884.	2.9	79
65	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.	7.5	25
66	Genome-wide association studies in East Asians identify new loci for waist-hip ratio and waist circumference. Scientific Reports, 2016, 6, 17958.	3.3	58
67	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	12.8	86
68	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.	2.9	50
69	Identification of Susceptibility Loci and Genes for Colorectal Cancer Risk. Gastroenterology, 2016, 150, 1633-1645.	1.3	97
70	Genome-wide association study of gastric adenocarcinoma in Asia: a comparison of associations between cardia and non-cardia tumours. Gut, 2016, 65, 1611-1618.	12.1	99
71	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.	3.5	98
72	A single-nucleotide polymorphism in the 3â€²-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.	1.8	13

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73	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.	3.3	24
74	<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.	5.1	72
75	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.	6.3	152
76	Relatively Small Contribution of Methylation and Genomic Copy Number Aberration to the Aberrant Expression of Inflammation-Related Genes in HBV-Related Hepatocellular Carcinoma. PLoS ONE, 2015, 10, e0126836.	2.5	1
77	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	6.2	101
78	Systematical analyses of variants in CTCF-binding sites identified a novel lung cancer susceptibility locus among Chinese population. Scientific Reports, 2015, 5, 7833.	3.3	16
79	Pulmonary expression of CYP2A13 and ABCB1 is regulated by FOXA2, and their genetic interaction is associated with lung cancer. FASEB Journal, 2015, 29, 1986-1998.	0.5	15
80	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.	3.8	34
81	Suppression of CYP2C9 by MicroRNA hsa-miR-128-3p in Human Liver Cells and Association with Hepatocellular Carcinoma. Scientific Reports, 2015, 5, 8534.	3.3	92
82	Genomic Analyses Reveal Mutational Signatures and Frequently Altered Genes in Esophageal Squamous Cell Carcinoma. American Journal of Human Genetics, 2015, 96, 597-611.	6.2	290
83	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.	6.2	41
84	Two Novel Variants on 13q22.1 Are Associated with Risk of Esophageal Squamous Cell Carcinoma. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1774-1780.	2.5	12
85	Associations of ATM Polymorphisms With Survival in Advanced Esophageal Squamous Cell Carcinoma Patients Receiving Radiation Therapy. International Journal of Radiation Oncology Biology Physics, 2015, 93, 181-189.	0.8	4
86	Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. Human Molecular Genetics, 2015, 24, 1791-1800.	2.9	105
87	Exposure to airborne PM2.5 suppresses microRNA expression and deregulates target oncogenes that cause neoplastic transformation in NIH3T3 cells. Oncotarget, 2015, 6, 29428-29439.	1.8	46
88	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.	1.6	9
89	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.	2.5	8
90	A genome-wide geneâ€“gene interaction analysis identifies an epistatic gene pair for lung cancer susceptibility in Han Chinese. Carcinogenesis, 2014, 35, 572-577.	2.8	29

