Jian Gu

List of Publications by Year in descending order

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210 papers	10,664 citations	26567 56 h-index	39575 94 g-index
217 all docs	217 docs citations	217 times ranked	15265 citing authors

#	Article	IF	Citations
1	Genome-wide association scan of tag SNPs identifies a susceptibility locus for lung cancer at 15q25.1. Nature Genetics, 2008, 40, 616-622.	9.4	1,189
2	Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. Nature Genetics, 2014, 46, 736-741.	9.4	360
3	Genetic variation in the prostate stem cell antigen gene PSCA confers susceptibility to urinary bladder cancer. Nature Genetics, 2009, 41, 991-995.	9.4	321
4	Bladder Cancer Predisposition: A Multigenic Approach to DNA-Repair and Cell-Cycleâ€“Control Genes. American Journal of Human Genetics, 2006, 78, 464-479.	2.6	249
5	Mitochondrial DNA Content: Its Genetic Heritability and Association With Renal Cell Carcinoma. Journal of the National Cancer Institute, 2008, 100, 1104-1112.	3.0	237
6	Single Nucleotide Polymorphisms of microRNA Machinery Genes Modify the Risk of Renal Cell Carcinoma. Clinical Cancer Research, 2008, 14, 7956-7962.	3.2	218
7	Genetic Variations in MicroRNA-Related Genes Are Novel Susceptibility Loci for Esophageal Cancer Risk. Cancer Prevention Research, 2008, 1, 460-469.	0.7	206
8	Hsa-miR-9 methylation status is associated with cancer development and metastatic recurrence in patients with clear cell renal cell carcinoma. Oncogene, 2010, 29, 5724-5728.	2.6	196
9	Genetic Variations in Radiation and Chemotherapy Drug Action Pathways Predict Clinical Outcomes in Esophageal Cancer. Journal of Clinical Oncology, 2006, 24, 3789-3798.	0.8	165
10	Energy stress-induced lncRNA FILNC1 represses c-Myc-mediated energy metabolism and inhibits renal tumor development. Nature Communications, 2017, 8, 783.	5.8	157
11	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
12	Prostate Stem Cell Antigen: A Jekyll and Hyde Molecule?. Clinical Cancer Research, 2010, 16, 3533-3538.	3.2	147
13	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. Nature Genetics, 2014, 46, 1233-1238.	9.4	147
14	Systematic Evaluation of Genetic Variants in the Inflammation Pathway and Risk of Lung Cancer. Cancer Research, 2007, 67, 6520-6527.	0.4	139
15	Polymorphisms in Inflammation Genes and Bladder Cancer: From Initiation to Recurrence, Progression, and Survival. Journal of Clinical Oncology, 2005, 23, 5746-5756.	0.8	138
16	Genome-wide association study identifies multiple loci associated with bladder cancer risk. Human Molecular Genetics, 2014, 23, 1387-1398.	1.4	137
17	Mosaic loss of chromosome Y is associated with common variation near TCL1A. Nature Genetics, 2016, 48, 563-568.	9.4	134
18	Prognostic significance of pretreatment serum levels of albumin, LDH and total bilirubin in patients with non-metastatic breast cancer. Carcinogenesis, 2015, 36, 243-248.	1.3	124

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19	MicroRNA Expression Signatures in Barrett's Esophagus and Esophageal Adenocarcinoma. Clinical Cancer Research, 2009, 15, 5744-5752.	3.2	120
20	Long-term tumor-free survival from treatment with the GFPâ€“TRAIL fusion gene expressed from the hTERT promoter in breast cancer cells. Oncogene, 2002, 21, 8020-8028.	2.6	118
21	Genetic Variants in MicroRNA Biosynthesis Pathways and Binding Sites Modify Ovarian Cancer Risk, Survival, and Treatment Response. Cancer Research, 2010, 70, 9765-9776.	0.4	118
22	A genome-wide association study of bladder cancer identifies a new susceptibility locus within SLC14A1, a urea transporter gene on chromosome 18q12.3. Human Molecular Genetics, 2011, 20, 4282-4289.	1.4	100
23	Genome-wide Association Study Identifies Five Susceptibility Loci for Follicular Lymphoma outside the HLA Region. American Journal of Human Genetics, 2014, 95, 462-471.	2.6	96
24	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. Nature Communications, 2016, 7, 10933.	5.8	94
25	Effects of N-acetyl transferase 1 and 2 polymorphisms on bladder cancer risk in Caucasians. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2005, 581, 97-104.	0.9	92
26	Genetic Variants in Inflammation-Related Genes Are Associated with Radiation-Induced Toxicity Following Treatment for Non-Small Cell Lung Cancer. PLoS ONE, 2010, 5, e12402.	1.1	91
