Maria Teresa Landi

List of Publications by Year
in descending order

148	10,062	36303 51	40979 93
papers	citations	h-index	g-index

157	157	157	16505
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Novel MAPK/AKT-impairing germline NRAS variant identified in a melanoma-prone family. Familial Cancer, 2022, 21, 347-355.	1.9	1
2	Clinical Implications of Inter- and Intratumor Heterogeneity of Immune Cell Markers in Lung Cancer. Journal of the National Cancer Institute, 2022, 114, 280-289.	6.3	8
3	Characterizing the tumor microenvironment in rare renal cancer histological types. Journal of Pathology: Clinical Research, 2022, 8, 88-98.	3.0	8
4	Multi-Trait Genetic Analysis Identifies Autoimmune Loci Associated with Cutaneous Melanoma. Journal of Investigative Dermatology, 2022, 142, 1607-1616.	0.7	11
5	Accounting for EGFR Mutations in Epidemiologic Analyses of Nonâ€“Small Cell Lung Cancers: Examples Based on the International Lung Cancer Consortium Data. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 679-687.	2.5	1
6	Abstract PO-192: Comparing the association of self-reported race-ethnicity and genetic ancestry with all-cause mortality: A pan-cancer survivor analysis in the PLCO Screening Trial. , 2022, , .		0
7	Genome-wide interaction analysis identified low-frequency variants with sex disparity in lung cancer risk. Human Molecular Genetics, 2022, 31, 2831-2843.	2.9	4
8	Geneâ€“gene interaction of AhRwith and within the Wntcascade affects susceptibility to lung cancer. European Journal of Medical Research, 2022, 27, 14.	2.2	1
9	Mapping clustered mutations in cancer reveals APOBEC3 mutagenesis of ecDNA. Nature, 2022, 602, 510-517.	27.8	60
10	DNA Methylation in Lung Cancer: Mechanisms and Associations with Histological Subtypes, Molecular Alterations, and Major Epidemiological Factors. Cancers, 2022, 14, 961.	3.7	24
11	SUITOR: Selecting the number of mutational signatures through cross-validation. PLoS Computational Biology, 2022, 18, e1009309.	3.2	1
12	Autophagopathies: from autophagy gene polymorphisms to precision medicine for human diseases. Autophagy, 2022, 18, 2519-2536.	9.1	11
13	Rare germline deleterious variants increase susceptibility for lung cancer. Human Molecular Genetics, 2022, 31, 3558-3565.	2.9	5
14	A Penalized Regression Framework for Building Polygenic Risk Models Based on Summary Statistics From Genome-Wide Association Studies and Incorporating External Information. Journal of the American Statistical Association, 2021, 116, 133-143.	3.1	13
15	Lung cancer risk in painters: results from the SYNERGY pooled caseâ€“control study consortium. Occupational and Environmental Medicine, 2021, 78, 269-278.	2.8	11
16	Integration of multiomic annotation data to prioritize and characterize inflammation and immuneâ€related risk variants in squamous cell lung cancer. Genetic Epidemiology, 2021, 45, 99-114.	1.3	7
17	Tracing Lung Cancer Risk Factors Through Mutational Signatures in Never-Smokers. American Journal of Epidemiology, 2021, 190, 962-976.	3.4	16
18	Causal relationships between body mass index, smoking and lung cancer: Univariable and multivariable Mendelian randomization. International Journal of Cancer, 2021, 148, 1077-1086.	5.1	73

