

Hongliang Liu

List of Publications by Year in descending order

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121
papers

2,147
citations

236612

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315357

38
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all docs

123
docs citations

123
times ranked

4154
citing authors

#	ARTICLE	IF	CITATIONS
1	Polygenic Risk Score Effectively Predicts Depression Onset in Alzheimer's Disease Based on Major Depressive Disorder Risk Variants. <i>Frontiers in Neuroscience</i> , 2022, 16, 827447.	1.4	4
2	Genetic variants in <i>CYP2B6</i> and <i>HSD17B12</i> associated with risk of squamous cell carcinoma of the head and neck. <i>International Journal of Cancer</i> , 2022, 151, 553-564.	2.3	7
3	Genetic variants in <i>DDO</i> and <i>PEX5L</i> in peroxisome-related pathways predict non-small cell lung cancer survival. <i>Molecular Carcinogenesis</i> , 2022, 61, 619-628.	1.3	2
4	Deciphering associations between three RNA splicing-related genetic variants and lung cancer risk. <i>Npj Precision Oncology</i> , 2022, 6, .	2.3	1
5	Genetic Association Between Epigenetic Aging-Acceleration and the Progression of Mild Cognitive Impairment to Alzheimer's Disease. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2022, 77, 1734-1742.	1.7	6
6	Potentially functional variants of <i>ERAP1</i> , <i>PSMF1</i> and <i>NCF2</i> in the MHC-I-related pathway predict non-small cell lung cancer survival. <i>Cancer Immunology, Immunotherapy</i> , 2021, 70, 2819-2833.	2.0	8
7	Association of genetic variants of <i>TMEM135</i> and <i>PEX5</i> in the peroxisome pathway with cutaneous melanoma-specific survival. <i>Annals of Translational Medicine</i> , 2021, 9, 396-396.	0.7	3
8	Genetic variants of <i>CHEK1</i> , <i>PRIM2</i> and <i>CDK6</i> in the mitotic phase-related pathway are associated with non-small cell lung cancer survival. <i>International Journal of Cancer</i> , 2021, 149, 1302-1312.	2.3	9
9	Potentially functional variants of <i>HBEGF</i> and <i>ITPR3</i> in GnRH signaling pathway genes predict survival of non-small cell lung cancer patients. <i>Translational Research</i> , 2021, 233, 92-103.	2.2	14
10	Association of genetic variants of <i>FBXO32</i> and <i>FOXO6</i> in the FOXO pathway with breast cancer risk. <i>Molecular Carcinogenesis</i> , 2021, 60, 661-670.	1.3	4
11	Genetic variants of <i>SDCCAG8</i> and <i>MAGI2</i> in mitosis-related pathway genes are independent predictors of cutaneous melanoma-specific survival. <i>Cancer Science</i> , 2021, 112, 4355-4364.	1.7	1
12	Genetic Variants of <i>CLPP</i> and <i>M1AP</i> Are Associated With Risk of Non-Small Cell Lung Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 709829.	1.3	1
13	A pleiotropic <i>ATM</i> variant (rs1800057 C>G) is associated with risk of multiple cancers. <i>Carcinogenesis</i> , 2021, , .	1.3	1
14	Genetic Variants of <i>CLEC4E</i> and <i>BIRC3</i> in Damage-Associated Molecular Patterns-Related Pathway Genes Predict Non-Small Cell Lung Cancer Survival. <i>Frontiers in Oncology</i> , 2021, 11, 717109.	1.3	6
15	Association Between Polygenic Risk Score and the Progression from Mild Cognitive Impairment to Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2021, 84, 1323-1335.	1.2	7
16	Genetic variants of , and in the natural killer cell-related pathway are associated with non-small cell lung cancer survival. <i>American Journal of Cancer Research</i> , 2021, 11, 2264-2277.	1.4	0
17	Genetic variants of and in myeloid cell-related pathway genes independently predict cutaneous melanoma-specific survival. <i>American Journal of Cancer Research</i> , 2021, 11, 3252-3262.	1.4	0
18	Novel genetic variants in <i>KIF16B</i> and <i>NEDD4L</i> in the endosome-related genes are associated with non-small cell lung cancer survival. <i>International Journal of Cancer</i> , 2020, 147, 392-403.	2.3	6