27	MicroRNA Expression Signatures during Malignant Progression from Barrett's Esophagus to Esophageal Adenocarcinoma. Cancer Prevention Research, 2013, 6, 196-205.	0.7	91
28	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
29	MicroRNA in the Pathogenesis and Prognosis of Esophageal Cancer. Current Pharmaceutical Design, 2012, 19, 1292-1300.	0.9	89
30	Nucleotide Excision Repair Gene Polymorphisms and Recurrence after Treatment for Superficial Bladder Cancer. Clinical Cancer Research, 2005, 11, 1408-1415.	3.2	88
31	Genetic variations in PI3K-AKT-mTOR pathway and bladder cancer risk. Carcinogenesis, 2009, 30, 2047-2052.	1.3	85
32	hTERT promoter induces tumor-specific Bax gene expression and cell killing in syngenic mouse tumor model and prevents systemic toxicity. Gene Therapy, 2002, 9, 30-37.	2.3	84
33	Aberrant Promoter Methylation Profile and Association with Survival in Patients with Nonâ€“Small Cell Lung Cancer. Clinical Cancer Research, 2006, 12, 7329-7338.	3.2	84
34	Genome-Wide Association Study of Survival in Nonâ€“Small Cell Lung Cancer Patients Receiving Platinum-Based Chemotherapy. Journal of the National Cancer Institute, 2011, 103, 817-825.	3.0	81
35	A genome-wide association study identifies a novel susceptibility locus for renal cell carcinoma on 12p11.23. Human Molecular Genetics, 2012, 21, 456-462.	1.4	81
36	Genomeâ€wide profiling of chromosomal alterations in renal cell carcinoma using highâ€density single nucleotide polymorphism arrays. International Journal of Cancer, 2009, 125, 2342-2348.	2.3	80

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37	Pathway-Based Serum microRNA Profiling and Survival in Patients with Advanced Stage Nonâ€“Small Cell Lung Cancer. Cancer Research, 2013, 73, 4801-4809.	0.4	80
38	Telomere Length in Peripheral Blood Leukocytes and Lung Cancer Risk: A Large Caseâ€“Control Study in Caucasians. Cancer Research, 2014, 74, 2476-2486.	0.4	80
39	Mutagen Sensitivity Has High Heritability: Evidence from a Twin Study. Cancer Research, 2006, 66, 5993-5996.	0.4	78
40	Modulation of DNA damage/DNA repair capacity by XPC polymorphisms. DNA Repair, 2008, 7, 141-148.	1.3	76
41	Mutagen Sensitivity: A Genetic Predisposition Factor for Cancer: Table 1.. Cancer Research, 2007, 67, 3493-3495.	0.4	75
42	Genome-Wide Catalogue of Chromosomal Aberrations in Barrett's Esophagus and Esophageal Adenocarcinoma: A High-Density Single Nucleotide Polymorphism Array Analysis. Cancer Prevention Research, 2010, 3, 1176-1186.	0.7	73
43	A Genome-Wide Association Study Identifies a Locus on Chromosome 14q21 as a Predictor of Leukocyte Telomere Length and as a Marker of Susceptibility for Bladder Cancer. Cancer Prevention Research, 2011, 4, 514-521.	0.7	73
44	Targeted expression of green fluorescent protein/tumor necrosis factor-related apoptosis-inducing ligand fusion protein from human telomerase reverse transcriptase promoter elicits antitumor activity without toxic effects on primary human hepatocytes. Cancer Research, 2002, 62, 3620-5.	0.4	73
45	Matrix Metalloproteinase Polymorphisms and Bladder Cancer Risk. Cancer Research, 2006, 66, 11644-11648.	0.4	71
46	Constitutive Short Telomere Length of Chromosome 17p and 12q but not 11q and 2p Is Associated with an Increased Risk for Esophageal Cancer. Cancer Prevention Research, 2009, 2, 459-465.	0.7	69
47	Projecting Individualized Probabilities of Developing Bladder Cancer in White Individuals. Journal of Clinical Oncology, 2007, 25, 4974-4981.	0.8	67
48	Genetic Polymorphisms in MicroRNA-Related Genes as Predictors of Clinical Outcomes in Colorectal Adenocarcinoma Patients. Clinical Cancer Research, 2012, 18, 3982-3991.	3.2	67
49	Compilation of small RNA sequences. Nucleic Acids Research, 1994, 22, 3481-3482.	6.5	64
50	Matrix Metalloproteinase Polymorphisms Are Associated with Bladder Cancer Invasiveness. Clinical Cancer Research, 2007, 13, 2614-2620.	3.2	64
51	High-order interactions among genetic polymorphisms in nucleotide excision repair pathway genes and smoking in modulating bladder cancer risk. Carcinogenesis, 2007, 28, 2160-2165.	1.3	64
52	Pharmacogenomics of platinum-based chemotherapy in NSCLC. Expert Opinion on Drug Metabolism and Toxicology, 2009, 5, 745-755.	1.5	63
53	PI3K/PTEN/AKT/mTOR pathway genetic variation predicts toxicity and distant progression in lung cancer patients receiving platinum-based chemotherapy. Lung Cancer, 2011, 71, 82-88.	0.9	63