#	Article	IF	Citations
19	Assessing Lung Cancer Absolute Risk Trajectory Based on a Polygenic Risk Model. Cancer Research, 2021, 81, 1607-1615.	0.9	50
20	Sub-multiplicative interaction between polygenic risk score and household coal use in relation to lung adenocarcinoma among never-smoking women in Asia. Environment International, 2021, 147, 105975.	10.0	12
21	Genome-wide association meta-analysis identifies pleiotropic risk loci for aerodigestive squamous cell cancers. PLoS Genetics, 2021, 17, e1009254.	3.5	19
22	Large-scale cross-cancer fine-mapping of the 5p15.33 region reveals multiple independent signals. Human Genetics and Genomics Advances, 2021, 2, 100041.	1.7	6
23	Genetic Relationship Between Endometriosis and Melanoma. Frontiers in Reproductive Health, 2021, 3, .	1.9	5
24	Genomic and evolutionary classification of lung cancer in never smokers. Nature Genetics, 2021, 53, 1348-1359.	21.4	81
25	Cell-type-specific meQTLs extend melanoma GWAS annotation beyond eQTLs and inform melanocyte gene-regulatory mechanisms. American Journal of Human Genetics, 2021, 108, 1631-1646.	6.2	12
26	A UVB-responsive common variant at chromosome band 7p21.1 confers tanning response and melanoma risk via regulation of the aryl hydrocarbon receptor, AHR. American Journal of Human Genetics, 2021, 108, 1611-1630.	6.2	7
27	Impact of Histology and Tumor Grade on Clinical Outcomes Beyond 5 Years of Follow-Up in a Large Cohort of Renal Cell Carcinomas. Clinical Genitourinary Cancer, 2021, 19, e280-e285.	1.9	2
28	Identification of Genetic Risk Factors for Familial Urinary Bladder Cancer: An Exome Sequencing Study. JCO Precision Oncology, 2021, 5, 1830-1839.	3.0	3
29	Genome-Wide Meta-Analyses of FTND and TTFC Phenotypes. Nicotine and Tobacco Research, 2020, 22, 900-909.	2.6	17
30	Genomeâ€wide association study of INDELs identified four novel susceptibility loci associated with lung cancer risk. International Journal of Cancer, 2020, 146, 2855-2864.	5.1	7
31	Immune-mediated genetic pathways resulting in pulmonary function impairment increase lung cancer susceptibility. Nature Communications, 2020, 11, 27.	12.8	23
32	Assessment of HER2 Protein Overexpression and Gene Amplification in Renal Collecting Duct Carcinoma: Therapeutic Implication. Cancers, 2020, 12, 3345.	3.7	3
33	A multifactorial score including autophagy for prognosis and care of COVID-19 patients. Autophagy, 2020, 16, 2276-2281.	9.1	11
34	MC1R variants and cutaneous melanoma risk according to histological type, body site, and Breslow thickness: a pooled analysis from the M-SKIP project. Melanoma Research, 2020, 30, 500-510.	1.2	6
35	Expanding the genetic architecture of nicotine dependence and its shared genetics with multiple traits. Nature Communications, 2020, 11, 5562.	12.8	80
36	Genetic and epigenetic intratumor heterogeneity impacts prognosis of lung adenocarcinoma. Nature Communications, 2020, 11, 2459.	12.8	77

#	Article	IF	Citations
37	Protein-altering germline mutations implicate novel genes related to lung cancer development. Nature Communications, 2020, 11, 2220.	12.8	31
38	The genomic and epigenomic evolutionary history of papillary renal cell carcinomas. Nature Communications, 2020, 11, 3096.	12.8	19
39	Frequency of Pathogenic Germline Variants in Cancer-Susceptibility Genes in Patients With Osteosarcoma. JAMA Oncology, 2020, 6, 724.	7.1	139
40	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	12.8	75
41	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. Nature Genetics, 2020, 52, 494-504.	21.4	138
42	Histologic features of melanoma associated with germline mutations of CDKN2A, CDK4, and POT1 in melanoma-prone families from the United States, Italy, and Spain. Journal of the American Academy of Dermatology, 2020, 83, 860-869.	1.2	5
43	Peritoneal mesothelioma and asbestos exposure: a population-based caseâ€“control study in Lombardy, Italy. Occupational and Environmental Medicine, 2019, 76, 545-553.	2.8	20
44	Estimating CDKN2A mutation carrier probability among global familial melanoma cases using GenoMELPREDICT. Journal of the American Academy of Dermatology, 2019, 81, 386-394.	1.2	17
45	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
46	Elevated Platelet Count Appears to Be Causally Associated with Increased Risk of Lung Cancer: A Mendelian Randomization Analysis. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 935-942.	2.5	21
47	MC1R variants in childhood and adolescent melanoma: a retrospective pooled analysis of a multicentre cohort. The Lancet Child and Adolescent Health, 2019, 3, 332-342.	5.6	16
48	Alcohol consumption and lung cancer risk: A pooled analysis from the International Lung Cancer Consortium and the SYNERGY study. Cancer Epidemiology, 2019, 58, 25-32.	1.9	22
49	Mendelian Randomization and mediation analysis of leukocyte telomere length and risk of lung and head and neck cancers. International Journal of Epidemiology, 2019, 48, 751-766.	1.9	32
50	Use of Big Data to Estimate Prevalence of Defective DNA Repair Variants in the US Population. JAMA Dermatology, 2019, 155, 72.	4.1	11
51	Using imputed genotype data in the joint score tests for genetic association and geneâ€“environment interactions in caseâ€control studies. Genetic Epidemiology, 2018, 42, 146-155.	1.3	8
52	Germline mutations in Protection of Telomeres 1 in two families with Hodgkin lymphoma. British Journal of Haematology, 2018, 181, 372-377.	2.5	48
53	Novel genetic variants in the P38MAPK pathway gene ZAK and susceptibility to lung cancer. Molecular Carcinogenesis, 2018, 57, 216-224.	2.7	9
54	Prevalence of pathogenic/likely pathogenic variants in the 24 cancer genes of the ACMG Secondary Findings v2.0 list in a large cancer cohort and ethnicity-matched controls. Genome Medicine, 2018, 10, 99.	8.2	15