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19	Novel genetic variants in <i>HDAC2</i> and <i>PPARGC1A</i> of the CREB-binding protein pathway predict survival of non-small cell lung cancer. <i>Molecular Carcinogenesis</i> , 2020, 59, 104-115.	1.3	13
20	Genetic variants in TKT and DERA in the nicotinamide adenine dinucleotide phosphate pathway predict melanoma survival. <i>European Journal of Cancer</i> , 2020, 136, 84-94.	1.3	3
21	Novel genetic variants in genes of the Fc gamma receptor-mediated phagocytosis pathway predict non-small cell lung cancer survival. <i>Translational Lung Cancer Research</i> , 2020, 9, 575-586.	1.3	6
22	Associations between genetic variants of KIF5B, FMN1, and MGAT3 in the cadherin pathway and pancreatic cancer risk. <i>Cancer Medicine</i> , 2020, 9, 9620-9631.	1.3	1
23	Genetic variants of the peroxisome proliferator-activated receptor (PPAR) signaling pathway genes and risk of pancreatic cancer. <i>Molecular Carcinogenesis</i> , 2020, 59, 930-939.	1.3	11
24	Novel Variants of ELP2 and PIAS1 in the Interferon Gamma Signaling Pathway Are Associated with Non-Small Cell Lung Cancer Survival. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 1679-1688.	1.1	2
25	Potentially functional genetic variants in <i>PLIN2</i> , <i>SULT2A1</i> and <i>UGT1A9</i> genes of the ketone pathway and survival of nonsmall cell lung cancer. <i>International Journal of Cancer</i> , 2020, 147, 1559-1570.	2.3	8
26	Novel Genetic Variants of ALG6 and GALNTL4 of the Glycosylation Pathway Predict Cutaneous Melanoma-Specific Survival. <i>Cancers</i> , 2020, 12, 288.	1.7	7
27	Genetic variants in <i>PDSS1</i> and <i>SLC16A6</i> of the ketone body metabolic pathway predict cutaneous melanoma-specific survival. <i>Molecular Carcinogenesis</i> , 2020, 59, 640-650.	1.3	9
28	<i>APOB</i> Genotypes and <i>CDH13</i> Haplotypes in the Cholesterol-Related Pathway Genes Predict Non-Small Cell Lung Cancer Survival. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 1204-1213.	1.1	7
29	A Genome-Wide Association Study Identifies Two Novel Susceptible Regions for Squamous Cell Carcinoma of the Head and Neck. <i>Cancer Research</i> , 2020, 80, 2451-2460.	0.4	33
30	Novel genetic variants of and involved in immunoregulatory interactions are associated with non-small cell lung cancer survival. <i>American Journal of Cancer Research</i> , 2020, 10, 1770-1784.	1.4	2
31	Variants in , and in vitamin D pathway genes are associated with breast cancer risk: a large-scale analysis of 14 GWASs in the DRIVE study. <i>American Journal of Cancer Research</i> , 2020, 10, 2160-2173.	1.4	2
32	Novel genetic variants of and related lymphangiogenesis signaling pathway predict non-small cell lung cancer survival. <i>American Journal of Cancer Research</i> , 2020, 10, 2603-2616.	1.4	1
33	Genetic variants of and in the NLRP3 inflammasome pathway are associated with non-small cell lung cancer survival. <i>American Journal of Cancer Research</i> , 2020, 10, 2582-2595.	1.4	6
34	Novel genetic variants of and of the endosome-related pathway predict cutaneous melanoma-specific survival. <i>American Journal of Cancer Research</i> , 2020, 10, 3382-3394.	1.4	0
35	A genetic variant within <i>MDM4</i> 3'UTR miRNA binding site is associated with HPV16-positive tumors and survival of oropharyngeal cancer. <i>Molecular Carcinogenesis</i> , 2019, 58, 2276-2285.	1.3	5
36	Genetic variants in glutamine metabolic pathway genes predict cutaneous melanoma-specific survival. <i>Molecular Carcinogenesis</i> , 2019, 58, 2091-2103.	1.3	5