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91	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.	2.9	90
92	A genome wide association study of genetic loci that influence tumour biomarkers cancer antigen 19-9, carcinoembryonic antigen and Î± fetoprotein and their associations with cancer risk. Gut, 2014, 63, 143-151.	12.1	67
93	Stability SCAD: a powerful approach to detect interactions in large-scale genomic study. BMC Bioinformatics, 2014, 15, 62.	2.6	1
94	Genome-wide association study of survival in patients with pancreatic adenocarcinoma. Gut, 2014, 63, 152-160.	12.1	59
95	A genome-wide association study identifies common variants influencing serum uric acid concentrations in a Chinese population. BMC Medical Genomics, 2014, 7, 10.	1.5	57
96	Identification of genomic alterations in oesophageal squamous cell cancer. Nature, 2014, 509, 91-95.	27.8	903
97	Joint analysis of three genome-wide association studies of esophageal squamous cell carcinoma in Chinese populations. Nature Genetics, 2014, 46, 1001-1006.	21.4	148
98	Genome-wide association study identifies three susceptibility loci for laryngeal squamous cell carcinoma in the Chinese population. Nature Genetics, 2014, 46, 1110-1114.	21.4	57
99	Genome-wide association study identifies new susceptibility loci for epithelial ovarian cancer in Han Chinese women. Nature Communications, 2014, 5, 4682.	12.8	59
100	A genome-wide gene-environment interaction analysis for tobacco smoke and lung cancer susceptibility. Carcinogenesis, 2014, 35, 1528-1535.	2.8	47
101	Population distribution and ancestry of the cancer protective MDM2 SNP285 (rs117039649). Oncotarget, 2014, 5, 8223-8234.	1.8	22
102	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.	2.7	25
103	A Genomeâ€Wide Association Study for Serum Bilirubin Levels and Geneâ€Environment Interaction in a Chinese Population. Genetic Epidemiology, 2013, 37, 293-300.	1.3	34
104	A functional BRCA1 coding sequence genetic variant contributes to risk of esophageal squamous cell carcinoma. Carcinogenesis, 2013, 34, 2309-2313.	2.8	54
105	Genome-wide association study on serum alkaline phosphatase levels in a Chinese population. BMC Genomics, 2013, 14, 684.	2.8	11
106	Evidence of associations of APOBEC3B gene deletion with susceptibility to persistent HBV infection and hepatocellular carcinoma. Human Molecular Genetics, 2013, 22, 1262-1269.	2.9	52
107	Identification of common variants in BRCA2 and MAP2K4 for susceptibility to sporadic pancreatic cancer. Carcinogenesis, 2013, 34, 1001-1005.	2.8	19
108	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.	21.4	97

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109	Genetic variants in STAT4 and HLA-DQ genes confer risk of hepatitis B virusâ€“related hepatocellular carcinoma. Nature Genetics, 2013, 45, 72-75.	21.4	259
110	A genome-wide association study identifies two new cervical cancer susceptibility loci at 4q12 and 17q12. Nature Genetics, 2013, 45, 918-922.	21.4	108
111	Risk prediction of esophageal squamous-cell carcinoma with common genetic variants and lifestyle factors in Chinese population. Carcinogenesis, 2013, 34, 1782-1786.	2.8	37
112	Risk of genome-wide association study-identified genetic variants for non-Hodgkin lymphoma in a Chinese population. Carcinogenesis, 2013, 34, 1516-1519.	2.8	11
113	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.	3.5	41
114	Genetic variants at 5p15 are associated with risk and early onset of gastric cancer in Chinese populations. Carcinogenesis, 2013, 34, 2539-2542.	2.8	13
115	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.	2.8	7
116	The Caseâ€Only Test for Geneâ€“Environment Interaction is Not Uniformly Powerful: An Empirical Example. Genetic Epidemiology, 2013, 37, 402-407.	1.3	8
117	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.	21.4	43
118	Pathway Analysis for Genome-Wide Association Study of Lung Cancer in Han Chinese Population. PLoS ONE, 2013, 8, e57763.	2.5	9
119	A Genome Wide Association Study Identifies Common Variants Associated with Lipid Levels in the Chinese Population. PLoS ONE, 2013, 8, e82420.	2.5	57
120	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.	2.5	25
121	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.	3.5	177
122	Copy number variation at 6q13 functions as a long-range regulator and is associated with pancreatic cancer risk. Carcinogenesis, 2012, 33, 94-100.	2.8	34
123	Association analyses identify multiple new lung cancer susceptibility loci and their interactions with smoking in the Chinese population. Nature Genetics, 2012, 44, 895-899.	21.4	129
124	Cytokine BAFF Gene Variation Is Associated with Survival of Patients with T-cell Lymphomas. Clinical Cancer Research, 2012, 18, 2250-2256.	7.0	13
125	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.	6.2	76
126	Genome-wide association analysis identifies new lung cancer susceptibility loci in never-smoking women in Asia. Nature Genetics, 2012, 44, 1330-1335.	21.4	286