#	Article	IF	Citations
55	Fine mapping of MHC region in lung cancer highlights independent susceptibility loci by ethnicity. Nature Communications, 2018, 9, 3927.	12.8	43
56	Outdoor particulate matter (PM10) exposure and lung cancer risk in the EAGLE study. PLoS ONE, 2018, 13, e0203539.	2.5	57
57	Genetic modifiers of radon-induced lung cancer risk: a genome-wide interaction study in former uranium miners. International Archives of Occupational and Environmental Health, 2018, 91, 937-950.	2.3	27
58	Combining common genetic variants and non-genetic risk factors to predict risk of cutaneous melanoma. Human Molecular Genetics, 2018, 27, 4145-4156.	2.9	34
59	Weak sharing of genetic association signals in three lung cancer subtypes: evidence at the SNP, gene, regulation, and pathway levels. Genome Medicine, 2018, 10, 16.	8.2	32
60	MelaNostrum: a consensus questionnaire of standardized epidemiologic and clinical variables for melanoma risk assessment by the melanostrum consortium. Journal of the European Academy of Dermatology and Venereology, 2018, 32, 2134-2141.	2.4	9
61	MC1R variants as melanoma risk factors independent of at-risk phenotypic characteristics: a pooled analysis from the M-SKIP project. Cancer Management and Research, 2018, Volume 10, 1143-1154.	1.9	57
62	Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. Nature Communications, 2018, 9, 3221.	12.8	60
63	Assessing the Incremental Contribution of Common Genomic Variants to Melanoma Risk Prediction in Two Population-Based Studies. Journal of Investigative Dermatology, 2018, 138, 2617-2624.	0.7	52
64	Lung cancer and socioeconomic status in a pooled analysis of case-control studies. PLoS ONE, 2018, 13, e0192999.	2.5	107
65	Genome-wide association study of familial lung cancer. Carcinogenesis, 2018, 39, 1135-1140.	2.8	42
66	Pathwayâ€analysis of published genomeâ€wide association studies of lung cancer: A potential role for the CYP4F3 locus. Molecular Carcinogenesis, 2017, 56, 1663-1672.	2.7	13
67	Nut Consumption and Lung Cancer Risk: Results from Two Large Observational Studies. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 826-836.	2.5	23
68	Alcohol and lung cancer risk among never smokers: A pooled analysis from the international lung cancer consortium and the SYNERGY study. International Journal of Cancer, 2017, 140, 1976-1984.	5.1	35
69	Genetic variants of PTPN2 are associated with lung cancer risk: a re-analysis of eight GWASs in the TRICL-ILCCO consortium. Scientific Reports, 2017, 7, 825.	3.3	10
70	Menstrual and reproductive factors and lung cancer risk: A pooled analysis from the international lung cancer consortium. International Journal of Cancer, 2017, 141, 309-323.	5.1	28
71	Functional characterization of a multi-cancer risk locus on chr5p15.33 reveals regulation of TERT by ZNF148. Nature Communications, 2017, 8, 15034.	12.8	40
72	Epigenome-wide analysis of DNA methylation in lung tissue shows concordance with blood studies and identifies tobacco smoke-inducible enhancers. Human Molecular Genetics, 2017, 26, 3014-3027.	2.9	97