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37	Three novel genetic variants in NRF2 signaling pathway genes are associated with pancreatic cancer risk. <i>Cancer Science</i> , 2019, 110, 2022-2032.	1.7	14
38	Genetic variants in the liver kinase B1-AMP-activated protein kinase pathway genes and pancreatic cancer risk. <i>Molecular Carcinogenesis</i> , 2019, 58, 1338-1348.	1.3	14
39	Potentially functional genetic variants in the TNF/TNFR signaling pathway genes predict survival of patients with non-small cell lung cancer in the PLCO cancer screening trial. <i>Molecular Carcinogenesis</i> , 2019, 58, 1094-1104.	1.3	9
40	Genetic variants of genes in the NER pathway associated with risk of breast cancer: A large-scale analysis of 14 published GWAS datasets in the DRIVE study. <i>International Journal of Cancer</i> , 2019, 145, 1270-1279.	2.3	13
41	Potential functional variants in SMC2 and TP53 in the AURORA pathway genes and risk of pancreatic cancer. <i>Carcinogenesis</i> , 2019, 40, 521-528.	1.3	17
42	Genetic variants in <i>ELOVL2</i> and <i>HSD17B12</i> predict melanoma-specific survival. <i>International Journal of Cancer</i> , 2019, 145, 2619-2628.	2.3	11
43	Genetic variants in the calcium signaling pathway genes are associated with cutaneous melanoma-specific survival. <i>Carcinogenesis</i> , 2019, 40, 279-288.	1.3	6
44	Genetic variants in <i>RUNX3</i> , <i>AMD1</i> and <i>MSRA</i> in the methionine metabolic pathway and survival in nonsmall cell lung cancer patients. <i>International Journal of Cancer</i> , 2019, 145, 621-631.	2.3	21
45	Potentially functional genetic variants in the complement-related immunity gene set are associated with non-small cell lung cancer survival. <i>International Journal of Cancer</i> , 2019, 144, 1867-1876.	2.3	14
46	Genetic variants in <i>RORA</i> and <i>DNMT1</i> associated with cutaneous melanoma survival. <i>International Journal of Cancer</i> , 2018, 142, 2303-2312.	2.3	13
47	Potentially Functional Variants of ATG16L2 Predict Radiation Pneumonitis and Outcomes in Patients with Non-Small Cell Lung Cancer after Definitive Radiotherapy. <i>Journal of Thoracic Oncology</i> , 2018, 13, 660-675.	0.5	29
48	Associations between expression levels of nucleotide excision repair proteins in lymphoblastoid cells and risk of squamous cell carcinoma of the head and neck. <i>Molecular Carcinogenesis</i> , 2018, 57, 784-793.	1.3	5
49	Novel genetic variants in the P38MAPK pathway gene <i>ZAK</i> and susceptibility to lung cancer. <i>Molecular Carcinogenesis</i> , 2018, 57, 216-224.	1.3	9
50	Genetic variants in the platelet-derived growth factor subunit B gene associated with pancreatic cancer risk. <i>International Journal of Cancer</i> , 2018, 142, 1322-1331.	2.3	20
51	Genetic variants in the metzincin metallopeptidase family genes predict melanoma survival. <i>Molecular Carcinogenesis</i> , 2018, 57, 22-31.	1.3	5
52	Genetic variant of IRAK2 in the toll-like receptor signaling pathway and survival of non-small cell lung cancer. <i>International Journal of Cancer</i> , 2018, 143, 2400-2408.	2.3	14
53	Single-nucleotide polymorphisms of stemness genes predicted to regulate RNA splicing, microRNA and oncogenic signaling are associated with prostate cancer survival. <i>Carcinogenesis</i> , 2018, 39, 879-888.	1.3	9
54	Expression and Comparison of Cbl-b in Lung Squamous Cell Carcinoma and Adenocarcinoma. <i>Medical Science Monitor</i> , 2018, 24, 623-635.	0.5	3