54	Prognostic significance of ataxiaâ€telangiectasia mutated, DNAâ€dependent protein kinase catalytic subunit, and Ku heterodimeric regulatory complex 86â€kD subunit expression in patients with nonsmall cell lung cancer. Cancer, 2008, 112, 2756-2764.	2.0	62

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55	A nonsynonymous single-nucleotide polymorphism in the PDZ-Rho guanine nucleotide exchange factor (Ser1416Gly) modulates the risk of lung cancer in Mexican Americans. Cancer, 2006, 106, 2707-2715.	2.0	59
56	Epidemiology and genetic susceptibility to bladder cancer. BJU International, 2008, 102, 1207-1215.	1.3	59
57	A genome-wide association study of marginal zone lymphoma shows association to the HLA region. Nature Communications, 2015, 6, 5751.	5.8	58
58	Role of Inflammation Gene Polymorphisms on Pain Severity in Lung Cancer Patients. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 2636-2642.	1.1	57
59	Combination of TRAIL gene therapy and chemotherapy enhances antitumor and antimetastasis effects in chemosensitive and chemoresistant breast cancers. Molecular Therapy, 2003, 8, 441-448.	3.7	56
60	Expression of Telomere-Associated Genes as Prognostic Markers for Overall Survival in Patients with Nonâ€“Small Cell Lung Cancer. Clinical Cancer Research, 2006, 12, 5720-5725.	3.2	56
61	Novel Susceptibility Loci for Second Primary Tumors/Recurrence in Head and Neck Cancer Patients: Large-Scale Evaluation of Genetic Variants. Cancer Prevention Research, 2009, 2, 617-624.	0.7	55
62	A novel single tetracycline-regulative adenoviral vector for tumor-specific Bax gene expression and cell killing in vitro and in vivo. Oncogene, 2002, 21, 4757-4764.	2.6	53
63	Genetic variations of the PI3K-AKT-mTOR pathway and clinical outcome in muscle invasive and metastatic bladder cancer patients. Carcinogenesis, 2010, 31, 1387-1391.	1.3	53
64	Genetic variants in cell cycle control pathway confer susceptibility to bladder cancer. Cancer, 2008, 112, 2467-2474.	2.0	52
65	Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. Human Molecular Genetics, 2016, 25, 1663-1676.	1.4	52
66	The somatic mutation landscape of premalignant colorectal adenoma. Gut, 2018, 67, 1299-1305.	6.1	52
67	The Ability of Bilirubin in Identifying Smokers with Higher Risk of Lung Cancer: A Large Cohort Study in Conjunction with Global Metabolomic Profiling. Clinical Cancer Research, 2015, 21, 193-200.	3.2	51
68	Profiling of Genetic Variations in Inflammation Pathway Genes in Relation to Bladder Cancer Predisposition. Clinical Cancer Research, 2008, 14, 2236-2244.	3.2	49
69	Combined TRAIL and Bax gene therapy prolonged survival in mice with ovarian cancer xenograft. Gene Therapy, 2002, 9, 1379-1386.	2.3	47
70	Mechanisms involved in development of resistance to adenovirus-mediated proapoptotic gene therapy in DLD1 human colon cancer cell line. Gene Therapy, 2002, 9, 1262-1270.	2.3	46
71	Genetic susceptibility to bladder cancer risk and outcome. Personalized Medicine, 2011, 8, 365-374.	0.8	46
72	GWAS-identified colorectal cancer susceptibility loci associated with clinical outcomes. Carcinogenesis, 2012, 33, 1327-1331.	1.3	46

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73	Association of mitochondrial DNA copy number in peripheral blood leukocytes with risk of esophageal adenocarcinoma. Carcinogenesis, 2013, 34, 2521-2524.	1.3	46
74	Genome-Wide Association Study Identifies Variants in Casein Kinase II (CSNK2A2) to be Associated With Leukocyte Telomere Length in a Punjabi Sikh Diabetic Cohort. Circulation: Cardiovascular Genetics, 2014, 7, 287-295.	5.1	46
75	Combined Effects of the p53 and p73 Polymorphisms on Lung Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 158-161.	1.1	45
76	Genetic Variations in the Sonic Hedgehog Pathway Affect Clinical Outcomes in Nonâ€“Muscle-Invasive Bladder Cancer. Cancer Prevention Research, 2010, 3, 1235-1245.	0.7	45
77	Augmenting Transgene Expression from Carcinoembryonic Antigen (CEA) Promoter via a GAL4 Gene Regulatory System. Molecular Therapy, 2001, 3, 278-283.	3.7	44
78	Cyclin D1 gene polymorphism as a risk factor for oral premalignant lesions. Carcinogenesis, 2006, 27, 2034-2037.	1.3	44
79	Dietary Intake of Vegetables and Fruits and the Modification Effects of GSTM1 and NAT2 Genotypes on Bladder Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 2090-2097.	1.1	44