#	Article	IF	Citations
73	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. Nature Genetics, 2017, 49, 1126-1132.	21.4	472
74	Functional variants in DCAF4 associated with lung cancer risk in European populations. Carcinogenesis, 2017, 38, 541-551.	2.8	16
75	Associations between genetic variants in mRNA splicing-related genes and risk of lung cancer: a pathway-based analysis from published GWASs. Scientific Reports, 2017, 7, 44634.	3.3	10
76	Common TDP1 Polymorphisms in Relation to Survival among Small Cell Lung Cancer Patients: A Multicenter Study from the International Lung Cancer Consortium. Clinical Cancer Research, 2017, 23, 7550-7557.	7.0	6
77	Higher-than-expected population prevalence of potentially pathogenic germlineTP53variants in individuals unselected for cancer history. Human Mutation, 2017, 38, 1723-1730.	2.5	40
78	Germline Variation at CDKN2A and Associations with Nevus Phenotypes amongÂMembers of Melanoma Families. Journal of Investigative Dermatology, 2017, 137, 2606-2612.	0.7	18
79	Inherited variation in circadian rhythm genes and risks of prostate cancer and three other cancer sites in combined cancer consortia. International Journal of Cancer, 2017, 141, 1794-1802.	5.1	28
80	Integrating Clinical and Multiple Omics Data for Prognostic Assessment across Human Cancers. Scientific Reports, 2017, 7, 16954.	3.3	79
81	Susceptibility loci of CNOT6 in the general mRNA degradation pathway and lung cancer riskâ€"A reâ€analysis of eight GWASs. Molecular Carcinogenesis, 2017, 56, 1227-1238.	2.7	10
82	Gene-set meta-analysis of lung cancer identifies pathway related to systemic lupus erythematosus. PLoS ONE, 2017, 12, e0173339.	2.5	15
83	Obesity, metabolic factors and risk of different histological types of lung cancer: A Mendelian randomization study. PLoS ONE, 2017, 12, e0177875.	2.5	79
84	Three new pancreatic cancer susceptibility signals identified on chromosomes 1q32.1, 5p15.33 and 8q24.21. Oncotarget, 2016, 7, 66328-66343.	1.8	88
85	<scp>TERT</scp> promoter mutations in melanoma survival. International Journal of Cancer, 2016, 139, 75-84.	5.1	101
86	Characterizing human lung tissue microbiota and its relationship to epidemiological and clinical features. Genome Biology, 2016, 17, 163.	8.8	264
87	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
88	Nonsyndromic cleft lip with or without cleft palate and cancer: Evaluation of a possible common genetic background through the analysis of GWAS data. Genomics Data, 2016, 10, 22-29.	1.3	19
89	Novel Association of Genetic Markers Affecting CYP2A6 Activity and Lung Cancer Risk. Cancer Research, 2016, 76, 5768-5776.	0.9	57
90	Occupational prestige, social mobility and the association with lung cancer in men. BMC Cancer, 2016, 16, 395.	2.6	18