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55	Apoptotic capacity and risk of squamous cell carcinoma of the head and neck. <i>European Journal of Cancer</i> , 2017, 72, 166-176.	1.3	19
56	Pathway analysis of published genome-wide association studies of lung cancer: A potential role for the <i>CYP4F3</i> locus. <i>Molecular Carcinogenesis</i> , 2017, 56, 1663-1672.	1.3	13
57	Reduced mRNA expression of nucleotide excision repair genes in lymphocytes and risk of squamous cell carcinoma of the head and neck. <i>Carcinogenesis</i> , 2017, 38, 504-510.	1.3	6
58	Genetic Variants in WNT2B and BTRC Predict Melanoma Survival. <i>Journal of Investigative Dermatology</i> , 2017, 137, 1749-1756.	0.3	5
59	Associations between RNA splicing regulatory variants of stemness-related genes and racial disparities in susceptibility to prostate cancer. <i>International Journal of Cancer</i> , 2017, 141, 731-743.	2.3	20
60	Genetic variants of PTPN2 are associated with lung cancer risk: a re-analysis of eight GWASs in the TRICL-ILCCO consortium. <i>Scientific Reports</i> , 2017, 7, 825.	1.6	10
61	Genetic variants in the integrin signaling pathway genes predict cutaneous melanoma survival. <i>International Journal of Cancer</i> , 2017, 140, 1270-1279.	2.3	4
62	Genetic variants in the genes encoding rho GTPases and related regulators predict cutaneous melanoma-specific survival. <i>International Journal of Cancer</i> , 2017, 141, 721-730.	2.3	8
63	A <i>PGC1β</i> genetic variant associated with nevus count and melanoma mortality. <i>International Journal of Cancer</i> , 2017, 141, 1066-1067.	2.3	5
64	Functional variants in DCAF4 associated with lung cancer risk in European populations. <i>Carcinogenesis</i> , 2017, 38, 541-551.	1.3	16
65	Associations between genetic variants in mRNA splicing-related genes and risk of lung cancer: a pathway-based analysis from published GWASs. <i>Scientific Reports</i> , 2017, 7, 44634.	1.6	10
66	Susceptibility loci of <i>CNOT6</i> in the general mRNA degradation pathway and lung cancer risk: A re-analysis of eight GWASs. <i>Molecular Carcinogenesis</i> , 2017, 56, 1227-1238.	1.3	10
67	Genetic variants of PDGF signaling pathway genes predict cutaneous melanoma survival. <i>Oncotarget</i> , 2017, 8, 74595-74606.	0.8	3
68	Component-wise gradient boosting and false discovery control in survival analysis with high-dimensional covariates. <i>Bioinformatics</i> , 2016, 32, 50-57.	1.8	26
69	Genetic variants in the vitamin D pathway genes <i>VDBP</i> and <i>RXRA</i> modulate cutaneous melanoma disease-specific survival. <i>Pigment Cell and Melanoma Research</i> , 2016, 29, 176-185.	1.5	19
70	Genetic variants in <i>ABCG1</i> are associated with survival of nonsmall-cell lung cancer patients. <i>International Journal of Cancer</i> , 2016, 138, 2592-2601.	2.3	41
71	Genetic variants in the PIWI/piRNA pathway gene <i>DCP1A</i> predict melanoma disease-specific survival. <i>International Journal of Cancer</i> , 2016, 139, 2730-2737.	2.3	21
72	A Novel Genetic Variant in Long Non-coding RNA Gene NEXN-AS1 is Associated with Risk of Lung Cancer. <i>Scientific Reports</i> , 2016, 6, 34234.	1.6	48