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127	Genome-Wide Association Study of Prognosis in Advanced Nonâ€“Small Cell Lung Cancer Patients Receiving Platinum-Based Chemotherapy. Clinical Cancer Research, 2012, 18, 5507-5514.	7.0	56
128	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.	21.4	238
129	Genome-wide association study identifies five loci associated with susceptibility to pancreatic cancer in Chinese populations. Nature Genetics, 2012, 44, 62-66.	21.4	164
130	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.	1.3	69
131	Functional regulatory variants of MCL1 contribute to enhanced promoter activity and reduced risk of lung cancer in nonsmokers: Implications for contextâ€dependent phenotype of an antiapoptotic and antiproliferative gene in solid tumor. Cancer, 2012, 118, 2085-2095.	4.1	5
132	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.	3.8	39
133	Increased risk of lung cancer associated with a functionally impaired polymorphic variant of the human DNA glycosylase NEIL2. DNA Repair, 2012, 11, 570-578.	2.8	42
134	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.	21.4	340
135	Association of candidate genetic variations with gastric cardia adenocarcinoma in Chinese population: a multiple interaction analysis. Carcinogenesis, 2011, 32, 336-342.	2.8	45
136	Genome-wide association study identifies three new susceptibility loci for esophageal squamous-cell carcinoma in Chinese populations. Nature Genetics, 2011, 43, 679-684.	21.4	260
137	Assessment of XPD Lys751Gln and XRCC1 Tâ€“77C polymorphisms in advanced non-small-cell lung cancer patients treated with platinum-based chemotherapy. Lung Cancer, 2011, 73, 110-115.	2.0	31
138	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.	21.4	250
139	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.	1.1	38
140	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.	16.8	104
141	A functional â^'77T>C polymorphism in XRCC1 is associated with risk of breast cancer. Breast Cancer Research and Treatment, 2011, 125, 479-487.	2.5	32
142	Circulating MicroRNAs, miR-21, miR-122, and miR-223, in patients with hepatocellular carcinoma or chronic hepatitis. Molecular Carcinogenesis, 2011, 50, 136-142.	2.7	494
143	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.	4.1	35
144	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.	0.8	53

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145	Genetic Variation in an miRNA-1827 Binding Site in MYCL1 Alters Susceptibility to Small-Cell Lung Cancer. Cancer Research, 2011, 71, 5175-5181.	0.9	73
146	Variations in HSPA1B at 6p21.3 Are Associated with Lung Cancer Risk and Prognosis in Chinese Populations. Cancer Research, 2011, 71, 7576-7586.	0.9	30
147	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
148	ATM Polymorphisms Are Associated With Risk of Radiation-Induced Pneumonitis. International Journal of Radiation Oncology Biology Physics, 2010, 77, 1360-1368.	0.8	77
149	An estrogen receptor Î± suppressor, microRNAâ€22, is downregulated in estrogen receptor Î±â€positive human breast cancer cell lines and clinical samples. FEBS Journal, 2010, 277, 1684-1694.	4.7	148
150	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.	21.4	319
151	Cyclooxygenase-2 Genetic Variants Are Associated with Survival in Unresectable Locally Advanced Nonâ€“Small Cell Lung Cancer. Clinical Cancer Research, 2010, 16, 2383-2390.	7.0	37
152	Risk of Genome-Wide Association Studyâ€“Identified Genetic Variants for Colorectal Cancer in a Chinese Population. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 1855-1861.	2.5	58
153	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.	3.2	42
154	The 5p15.33 Locus Is Associated with Risk of Lung Adenocarcinoma in Never-Smoking Females in Asia. PLoS Genetics, 2010, 6, e1001051.	3.5	168
155	Genome-Wide Interrogation Identifies YAP1 Variants Associated with Survival of Small-Cell Lung Cancer Patients. Cancer Research, 2010, 70, 9721-9729.	0.9	53
156	No association betweenXRCC1polymorphisms and survival in non-small-cell lung cancer patients treated with platinum-based chemotherapy. Cancer Biology and Therapy, 2010, 10, 854-859.	3.4	12
157	Association of TGF-Î²1 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.	0.6	47
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