#	Article	IF	Citations
91	Multiple rare variants in high-risk pancreatic cancer-related genes may increase risk for pancreatic cancer in a subset of patients with and without germline CDKN2A mutations. Human Genetics, 2016, 135, 1241-1249.	3.8	24
92	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	12.8	86
93	A Novel Genetic Variant in Long Non-coding RNA Gene NEXN-AS1 is Associated with Risk of Lung Cancer. Scientific Reports, 2016, 6, 34234.	3.3	48
94	Association of Melanocortin-1 Receptor Variants with Pigmentary Traits in Humans: AÂPooled Analysis from the M-Skip Project. Journal of Investigative Dermatology, 2016, 136, 1914-1917.	0.7	16
95	Genetic variant in DNA repair geneGTF2H4is associated with lung cancer risk: a large-scale analysis of six published GWAS datasets in the TRICL consortium. Carcinogenesis, 2016, 37, 888-896.	2.8	15
96	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
97	Fine mapping of chromosome 5p15.33 based on a targeted deep sequencing and high density genotyping identifies novel lung cancer susceptibility loci. Carcinogenesis, 2016, 37, 96-105.	2.8	36
98	Identification of a novel susceptibility locus at 13q34 and refinement of the 20p12.2 region as a multi-signal locus associated with bladder cancer risk in individuals of European ancestry. Human Molecular Genetics, 2016, 25, 1203-1214.	2.9	38
99	Phenotypic and Histopathological Tumor Characteristics According to CDKN2A Mutation Status among Affected Members ofÂMelanoma Families. Journal of Investigative Dermatology, 2016, 136, 1066-1069.	0.7	13
100	Polymorphisms of the centrosomal gene (FGFR1OP) and lung cancer risk: a meta-analysis of 14 463 cases and 44 188 controls. Carcinogenesis, 2016, 37, 280-289.	2.8	7
101	MEGSA: A Powerful and Flexible Framework for Analyzing Mutual Exclusivity of Tumor Mutations. American Journal of Human Genetics, 2016, 98, 442-455.	6.2	40
102	Cigarette smoking behaviour and blood metabolomics. International Journal of Epidemiology, 2016, 45, 1421-1432.	1.9	63
103	Risk factors for keratinocyte skin cancer in patients diagnosed with melanoma, a large retrospective study. European Journal of Cancer, 2016, 53, 115-124.	2.8	15
104	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
105	Somatic Genomics and Clinical Features of Lung Adenocarcinoma: A Retrospective Study. PLoS Medicine, 2016, 13, e1002162.	8.4	148
106	A hybrid parametric and empirical likelihood model for evaluating interactions in case-control studies. Statistics and Its Interface, 2016, 9, 147-158.	0.3	1
107	<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
108	An exposureâ€weighted score test for genetic associations integrating environmental risk factors. Biometrics, 2015, 71, 596-605.	1.4	11

#	Article	IF	Citations
109	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
110	Lung Cancer Prognosis Before and After Recurrence in a Population-Based Setting. Journal of the National Cancer Institute, 2015, 107, djv059.	6.3	86
111	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	6.2	101
112	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. Nature Genetics, 2015, 47, 987-995.	21.4	218
113	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. Human Molecular Genetics, 2015, 24, 5356-5366.	2.9	128
114	Identification of lung cancer histology-specific variants applying Bayesian framework variant prioritization approaches within the TRICL and ILCCO consortia. Carcinogenesis, 2015, 36, 1314-1326.	2.8	15
115	The role of haplotype in 15q25.1 locus in lung cancer risk: results of scanning chromosome 15. Carcinogenesis, 2015, 36, 1275-1283.	2.8	15
116	Deciphering associations for lung cancer risk through imputation and analysis of 12â€‰316 cases and 16â€‰831 controls. European Journal of Human Genetics, 2015, 23, 1723-1728.	2.8	22
117	VTET: a variable threshold exact test for identifying disease-associated copy number variations enriched in short genomic regions. Frontiers in Genetics, 2014, 5, 53.	2.3	2
118	Is Previous Respiratory Disease a Risk Factor for Lung Cancer?. American Journal of Respiratory and Critical Care Medicine, 2014, 190, 549-559.	5.6	97
119	The Effect on Melanoma Risk of Genes Previously Associated With Telomere Length. Journal of the National Cancer Institute, 2014, 106, .	6.3	109
120	Time to Smoke First Morning Cigarette and Lung Cancer in a Caseâ€“Control Study. Journal of the National Cancer Institute, 2014, 106, dju118.	6.3	35
121	Genome-wide interaction study of smoking and bladder cancer risk. Carcinogenesis, 2014, 35, 1737-1744.	2.8	50
122	Rare missense variants in POT1 predispose to familial cutaneous malignant melanoma. Nature Genetics, 2014, 46, 482-486.	21.4	283
123	The 19q12 Bladder Cancer GWAS Signal: Association with Cyclin E Function and Aggressive Disease. Cancer Research, 2014, 74, 5808-5818.	0.9	24
124	HPV-associated lung cancers: an international pooled analysis. Carcinogenesis, 2014, 35, 1267-1275.	2.8	57
125	Genetic polymorphisms in the 9p21 region associated with risk of multiple cancers. Carcinogenesis, 2014, 35, 2698-2705.	2.8	67
126	Characterizing the genetic basis of methylome diversity in histologically normal human lung tissue. Nature Communications, 2014, 5, 3365.	12.8	123