80	Mutagen Sensitivity and Genetic Variants in Nucleotide Excision Repair Pathway: Genotype-Phenotype Correlation. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 2065-2071.	1.1	43
81	Expression of methylation-related genes is associated with overall survival in patients with non-small cell lung cancer. British Journal of Cancer, 2008, 98, 1716-1722.	2.9	43
82	Germline genetic variations in drug action pathways predict clinical outcomes in advanced lung cancer treated with platinum-based chemotherapy. Pharmacogenetics and Genomics, 2008, 18, 955-965.	0.7	43
83	Polymorphisms of STK15 (Aurora-A) gene and lung cancer risk in Caucasians. Carcinogenesis, 2006, 28, 350-355.	1.3	42
84	Genome-wide methylation analysis shows similar patterns in Barrettâ€™s esophagus and esophageal adenocarcinoma. Carcinogenesis, 2013, 34, 2750-2756.	1.3	42
85	Adenylation of Small RNAs in Human Cells. Journal of Biological Chemistry, 1998, 273, 6853-6859.	1.6	39
86	Genetic and intermediate phenotypic susceptibility markers of gastric cancer in Hispanic Americans: A caseâ€control study. Cancer, 2014, 120, 3040-3048.	2.0	38
87	Reduced mitochondrial DNA copy number in peripheral blood leukocytes increases the risk of soft tissue sarcoma. Carcinogenesis, 2013, 34, 1039-1043.	1.3	37
88	MicroRNA profiling in clear cell renal cell carcinoma tissues potentially links tumorigenesis and recurrence with obesity. British Journal of Cancer, 2017, 116, 77-84.	2.9	37
89	Bax-Induction Gene Therapy of Pancreatic Cancer. Journal of Surgical Research, 2002, 106, 346-351.	0.8	36
90	Global Assessment of Genetic Variation Influencing Response to Retinoid Chemoprevention in Head and Neck Cancer Patients. Cancer Prevention Research, 2011, 4, 185-193.	0.7	36

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91	Long telomeres in peripheral blood leukocytes are associated with an increased risk of soft tissue sarcoma. Cancer, 2013, 119, 1885-1891.	2.0	35
92	Severe obesity prior to diagnosis limits survival in colorectal cancer patients evaluated at a large cancer centre. British Journal of Cancer, 2016, 114, 103-109.	2.9	35
93	Formation of 2â€²,3â€²-Cyclic Phosphates at the 3â€² End of Human U6 Small Nuclear RNA in Vitro. Journal of Biological Chemistry, 1997, 272, 21989-21993.	1.6	34
94	Accurate 3â€² End Processing and Adenylation of Human Signal Recognition Particle RNA and Alu RNA in Vitro. Journal of Biological Chemistry, 1998, 273, 35023-35031.	1.6	34
95	Depressive Symptoms and Short Telomere Length Are Associated with Increased Mortality in Bladder Cancer Patients. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 336-343.	1.1	33
96	Moving toward individualized therapy based on NER polymorphisms that predict platinum sensitivity in ovarian cancer patients. Gynecologic Oncology, 2007, 107, S223-S229.	0.6	32
97	Genetic variations in the transforming growth factor-beta pathway as predictors of survival in advanced non-small cell lung cancer. Carcinogenesis, 2011, 32, 1050-1056.	1.3	32
98	Short telomere lengths in peripheral blood leukocytes are associated with an increased risk of oral premalignant lesion and oral squamous cell carcinoma. Cancer, 2013, 119, 4277-4283.	2.0	32
99	Induction of Apoptosis and Down-Regulation of Bcl-XL in Cancer Cells by a Novel Small Molecule, 2[[3-(2,3-Dichlorophenoxy)propyl]amino]ethanol. Cancer Research, 2004, 64, 1110-1113.	0.4	31
100	The Prostate Cancer Susceptibility Variant rs2735839 Near KLK3 Gene Is Associated with Aggressive Prostate Cancer and Can Stratify Gleason Score 7 Patients. Clinical Cancer Research, 2014, 20, 5133-5139.	3.2	31
101	Serum MicroRNAâ€150 Predicts Prognosis for Earlyâ€Stage Nonâ€Small Cell Lung Cancer and Promotes Tumor Cell Proliferation by Targeting Tumor Suppressor Gene SRCIN1. Clinical Pharmacology and Therapeutics, 2018, 103, 1061-1073.	2.3	31
102	Identification of Serum Markers of Esophageal Adenocarcinoma by Global and Targeted Metabolic Profiling. Clinical Gastroenterology and Hepatology, 2015, 13, 1730-1737.e9.	2.4	29
103	Personalized Risk Assessment in Never, Light, and Heavy Smokers in a prospective cohort in Taiwan. Scientific Reports, 2016, 6, 36482.	1.6	29
104	Genetic polymorphism in bladder cancer. Frontiers in Bioscience - Landmark, 2007, 12, 192.	3.0	29
105	Induction of p53-regulated genes in lung cancer cells: implications of the mechanism for adenoviral p53-mediated apoptosis. Oncogene, 2004, 23, 1300-1307.	2.6	28
