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	Gene Expression Signature of Cigarette Smoking and Its Role in Lung Adenocarcinoma Development and Survival. PLoS ONE, 2008, 3, e1651.	2.5	563
2	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
3	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
4	Genome-wide association study identifies three loci associated with melanoma risk. Nature Genetics, 2009, 41, 920-925.	21.4	422
5	Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. Nature Genetics, 2014, 46, 736-741.	21.4	360
6	MC1R Germline Variants Confer Risk for BRAF-Mutant Melanoma. Science, 2006, 313, 521-522.	12.6	318
7	MicroRNA Expression Differentiates Histology and Predicts Survival of Lung Cancer. Clinical Cancer Research, 2010, 16, 430-441.	7.0	316
8	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. Nature Genetics, 2014, 46, 994-1000.	21.4	294
9	Rare missense variants in POT1 predispose to familial cutaneous malignant melanoma. Nature Genetics, 2014, 46, 482-486.	21.4	283
10	Characterizing human lung tissue microbiota and its relationship to epidemiological and clinical features. Genome Biology, 2016, 17, 163.	8.8	264
11	Genome-wide association study identifies three new melanoma susceptibility loci. Nature Genetics, 2011, 43, 1108-1113.	21.4	230
12	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. Nature Genetics, 2015, 47, 987-995.	21.4	218
13	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
14	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
15	Somatic Genomics and Clinical Features of Lung Adenocarcinoma: A Retrospective Study. PLoS Medicine, 2016, 13, e1002162.	8.4	148
16	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. Nature Genetics, 2011, 43, 1114-1118.	21.4	140
17	Frequency of Pathogenic Germline Variants in Cancer-Susceptibility Genes in Patients With Osteosarcoma. JAMA Oncology, 2020, 6, 724.	7.1	139
18	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

#	Article	IF	Citations
19	Comprehensive evaluation of allele frequency differences ofMC1Rvariants across populations. Human Mutation, 2007, 28, 495-505.	2.5	135
20	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. Human Molecular Genetics, 2015, 24, 5356-5366.	2.9	128
21	Characterizing the genetic basis of methylome diversity in histologically normal human lung tissue. Nature Communications, 2014, 5, 3365.	12.8	123
22	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
23	A variant in FTO shows association with melanoma risk not due to BMI. Nature Genetics, 2013, 45, 428-432.	21.4	111
24	The Effect on Melanoma Risk of Genes Previously Associated With Telomere Length. Journal of the National Cancer Institute, 2014, 106, .	6.3	109
25	Common Genetic Polymorphisms Modify the Effect of Smoking on Absolute Risk of Bladder Cancer. Cancer Research, 2013, 73, 2211-2220.	0.9	107
26	Lung cancer and socioeconomic status in a pooled analysis of case-control studies. PLoS ONE, 2018, 13, e0192999.	2.5	107
27	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	6.2	101
28	<scp>TERT</scp> promoter mutations in melanoma survival. International Journal of Cancer, 2016, 139, 75-84.	5.1	101
29	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
30	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
31	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
32	Phase I Metabolic Genes and Risk of Lung Cancer: Multiple Polymorphisms and mRNA Expression. PLoS ONE, 2009, 4, e5652.	2.5	91
33	Three new pancreatic cancer susceptibility signals identified on chromosomes 1q32.1, 5p15.33 and 8q24.21. Oncotarget, 2016, 7, 66328-66343.	1.8	88
34	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
35	Lung Cancer Prognosis Before and After Recurrence in a Population-Based Setting. Journal of the National Cancer Institute, 2015, 107, djv059.	6.3	86
36	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	12.8	86