#	Article	IF	Citations
127	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. Nature Genetics, 2014, 46, 994-1000.	21.4	294
128	Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. Nature Genetics, 2014, 46, 736-741.	21.4	360
129	Common Genetic Polymorphisms Modify the Effect of Smoking on Absolute Risk of Bladder Cancer. Cancer Research, 2013, 73, 2211-2220.	0.9	107
130	A variant in FTO shows association with melanoma risk not due to BMI. Nature Genetics, 2013, 45, 428-432.	21.4	111
131	Mood Disorders and Risk of Lung Cancer in the EAGLE Case-Control Study and in the U.S. Veterans Affairs Inpatient Cohort. PLoS ONE, 2012, 7, e42945.	2.5	9
132	On the Interplay of Telomeres, Nevi and the Risk of Melanoma. PLoS ONE, 2012, 7, e52466.	2.5	18
133	Genome-wide association study identifies three new melanoma susceptibility loci. Nature Genetics, 2011, 43, 1108-1113.	21.4	230
134	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. Nature Genetics, 2011, 43, 1114-1118.	21.4	140
135	MicroRNA Expression Differentiates Histology and Predicts Survival of Lung Cancer. Clinical Cancer Research, 2010, 16, 430-441.	7.0	316
136	Phase I Metabolic Genes and Risk of Lung Cancer: Multiple Polymorphisms and mRNA Expression. PLoS ONE, 2009, 4, e5652.	2.5	91
137	Family history of cancer and nonmalignant lung diseases as risk factors for lung cancer. International Journal of Cancer, 2009, 125, 146-152.	5.1	46
138	Genome-wide association study identifies three loci associated with melanoma risk. Nature Genetics, 2009, 41, 920-925.	21.4	422
139	A Genome-wide Association Study of Lung Cancer Identifies a Region of Chromosome 5p15 Associated with Risk for Adenocarcinoma. American Journal of Human Genetics, 2009, 85, 679-691.	6.2	489
140	Environment And Genetics in Lung cancer Etiology (EAGLE) study: An integrative population-based case-control study of lung cancer. BMC Public Health, 2008, 8, 203.	2.9	114
141	Gene Expression Signature of Cigarette Smoking and Its Role in Lung Adenocarcinoma Development and Survival. PLoS ONE, 2008, 3, e1651.	2.5	563
142	Comprehensive evaluation of allele frequency differences ofMC1Rvariants across populations. Human Mutation, 2007, 28, 495-505.	2.5	135
143	MC1R Germline Variants Confer Risk for BRAF-Mutant Melanoma. Science, 2006, 313, 521-522.	12.6	318
144	CYP1A1 and CYP1B1 genotypes, haplotypes, and TCDD-induced gene expression in subjects from Seveso, Italy. Toxicology, 2005, 207, 191-202.	4.2	61

#	Article	IF	Citations
145	MC1R, ASIP, and DNA Repair in Sporadic and Familial Melanoma in a Mediterranean Population. Journal of the National Cancer Institute, 2005, 97, 998-1007.	6.3	150
146	TCDD-mediated alterations in the AhR-dependent pathway in Seveso, Italy, 20 years after the accident. Carcinogenesis, 2003, 24, 673-680.	2.8	42
147	DNA Repair, Dysplastic Nevi, and Sunlight Sensitivity in the Development of Cutaneous Malignant Melanoma. Journal of the National Cancer Institute, 2002, 94, 94-101.	6.3	85
148	Glucocorticoid use and melanoma risk. International Journal of Cancer, 2001, 94, 302-303.	5.1	8