106	Genetic Variations in the Regulator of G-Protein Signaling Genes Are Associated with Survival in Late-Stage Non-Small Cell Lung Cancer. PLoS ONE, 2011, 6, e21120.	1.1	27
107	Systematic evaluation of apoptotic pathway gene polymorphisms and lung cancer risk. Carcinogenesis, 2012, 33, 1699-1706.	1.3	26
108	Mitochondrial DNA copy number in peripheral blood leukocytes and the aggressiveness of localized prostate cancer. Oncotarget, 2015, 6, 41988-41996.	0.8	26

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109	Roles of tumor suppressor and telomere maintenance genes in cancer and agingâ€"an epidemiological study. Carcinogenesis, 2005, 26, 1741-1747.	1.3	25
110	Genetic susceptibility to bladder cancer with an emphasis on geneâ€"gene and geneâ€"environmental interactions. Current Opinion in Urology, 2008, 18, 493-498.	0.9	25
111	Mitochondrial DNA copy number in peripheral blood leukocytes and the risk of clear cell renal cell carcinoma. Carcinogenesis, 2015, 36, 249-255.	1.3	25
112	Prognostic significance of promoter CpG island methylation of obesityâ€related genes in patients with nonmetastatic renal cell carcinoma. Cancer, 2017, 123, 3617-3627.	2.0	25
113	Telomerase Promoter-Driven Cancer Cell Suicide. Cancer Biology and Therapy, 2003, 2, 63-69.	1.5	23
114	STK15 F31I polymorphism is associated with increased uterine cancer risk: A pilot studyâ˜†. Gynecologic Oncology, 2007, 107, 71-74.	0.6	23
115	Prospective analysis of DNA damage and repair markers of lung cancer risk from the Prostate, Lung, Colorectal and Ovarian (PLCO) Cancer Screening Trial. Carcinogenesis, 2011, 32, 69-73.	1.3	23
116	Association of Auroraâ€A (STK15) kinase polymorphisms with clinical outcome of esophageal cancer treated with preoperative chemoradiation. Cancer, 2012, 118, 4346-4353.	2.0	23
117	Social-demographics, health behaviors, and telomere length in the Mexican American Mano a Mano Cohort. Oncotarget, 2017, 8, 96553-96567.	0.8	23
118	Leukocyte mitochondrial DNA content: a novel biomarker associated with prognosis and therapeutic outcome in colorectal cancer. Carcinogenesis, 2015, 36, 543-552.	1.3	22
119	Genomic DNA Hypomethylation and Risk of Renal Cell Carcinoma: A Caseâ€"Control Study. Clinical Cancer Research, 2016, 22, 2074-2082.	3.2	22
120	Low serum testosterone is associated with tumor aggressiveness and poor prognosis in prostate cancer. Oncology Letters, 2017, 13, 1949-1957.	0.8	22
121	Telomerase promoter-driven cancer gene therapy. Cancer Biology and Therapy, 2003, 2, S64-70.	1.5	22
122	Germline prognostic markers for urinary bladder cancer: Obstacles and opportunities. Urologic Oncology: Seminars and Original Investigations, 2012, 30, 524-532.	0.8	21
123	Enhancing adenovirus-mediated gene transferin vitroandin vivoby addition of protamine and hydrocortisone. Journal of Gene Medicine, 2003, 5, 868-875.	1.4	20
124	Increased leukocyte mitochondrial DNA copy number is associated with oral premalignant lesions: an epidemiology study. Carcinogenesis, 2014, 35, 1760-1764.	1.3	20
125	Genetic variants of the Wnt signaling pathway as predictors of recurrence and survival in early-stage non-small cell lung cancer patients. Carcinogenesis, 2014, 35, 1284-1291.	1.3	19
126	Lower mitochondrial DNA copy number in peripheral blood leukocytes increases the risk of endometrial cancer. Molecular Carcinogenesis, 2016, 55, 1111-1117.	1.3	19

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127	Small RNA database. Nucleic Acids Research, 1998, 26, 160-162.	6.5	18
128	HSD3B and Gene-Gene Interactions in a Pathway-Based Analysis of Genetic Susceptibility to Bladder Cancer. PLoS ONE, 2012, 7, e51301.	1.1	18
129	Epigenetic analysis of microRNA genes in tumors from surgically resected lung cancer patients and association with survival. Molecular Carcinogenesis, 2015, 54, E45-51.	1.3	18
130	High baseline levels of interleukin-8 in leukocytes and urine predict tumor recurrence in non-muscle invasive bladder cancer patients receiving bacillus Calmetteâ€“Guerin therapy: A long-term survival analysis. OncoImmunology, 2017, 6, e1265719.	2.1	18
131	Polymorphisms in genes related to epithelialâ€“mesenchymal transition and risk of non-small cell lung cancer. Carcinogenesis, 2017, 38, 1029-1035.	1.3	18