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73	Genetic variant in DNA repair gene <i>GTF2H4</i> is associated with lung cancer risk: a large-scale analysis of six published GWAS datasets in the TRICL consortium. <i>Carcinogenesis</i> , 2016, 37, 888-896.	1.3	15
74	Single Nucleotide Polymorphisms in CBLB, a Regulator of T-Cell Response, Predict Radiation Pneumonitis and Outcomes After Definitive Radiotherapy for Non-Small-Cell Lung Cancer. <i>Clinical Lung Cancer</i> , 2016, 17, 253-262.e5.	1.1	16
75	Reduced DNA double-strand break repair capacity and risk of squamous cell carcinoma of the head and neck—A case-control study. <i>DNA Repair</i> , 2016, 40, 18-26.	1.3	14
76	A variant at a potentially functional microRNA-binding site in BRIP1 was associated with risk of squamous cell carcinoma of the head and neck. <i>Tumor Biology</i> , 2016, 37, 8057-8066.	0.8	12
77	Associations between smoking behavior-related alleles and the risk of melanoma. <i>Oncotarget</i> , 2016, 7, 47366-47375.	0.8	15
78	Genetic variants of genes in the Notch signaling pathway predict overall survival of non-small cell lung cancer patients in the PLCO study. <i>Oncotarget</i> , 2016, 7, 61716-61727.	0.8	17
79	Genetic variants in Hippo pathway genes <i>YAP1</i> and <i>TEAD1</i> and <i>TEAD4</i> are associated with melanoma-specific survival. <i>International Journal of Cancer</i> , 2015, 137, 638-645.	2.3	48
80	Functional Variants in Notch Pathway Genes <i>NCOR2</i> , <i>NCSTN</i> , and <i>MAML2</i> Predict Survival of Patients with Cutaneous Melanoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1101-1110.	1.1	20
81	Genetic Variants of the MDM2 Gene Are Predictive of Treatment-Related Toxicities and Overall Survival in Patients With Advanced NSCLC. <i>Clinical Lung Cancer</i> , 2015, 16, e37-e53.	1.1	13
82	Genetic polymorphisms in the microRNA binding-sites of the thymidylate synthase gene predict risk and survival in gastric cancer. <i>Molecular Carcinogenesis</i> , 2015, 54, 880-888.	1.3	20
83	Genetic Variants in Fanconi Anemia Pathway Genes BRCA2 and FANCA Predict Melanoma Survival. <i>Journal of Investigative Dermatology</i> , 2015, 135, 542-550.	0.3	28
84	Identification of a melanoma susceptibility locus and somatic mutation in <i>TET2</i> . <i>Carcinogenesis</i> , 2014, 35, 2097-2101.	1.3	41
85	Potentially functional variants in the core nucleotide excision repair genes predict survival in Japanese gastric cancer patients. <i>Carcinogenesis</i> , 2014, 35, 2031-2038.	1.3	14
86	Functional single nucleotide polymorphisms of the RASSF3 gene and susceptibility to squamous cell carcinoma of the head and neck. <i>European Journal of Cancer</i> , 2014, 50, 582-592.	1.3	8
87	Genetic variants of the LIN28B gene predict severe radiation pneumonitis in patients with non-small cell lung cancer treated with definitive radiation therapy. <i>European Journal of Cancer</i> , 2014, 50, 1706-1716.	1.3	38
88	A functional variant at the miR-885-5p binding site of CASP3 confers risk of both index and second primary malignancies in patients with head and neck cancer. <i>FASEB Journal</i> , 2013, 27, 1404-1412.	0.2	32
89	Genome-wide association studies identify several new loci associated with pigmentation traits and skin cancer risk in European Americans. <i>Human Molecular Genetics</i> , 2013, 22, 2948-2959.	1.4	104
90	ATM Polymorphisms Predict Severe Radiation Pneumonitis in Patients With Non-Small Cell Lung Cancer Treated With Definitive Radiation Therapy. <i>International Journal of Radiation Oncology Biology Physics</i> , 2013, 85, 1066-1073.	0.4	57

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91	Association between putative functional variants in the <i>PSMB9</i> gene and risk of melanoma – re-analysis of published melanoma genome-wide association studies. <i>Pigment Cell and Melanoma Research</i> , 2013, 26, 392-401.	1.5	5
92	Association between functional polymorphisms in genes involved in the MAPK signaling pathways and cutaneous melanoma risk. <i>Carcinogenesis</i> , 2013, 34, 885-892.	1.3	10
93	Telomere Length in Peripheral Blood Lymphocytes Contributes to the Development of HPV-Associated Oropharyngeal Carcinoma. <i>Cancer Research</i> , 2013, 73, 5996-6003.	0.4	24
94	ERCC1 and ERCC2 Variants Predict Survival in Gastric Cancer Patients. <i>PLoS ONE</i> , 2013, 8, e71994.	1.1	37
95	Influence of single nucleotide polymorphisms in the MMP1 promoter region on cutaneous melanoma progression. <i>Melanoma Research</i> , 2012, 22, 169-175.	0.6	15
96	Roles of genetic variants in the PI3K and RAS/RAF pathways in susceptibility to endometrial cancer and clinical outcomes. <i>Journal of Cancer Research and Clinical Oncology</i> , 2012, 138, 377-385.	1.2	55
97	A Functional NQO1 609C>T Polymorphism and Risk of Gastrointestinal Cancers: A Meta-Analysis. <i>PLoS ONE</i> , 2012, 7, e30566.	1.1	18
98	A genetic variant in the APE1/Ref-1 gene promoter -141T/G may modulate risk of glioblastoma in a Chinese Han population. <i>BMC Cancer</i> , 2011, 11, 104.	1.1	16
99	Comparative proteomics study of freshly isolated, in vitro cultured, and proliferating islet preparation cells. <i>Journal of Endocrinological Investigation</i> , 2011, 34, 816-23.	1.8	0
100	Association of human aryl hydrocarbon receptor gene polymorphisms with risk of lung cancer among cigarette smokers in a Chinese population. <i>Pharmacogenetics and Genomics</i> , 2009, 19, 25-34.	0.7	49
101	<i>XRCC3</i> haplotypes and risk of gliomas in a Chinese population: A hospital-based case-control study. <i>International Journal of Cancer</i> , 2009, 124, 2948-2953.	2.3	41
102	Association between polymorphisms in the <i>GSTA4</i> gene and risk of lung cancer: A case-control study in a Southeastern Chinese population. <i>Molecular Carcinogenesis</i> , 2009, 48, 253-259.	1.3	7
103	Genetic variants in GTF2H1 and risk of lung cancer: A case-control analysis in a Chinese population. <i>Lung Cancer</i> , 2009, 63, 180-186.	0.9	10
104	Polymorphisms of <i>LIG4</i> and <i>XRCC4</i> involved in the NHEJ pathway interact to modify risk of glioma. <i>Human Mutation</i> , 2008, 29, 381-389.	1.1	64
105	Polymorphisms in hMLH1 and risk of early-onset lung cancer in a southeast Chinese population. <i>Lung Cancer</i> , 2008, 59, 164-170.	0.9	30
106	Polymorphisms in excision repair cross-complementing group 4 (ERCC4) and susceptibility to primary lung cancer in a Chinese Han population. <i>Lung Cancer</i> , 2008, 60, 332-339.	0.9	19
107	Potentially functional polymorphisms of EXO1 and risk of lung cancer in a Chinese population: A case-control analysis. <i>Lung Cancer</i> , 2008, 60, 340-346.	0.9	37
108	Association of polymorphisms in one-carbon metabolizing genes and lung cancer risk: a case-control study in Chinese population. <i>Lung Cancer</i> , 2008, 61, 21-29.	0.9	44