#	Article	IF	Citations
37	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
38	Genomic and evolutionary classification of lung cancer in never smokers. Nature Genetics, 2021, 53, 1348-1359.	21.4	81
39	Expanding the genetic architecture of nicotine dependence and its shared genetics with multiple traits. Nature Communications, 2020, 11, 5562.	12.8	80
40	Integrating Clinical and Multiple Omics Data for Prognostic Assessment across Human Cancers. Scientific Reports, 2017, 7, 16954.	3.3	79
41	Obesity, metabolic factors and risk of different histological types of lung cancer: A Mendelian randomization study. PLoS ONE, 2017, 12, e0177875.	2.5	79
42	Genetic and epigenetic intratumor heterogeneity impacts prognosis of lung adenocarcinoma. Nature Communications, 2020, 11, 2459.	12.8	77
43	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	12.8	75
44	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
45	<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
46	Genetic polymorphisms in the 9p21 region associated with risk of multiple cancers. Carcinogenesis, 2014, 35, 2698-2705.	2.8	67
47	Cigarette smoking behaviour and blood metabolomics. International Journal of Epidemiology, 2016, 45, 1421-1432.	1.9	63
48	CYP1A1 and CYP1B1 genotypes, haplotypes, and TCDD-induced gene expression in subjects from Seveso, Italy. Toxicology, 2005, 207, 191-202.	4.2	61
49	Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. Nature Communications, 2018, 9, 3221.	12.8	60
50	Mapping clustered mutations in cancer reveals APOBEC3 mutagenesis of ecDNA. Nature, 2022, 602, 510-517.	27.8	60
51	HPV-associated lung cancers: an international pooled analysis. Carcinogenesis, 2014, 35, 1267-1275.	2.8	57
52	Novel Association of Genetic Markers Affecting CYP2A6 Activity and Lung Cancer Risk. Cancer Research, 2016, 76, 5768-5776.	0.9	57
53	Outdoor particulate matter (PM10) exposure and lung cancer risk in the EAGLE study. PLoS ONE, 2018, 13, e0203539.	2.5	57
54	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

#	Article	IF	Citations
55	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
56	Genome-wide interaction study of smoking and bladder cancer risk. Carcinogenesis, 2014, 35, 1737-1744.	2.8	50
57	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
58	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
59	Assessing Lung Cancer Absolute Risk Trajectory Based on a Polygenic Risk Model. Cancer Research, 2021, 81, 1607-1615.	0.9	50
60	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
61	Germline mutations in Protection of Telomeres 1 in two families with Hodgkin lymphoma. British Journal of Haematology, 2018, 181, 372-377.	2.5	48
62	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
63	Fine mapping of MHC region in lung cancer highlights independent susceptibility loci by ethnicity. Nature Communications, 2018, 9, 3927.	12.8	43
64	TCDD-mediated alterations in the AhR-dependent pathway in Seveso, Italy, 20 years after the accident. Carcinogenesis, 2003, 24, 673-680.	2.8	42
65	Genome-wide association study of familial lung cancer. Carcinogenesis, 2018, 39, 1135-1140.	2.8	42
66	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
67	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
68	Higher-than-expected population prevalence of potentially pathogenic germlineTP53variants in individuals unselected for cancer history. Human Mutation, 2017, 38, 1723-1730.	2.5	40
69	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
70	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
71	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
72	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

#	Article	IF	Citations
73	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
74	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
75	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
76	Protein-altering germline mutations implicate novel genes related to lung cancer development. Nature Communications, 2020, 11, 2220.	12.8	31
77	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
78	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
79	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
80	The 19q12 Bladder Cancer GWAS Signal: Association with Cyclin E Function and Aggressive Disease. Cancer Research, 2014, 74, 5808-5818.	0.9	24
81	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
82	DNA Methylation in Lung Cancer: Mechanisms and Associations with Histological Subtypes, Molecular Alterations, and Major Epidemiological Factors. Cancers, 2022, 14, 961.	3.7	24
83	Nut Consumption and Lung Cancer Risk: Results from Two Large Observational Studies. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 826-836.	2.5	23
84	Immune-mediated genetic pathways resulting in pulmonary function impairment increase lung cancer susceptibility. Nature Communications, 2020, 11, 27.	12.8	23
85	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
86	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
87	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
88	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
89	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
90	The genomic and epigenomic evolutionary history of papillary renal cell carcinomas. Nature Communications, 2020, 11, 3096.	12.8	19