132	A miR-SNP biomarker linked to an increased lung cancer survival by miRNA-mediated down-regulation of FZD4 expression and Wnt signaling. Scientific Reports, 2017, 7, 9029.	1.6	18
133	Genetic Variants in Telomere-Maintenance Genes and Bladder Cancer Risk. PLoS ONE, 2012, 7, e30665.	1.1	18
134	Identification of Tissue- and Cancer-Selective Promoters for the Introduction of Genes into Human Ovarian Cancer Cells. Gynecologic Oncology, 2002, 85, 451-458.	0.6	17
135	Joint Effect of Mutagen Sensitivity and Insulin-Like Growth Factors in Predicting the Risk of Developing Secondary Primary Tumors and Tumor Recurrence in Patients with Head and Neck Cancer. Clinical Cancer Research, 2006, 12, 7194-7201.	3.2	17
136	Telomere Length and Recurrence Risk after Curative Resection in Patients with Early-Stage Nonâ€“Small-Cell Lung Cancer: A Prospective Cohort Study. Journal of Thoracic Oncology, 2015, 10, 302-308.	0.5	17
137	Isolation and characterization of a new 110 kDa human nuclear RNA-binding protein (p110nrb). Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1998, 1399, 1-9.	2.4	16
138	Improved Prognostic Stratification Using Circulating Tumor Cell Clusters in Patients with Metastatic Castration-Resistant Prostate Cancer. Cancers, 2021, 13, 268.	1.7	16
139	Heritability of prostate cancer: a tale of rare variants and common single nucleotide polymorphisms. Annals of Translational Medicine, 2016, 4, 206-206.	0.7	16
140	Small RNA database. Nucleic Acids Research, 1996, 24, 73-75.	6.5	15
141	The pharmacogenetic impact of inflammatory genes on bladder cancer recurrence. Pharmacogenomics, 2005, 6, 575-584.	0.6	15
142	Ionizing Radiationâ€“Induced Î³-H2AX Activity in Whole Blood Culture and the Risk of Lung Cancer. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 443-451.	1.1	15
143	Risk Assessment of Esophageal Adenocarcinoma Using Î³-H2AX Assay. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 1797-1804.	1.1	15
144	Identification of polymorphisms in ultraconserved elements associated with clinical outcomes in locally advanced colorectal adenocarcinoma. Cancer, 2012, 118, 6188-6198.	2.0	14

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145	Leukocyte telomere length is associated with aggressive prostate cancer in localized prostate cancer patients. EBioMedicine, 2020, 52, 102616.	2.7	14
146	Integration of circulating tumor cell and neutrophil-lymphocyte ratio to identify high-risk metastatic castration-resistant prostate cancer patients. BMC Cancer, 2021, 21, 655.	1.1	14
147	Predictors of Survival in Never-Smokers with Nonâ€“Small Cell Lung Cancer: A Large-Scale, Two-Phase Genetic Study. Clinical Cancer Research, 2012, 18, 5983-5991.	3.2	13
148	Comprehensive pathwayâ€based interrogation of genetic variations in the nucleotide excision DNA repair pathway and risk of bladder cancer. Cancer, 2012, 118, 205-215.	2.0	13
149	Association of leukocyte telomere length in peripheral blood leukocytes with endometrial cancer risk in Caucasian Americans. Carcinogenesis, 2015, 36, 1327-1332.	1.3	13
150	Genetic variants in telomereâ€maintenance genes are associated with ovarian cancer risk and outcome. Journal of Cellular and Molecular Medicine, 2017, 21, 510-518.	1.6	13
151	Long Leukocyte Telomere Length Is Associated with Increased Risks of Soft Tissue Sarcoma: A Mendelian Randomization Study. Cancers, 2020, 12, 594.	1.7	13
152	Benzo(a)pyrene Diol Epoxide-Induced Chromosome 9p21 Aberrations Are Associated with Increased Risk of Bladder Cancer. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 2445-2450.	1.1	12
153	Re: Short Telomere Length, Cancer Survival, and Cancer Risk in 47 102 Individuals. Journal of the National Cancer Institute, 2013, 105, 1157-1157.	3.0	12
154	Genetic variations in base excision repair pathway and risk of bladder cancer: A caseâ€control study in the United States. Molecular Carcinogenesis, 2015, 54, 50-57.	1.3	12
155	Cohort Profile: The MD Anderson Cancer Patients and Survivors Cohort (MDA-CPSC). International Journal of Epidemiology, 2016, 45, 713-713f.	0.9	12
156	Pathway analysis of bladder cancer genome-wide association study identifies novel pathways involved in bladder cancer development. Genes and Cancer, 2016, 7, 229-239.	0.6	12
157	Evolutionary conservation of post-transcriptional 3' end adenylation of small RNAs: S. cerevisiae signal recognition particle RNA and U2 small nuclear RNA are post-transcriptionally adenylated. Molecular and Cellular Biochemistry, 2000, 208, 99-109.	1.4	11
