

Maria Teresa Landi

List of Publications by Year in descending order

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Version: 2024-02-01

148
papers

10,062
citations

36299

51
h-index

40976

93
g-index

157
all docs

157
docs citations

157
times ranked

16505
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

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19	Comprehensive evaluation of allele frequency differences of MC1R variants across populations. <i>Human Mutation</i> , 2007, 28, 495-505.	2.5	135
20	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. <i>Human Molecular Genetics</i> , 2015, 24, 5356-5366.	2.9	128
21	Characterizing the genetic basis of methylome diversity in histologically normal human lung tissue. <i>Nature Communications</i> , 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. <i>BMC Public Health</i> , 2008, 8, 203.	2.9	114
23	A variant in FTO shows association with melanoma risk not due to BMI. <i>Nature Genetics</i> , 2013, 45, 428-432.	21.4	111
24	The Effect on Melanoma Risk of Genes Previously Associated With Telomere Length. <i>Journal of the National Cancer Institute</i> , 2014, 106, .	6.3	109
25	Common Genetic Polymorphisms Modify the Effect of Smoking on Absolute Risk of Bladder Cancer. <i>Cancer Research</i> , 2013, 73, 2211-2220.	0.9	107
26	Lung cancer and socioeconomic status in a pooled analysis of case-control studies. <i>PLoS ONE</i> , 2018, 13, e0192999.	2.5	107
27	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. <i>American Journal of Human Genetics</i> , 2015, 96, 487-497.	6.2	101
28	<i>TERT</i> promoter mutations in melanoma survival. <i>International Journal of Cancer</i> , 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. <i>PLoS Genetics</i> , 2016, 12, e1006493.	3.5	98
30	Is Previous Respiratory Disease a Risk Factor for Lung Cancer?. <i>American Journal of Respiratory and Critical Care Medicine</i> , 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. <i>Human Molecular Genetics</i> , 2017, 26, 3014-3027.	2.9	97
32	Phase I Metabolic Genes and Risk of Lung Cancer: Multiple Polymorphisms and mRNA Expression. <i>PLoS ONE</i> , 2009, 4, e5652.	2.5	91
33	Three new pancreatic cancer susceptibility signals identified on chromosomes 1q32.1, 5p15.33 and 8q24.21. <i>Oncotarget</i> , 2016, 7, 66328-66343.	1.8	88
34	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	12.8	88
35	Lung Cancer Prognosis Before and After Recurrence in a Population-Based Setting. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv059.	6.3	86
36	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. <i>Nature Communications</i> , 2016, 7, 11843.	12.8	86

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37	DNA Repair, Dysplastic Nevi, and Sunlight Sensitivity in the Development of Cutaneous Malignant Melanoma. <i>Journal of the National Cancer Institute</i> , 2002, 94, 94-101.	6.3	85
38	Genomic and evolutionary classification of lung cancer in never smokers. <i>Nature Genetics</i> , 2021, 53, 1348-1359.	21.4	81
39	Expanding the genetic architecture of nicotine dependence and its shared genetics with multiple traits. <i>Nature Communications</i> , 2020, 11, 5562.	12.8	80
40	Integrating Clinical and Multiple Omics Data for Prognostic Assessment across Human Cancers. <i>Scientific Reports</i> , 2017, 7, 16954.	3.3	79
41	Obesity, metabolic factors and risk of different histological types of lung cancer: A Mendelian randomization study. <i>PLoS ONE</i> , 2017, 12, e0177875.	2.5	79
42	Genetic and epigenetic intratumor heterogeneity impacts prognosis of lung adenocarcinoma. <i>Nature Communications</i> , 2020, 11, 2459.	12.8	77
43	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. <i>Nature Communications</i> , 2020, 11, 3353.	12.8	75
44	Causal relationships between body mass index, smoking and lung cancer: Univariable and multivariable Mendelian randomization. <i>International Journal of Cancer</i> , 2021, 148, 1077-1086.	5.1	73
45	Genetic variants associated with longer telomere length are associated with increased lung cancer risk among never-smoking women in Asia: a report from the female lung cancer consortium in Asia. <i>International Journal of Cancer</i> , 2015, 137, 311-319.	5.1	72
46	Genetic polymorphisms in the 9p21 region associated with risk of multiple cancers. <i>Carcinogenesis</i> , 2014, 35, 2698-2705.	2.8	67
47	Cigarette smoking behaviour and blood metabolomics. <i>International Journal of Epidemiology</i> , 2016, 45, 1421-1432.	1.9	63
48	CYP1A1 and CYP1B1 genotypes, haplotypes, and TCDD-induced gene expression in subjects from Seveso, Italy. <i>Toxicology</i> , 2005, 207, 191-202.	4.2	61
49	Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. <i>Nature Communications</i> , 2018, 9, 3221.	12.8	60
50	Mapping clustered mutations in cancer reveals APOBEC3 mutagenesis of ecDNA. <i>Nature</i> , 2022, 602, 510-517.	27.8	60
51	HPV-associated lung cancers: an international pooled analysis. <i>Carcinogenesis</i> , 2014, 35, 1267-1275.	2.8	57
52	Novel Association of Genetic Markers Affecting CYP2A6 Activity and Lung Cancer Risk. <i>Cancer Research</i> , 2016, 76, 5768-5776.	0.9	57
53	Outdoor particulate matter (PM10) exposure and lung cancer risk in the EAGLE study. <i>PLoS ONE</i> , 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. <i>Cancer Management and Research</i> , 2018, Volume 10, 1143-1154.	1.9	57