#	Article	IF	Citations
91	Genome-wide association meta-analysis identifies pleiotropic risk loci for aerodigestive squamous cell cancers. PLoS Genetics, 2021, 17, e1009254.	3.5	19
92	Occupational prestige, social mobility and the association with lung cancer in men. BMC Cancer, 2016, 16, 395.	2.6	18
93	Germline Variation at CDKN2A and Associations with Nevus Phenotypes amongÂMembers of Melanoma Families. Journal of Investigative Dermatology, 2017, 137, 2606-2612.	0.7	18
94	On the Interplay of Telomeres, Nevi and the Risk of Melanoma. PLoS ONE, 2012, 7, e52466.	2.5	18
95	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
96	Genome-Wide Meta-Analyses of FTND and TTFC Phenotypes. Nicotine and Tobacco Research, 2020, 22, 900-909.	2.6	17
97	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
98	Functional variants in DCAF4 associated with lung cancer risk in European populations. Carcinogenesis, 2017, 38, 541-551.	2.8	16
99	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
100	Tracing Lung Cancer Risk Factors Through Mutational Signatures in Never-Smokers. American Journal of Epidemiology, 2021, 190, 962-976.	3.4	16
101	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
102	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
103	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
104	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
105	Gene-set meta-analysis of lung cancer identifies pathway related to systemic lupus erythematosus. PLoS ONE, 2017, 12, e0173339.	2.5	15
106	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
107	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
108	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

#	Article	IF	Citations
109	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
110	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
111	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
112	An exposureâ€weighted score test for genetic associations integrating environmental risk factors. Biometrics, 2015, 71, 596-605.	1.4	11
113	Use of Big Data to Estimate Prevalence of Defective DNA Repair Variants in the US Population. JAMA Dermatology, 2019, 155, 72.	4.1	11
114	A multifactorial score including autophagy for prognosis and care of COVID-19 patients. Autophagy, 2020, 16, 2276-2281.	9.1	11
115	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
116	Multi-Trait Genetic Analysis Identifies Autoimmune Loci Associated with Cutaneous Melanoma. Journal of Investigative Dermatology, 2022, 142, 1607-1616.	0.7	11
117	Autophagopathies: from autophagy gene polymorphisms to precision medicine for human diseases. Autophagy, 2022, 18, 2519-2536.	9.1	11
118	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
119	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
120	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
121	Novel genetic variants in the P38MAPK pathway gene ZAK and susceptibility to lung cancer. Molecular Carcinogenesis, 2018, 57, 216-224.	2.7	9
122	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
123	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
124	Glucocorticoid use and melanoma risk. International Journal of Cancer, 2001, 94, 302-303.	5.1	8
125	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
126	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

#	Article	IF	Citations
127	Characterizing the tumor microenvironment in rare renal cancer histological types. Journal of Pathology: Clinical Research, 2022, 8, 88-98.	3.0	8
128	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
129	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
130	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
131	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
132	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
133	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
134	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
135	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
136	Genetic Relationship Between Endometriosis and Melanoma. Frontiers in Reproductive Health, 2021, 3, .	1.9	5
137	Rare germline deleterious variants increase susceptibility for lung cancer. Human Molecular Genetics, 2022, 31, 3558-3565.	2.9	5
138	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
139	Assessment of HER2 Protein Overexpression and Gene Amplification in Renal Collecting Duct Carcinoma: Therapeutic Implication. Cancers, 2020, 12, 3345.	3.7	3
140	Identification of Genetic Risk Factors for Familial Urinary Bladder Cancer: An Exome Sequencing Study. JCO Precision Oncology, 2021, 5, 1830-1839.	3.0	3
141	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
142	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
143	Novel MAPK/AKT-impairing germline NRAS variant identified in a melanoma-prone family. Familial Cancer, 2022, 21, 347-355.	1.9	1
144	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

#	Article	IF	Citations
145	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
146	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
147	SUITOR: Selecting the number of mutational signatures through cross-validation. PLoS Computational Biology, 2022, 18, e1009309.	3.2	1
148	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