158	A genetic variant near the PMAIP1/Noxa gene is associated with increased bleomycin sensitivity. Human Molecular Genetics, 2011, 20, 820-826.	1.4	11
159	Common genetic variants in cell cycle pathway are associated with survival in stage IIIâ€“IV non-small-cell lung cancer. Carcinogenesis, 2011, 32, 1867-1871.	1.3	11
160	Mitochondrial DNA copy number in peripheral blood leukocytes is associated with biochemical recurrence in prostate cancer patients in African Americans. Carcinogenesis, 2020, 41, 267-273.	1.3	11
161	Cell to cell contact required for bystander effect of the TNF-related apoptosis-inducing ligand (TRAIL) gene. International Journal of Oncology, 2003, 22, 1241.	1.4	10
162	Hypoxia pathway genetic variants predict survival of non-small-cell lung cancer patients receiving platinum-based chemotherapy. Carcinogenesis, 2017, 38, 419-424.	1.3	10

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163	Associations of genetically predicted circulating insulinâ€like growth factorâ€1 and insulinâ€like growth factor binding proteinâ€3 with bladder cancer risk. Molecular Carcinogenesis, 2021, 60, 726-733.	1.3	10
164	Leukocyte telomere length is associated with aggressive prostate cancer in localized African American prostate cancer patients. Carcinogenesis, 2020, 41, 1213-1218.	1.3	9
165	Elevated systemic inflammatory responses, factors associated with physical and mental quality of life, and prognosis of hepatocellular carcinoma. Aging, 2020, 12, 4357-4370.	1.4	9
166	Identification of polymorphisms in ultraconserved elements (UCEs) associated with clinical outcomes in patients (pts) with stage II/III colorectal cancer (CRC).. Journal of Clinical Oncology, 2011, 29, 3529-3529.	0.8	8
167	Genetic variants within ultraconserved elements and susceptibility to right- and left-sided colorectal adenocarcinoma. Carcinogenesis, 2012, 33, 841-847.	1.3	7
168	Methylation of subtelomeric repeat D4Z4 in peripheral blood leukocytes is associated with biochemical recurrence in localized prostate cancer patients. Carcinogenesis, 2017, 38, 821-826.	1.3	7
169	Genetic associations of T cell cancer immune response with tumor aggressiveness in localized prostate cancer patients and disease reclassification in an active surveillance cohort. OncoImmunology, 2019, 8, e1483303.	2.1	7
170	Reply to â€˜Mosaic loss of chromosome Y in leukocytes mattersâ€™. Nature Genetics, 2019, 51, 7-9.	9.4	7
171	LINE-1 methylation in peripheral blood leukocytes and clinical characteristics and prognosis of prostate cancer patients. Oncotarget, 2017, 8, 94020-94027.	0.8	7
172	Epigenome-Wide Association Study of Prostate Cancer in African Americans Identifies DNA Methylation Biomarkers for Aggressive Disease. Biomolecules, 2021, 11, 1826.	1.8	7
173	High circulating insulin-like growth factor-1 reduces the risk of renal cell carcinoma: a Mendelian randomization study. Carcinogenesis, 2021, 42, 826-830.	1.3	6
174	Leukocyte Telomere Length and Cancer Risk: A Dynamic Problem. EBioMedicine, 2015, 2, 493-494.	2.7	5
175	Genetic variants in the nucleotide excision repair genes are associated with the risk of developing endometriosis. Biology of Reproduction, 2019, 101, 928-937.	1.2	5
176	Leukocyte Telomere Length and Bladder Cancer Risk: A Large Caseâ€“Control Study and Mendelian Randomization Analysis. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 203-209.	1.1	5
177	Genetic variants of the Wnt signaling pathway as predictors of aggressive disease and reclassification in men with early stage prostate cancer on active surveillance. Carcinogenesis, 2016, 37, 965-971.	1.3	4
178	Methylation of global DNA repeat LINE-1 and subtelomeric DNA repeats D4Z4 in leukocytes is associated with biochemical recurrence in African American prostate cancer patients. Carcinogenesis, 2019, 40, 1055-1060.	1.3	4
179	MicroRNAs in Esophageal Cancer. , 2011, , 201-221.		3
180	Irradiation-induced telomerase activity and the risk of lung cancer. Cancer, 2007, 109, 1157-1163.	2.0	2

#	Article	IF	Citations
181	Strategies to Identify Pharmacogenomic Biomarkers: Candidate Gene, Pathway-Based, and Genome-Wide Approaches. , 2008, , 353-370.		2
182	Genetic variations in apoptosis pathway and the risk of ovarian cancer. Oncotarget, 2016, 7, 56737-56745.	0.8	2