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109	Tagging single nucleotide polymorphisms in MBD4 are associated with risk of lung cancer in a Chinese population. <i>Lung Cancer</i> , 2008, 62, 281-286.	0.9	15
110	Tagging Single Nucleotide Polymorphisms in Phosphoinositide-3-Kinase-Related Protein Kinase Genes Involved in DNA Damage Checkpoints and Lung Cancer Susceptibility. <i>Clinical Cancer Research</i> , 2008, 14, 2887-2891.	3.2	9
111	Genetic variants in peroxisome proliferator-activated receptor- β gene are associated with risk of lung cancer in a Chinese population. <i>Carcinogenesis</i> , 2008, 29, 342-350.	1.3	24
112	Methyl-CpG binding domain 1 gene polymorphisms and lung cancer risk in a Chinese population. <i>Biomarkers</i> , 2008, 13, 607-617.	0.9	6
113	Tagging SNPs in non-homologous end-joining pathway genes and risk of glioma. <i>Carcinogenesis</i> , 2007, 28, 1906-1913.	1.3	82
114	Tagging single nucleotide polymorphisms in excision repair cross-complementing group 1 (ERCC1) and risk of primary lung cancer in a Chinese population. <i>Pharmacogenetics and Genomics</i> , 2007, 17, 417-423.	0.7	27
115	Polymorphisms of CAK genes and risk for lung cancer: A case-control study in Chinese population. <i>Lung Cancer</i> , 2007, 58, 171-183.	0.9	7
116	Genetic variants in MGMT and risk of lung cancer in Southeastern Chinese: a haplotype-based analysis. <i>Human Mutation</i> , 2007, 28, 431-440.	1.1	46
117	A meta-analysis of association between C677T polymorphism in the methylenetetrahydrofolate reductase gene and hypertension. <i>European Journal of Human Genetics</i> , 2007, 15, 1239-1245.	1.4	103
118	Sequence variations in DNA repair gene XPC is associated with lung cancer risk in a Chinese population: a case-control study. <i>BMC Cancer</i> , 2007, 7, 81.	1.1	31
119	The influence of metabolic gene polymorphisms on urinary 1-hydroxypyrene concentrations in Chinese coke oven workers. <i>Science of the Total Environment</i> , 2007, 381, 38-46.	3.9	28
120	Polymorphisms in DNA damage binding protein 2 (DDB2) and susceptibility of primary lung cancer in the Chinese: a case-control study. <i>Carcinogenesis</i> , 2006, 27, 1475-1480.	1.3	20
121	Polymorphisms in the Two Helicases ERCC2/XPD and ERCC3/XPB of the Transcription Factor IIIH Complex and Risk of Lung Cancer: A Case-Control Analysis in a Chinese Population. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2006, 15, 1336-1340.	1.1	45