183	Abstract 196: A SNP in the 3â€²-untranslated region of FZD4 linked to lung cancer survival modulates a miRNA-mediated FZD4 transcript binding, cleavage, expression, and Wnt-signaling in NSCLC cells. , 2015, , .		1
184	Pharmacogenetics in Cancer Chemotherapy. , 2008, , 113-128.		1
185	Abstract 2650: A combined bioinformatics and GWAS approach identifies a functional 3â€²UTR insertion/deletion inYES1associated with bladder cancer risk. , 2012, , .		1
186	Abstract 5038: Telomere length linking social contexts and cancer risk in Mexican Americans. , 2014, , .		1
187	Abstract LB-298: The use of lung cancer risk prediction model to stratify heavy smokers: The power of routinely collected lab data. Cancer Research, 2014, 74, LB-298-LB-298.	0.4	1
188	Prognostic value of leukocyte telomere length in renal cell carcinoma patients. American Journal of Cancer Research, 2020, 10, 3428-3439.	1.4	1
189	Genome-wide DNA methylation profiling of leukocytes identifies CpG methylation signatures of aggressive prostate cancer. American Journal of Cancer Research, 2021, 11, 968-978.	1.4	1
190	Biomarkers for Assessing Risk of Cancer. , 2015, , 317-330.e3.		0
191	Genetic variants in epithelialâ€“mesenchymal transition genes as predictors of clinical outcomes in localized prostate cancer. Carcinogenesis, 2020, 41, 1057-1064.	1.3	0
192	Pharmacogenetics of Lung Cancer. , 2010, , 87-106.		0
193	Use of telomere length in peripheral leukocytes to predict risk of recurrence in patients with early-stage non-small cell lung cancer after curative resection.. Journal of Clinical Oncology, 2010, 28, 7031-7031.	0.8	0
194	Abstract LB-424: A genome-wide association study identifies a locus on chromosome 14q21 as a predictor of leukocyte telomere length and as a marker of susceptibility to bladder cancer. , 2011, , .		0
195	Abstract 2249: Use of telomere length and genetic variations in maintenance genes to predict risk of recurrence and survival in patients with early-stage non-small cell lung cancer. , 2011, , .		0
196	Abstract 4485: Prediction of esophageal cancer risk through quantification of gamma-H2AX levels in peripheral blood lymphocytes. , 2012, , .		0
197	Abstract 4484: A novel objective, image-based phenotypic assay reveals higher Î±-radiation-induced Î³-H2AX level in peripheral blood lymphocytes as a risk predictor for lung cancer. , 2012, , .		0
198	Abstract 1728: Genetic variations in epidermal growth factor receptor pathway predict recurrence and response to chemotherapy in early stage non-small cell lung cancer. , 2012, , .		0

#	Article	IF	Citations
199	Abstract 2929: Predictors of survival in never-smokers with non-small cell lung cancer: A large-scale, two-phase genetic study. , 2012, , .		0
200	Abstract LB-27: Metabolomic profiling identifies bilirubin as a novel serum marker for lung cancer.. , 2013, , .		0
201	Abstract 2554: Constitutive short telomere length and lung cancer risk: a large case- control study.. , 2013, , .		0
202	Leukocyte telomere length and risk of secondary primary tumors in long-term breast cancer survivors.. Journal of Clinical Oncology, 2014, 32, 9599-9599.	0.8	0
203	Abstract 5062: Serum microRNA profiling in non-muscle invasive bladder cancer. , 2014, , .		0
204	Abstract 3850: Genetic and intermediate phenotypic susceptibility markers of gastric cancer in Hispanic-Americans: A case control study. , 2014, , .		0
205	Abstract 5547: A genetic variant nearKLK3gene is associated with aggressive prostate cancer and can stratify Gleason score 7 patients. , 2014, , .		0
206	Abstract 4594: Serum microRNA signatures predict recurrence and survival in Caucasian patients with early stage non-small cell lung cancer. , 2015, , .		0
207	Abstract 3737: Severe obesity and colorectal cancer patient survival. , 2015, , .		0
208	Genetically predicted high circulating insulin-like growth factor-1 and insulin-like growth factor binding protein-3 increase the risks of soft tissue sarcoma. American Journal of Cancer Research, 2021, 11, 3980-3989.	1.4	0
209	A whole-exome case-control association study to characterize the contribution of rare coding variation to pancreatic cancer risk. Human Genetics and Genomics Advances, 2022, 3, 100078.	1.0	0
210	Prognostic significance of circulating insulin growth-like factor 1 and insulin growth-like factor binding protein 3 in renal cell carcinoma patients.. American Journal of Cancer Research, 2022, 12, 852-860.	1.4	0