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55	Assessing the Incremental Contribution of Common Genomic Variants to Melanoma Risk Prediction in Two Population-Based Studies. <i>Journal of Investigative Dermatology</i> , 2018, 138, 2617-2624.	0.7	52
56	Genome-wide interaction study of smoking and bladder cancer risk. <i>Carcinogenesis</i> , 2014, 35, 1737-1744.	2.8	50
57	Association between GWAS-identified lung adenocarcinoma susceptibility loci and EGFR mutations in never-smoking Asian women, and comparison with findings from Western populations. <i>Human Molecular Genetics</i> , 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. <i>Human Molecular Genetics</i> , 2016, 25, 620-629.	2.9	50
59	Assessing Lung Cancer Absolute Risk Trajectory Based on a Polygenic Risk Model. <i>Cancer Research</i> , 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. <i>Scientific Reports</i> , 2016, 6, 34234.	3.3	48
61	Germline mutations in <i>Protection of Telomeres 1</i> in two families with Hodgkin lymphoma. <i>British Journal of Haematology</i> , 2018, 181, 372-377.	2.5	48
62	Family history of cancer and nonmalignant lung diseases as risk factors for lung cancer. <i>International Journal of Cancer</i> , 2009, 125, 146-152.	5.1	46
63	Fine mapping of MHC region in lung cancer highlights independent susceptibility loci by ethnicity. <i>Nature Communications</i> , 2018, 9, 3927.	12.8	43
64	TCDD-mediated alterations in the AhR-dependent pathway in Seveso, Italy, 20 years after the accident. <i>Carcinogenesis</i> , 2003, 24, 673-680.	2.8	42
65	Genome-wide association study of familial lung cancer. <i>Carcinogenesis</i> , 2018, 39, 1135-1140.	2.8	42
66	MEGSA: A Powerful and Flexible Framework for Analyzing Mutual Exclusivity of Tumor Mutations. <i>American Journal of Human Genetics</i> , 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. <i>Nature Communications</i> , 2017, 8, 15034.	12.8	40
68	Higher-than-expected population prevalence of potentially pathogenic germline <i>TP53</i> variants in individuals unselected for cancer history. <i>Human Mutation</i> , 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. <i>Human Molecular Genetics</i> , 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. <i>Carcinogenesis</i> , 2016, 37, 96-105.	2.8	36
71	Time to Smoke First Morning Cigarette and Lung Cancer in a Case-Control Study. <i>Journal of the National Cancer Institute</i> , 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. <i>International Journal of Cancer</i> , 2017, 140, 1976-1984.	5.1	35

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73	Combining common genetic variants and non-genetic risk factors to predict risk of cutaneous melanoma. <i>Human Molecular Genetics</i> , 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. <i>Genome Medicine</i> , 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. <i>International Journal of Epidemiology</i> , 2019, 48, 751-766.	1.9	32
76	Protein-altering germline mutations implicate novel genes related to lung cancer development. <i>Nature Communications</i> , 2020, 11, 2220.	12.8	31
77	Menstrual and reproductive factors and lung cancer risk: A pooled analysis from the international lung cancer consortium. <i>International Journal of Cancer</i> , 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. <i>International Journal of Cancer</i> , 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. <i>International Archives of Occupational and Environmental Health</i> , 2018, 91, 937-950.	2.3	27
80	The 19q12 Bladder Cancer GWAS Signal: Association with Cyclin E Function and Aggressive Disease. <i>Cancer Research</i> , 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. <i>Human Genetics</i> , 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. <i>Cancers</i> , 2022, 14, 961.	3.7	24
83	Nut Consumption and Lung Cancer Risk: Results from Two Large Observational Studies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 826-836.	2.5	23
84	Immune-mediated genetic pathways resulting in pulmonary function impairment increase lung cancer susceptibility. <i>Nature Communications</i> , 2020, 11, 27.	12.8	23
85	Deciphering associations for lung cancer risk through imputation and analysis of 12,316 cases and 16,831 controls. <i>European Journal of Human Genetics</i> , 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. <i>Cancer Epidemiology</i> , 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. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 935-942.	2.5	21
88	Peritoneal mesothelioma and asbestos exposure: a population-based case-control study in Lombardy, Italy. <i>Occupational and Environmental Medicine</i> , 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. <i>Genomics Data</i> , 2016, 10, 22-29.	1.3	19
90	The genomic and epigenomic evolutionary history of papillary renal cell carcinomas. <i>Nature Communications</i> , 2020, 11, 3096.	12.8	19

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91	Genome-wide association meta-analysis identifies pleiotropic risk loci for aerodigestive squamous cell cancers. <i>PLoS Genetics</i> , 2021, 17, e1009254.	3.5	19
92	Occupational prestige, social mobility and the association with lung cancer in men. <i>BMC Cancer</i> , 2016, 16, 395.	2.6	18
93	Germline Variation at CDKN2A and Associations with Nevus Phenotypes among Members of Melanoma Families. <i>Journal of Investigative Dermatology</i> , 2017, 137, 2606-2612.	0.7	18
94	On the Interplay of Telomeres, Nevi and the Risk of Melanoma. <i>PLoS ONE</i> , 2012, 7, e52466.	2.5	18
95	Estimating CDKN2A mutation carrier probability among global familial melanoma cases using GenOMELPREDICT. <i>Journal of the American Academy of Dermatology</i> , 2019, 81, 386-394.	1.2	17
96	Genome-Wide Meta-Analyses of FTND and TTFC Phenotypes. <i>Nicotine and Tobacco Research</i> , 2020, 22, 900-909.	2.6	17
97	Association of Melanocortin-1 Receptor Variants with Pigmentary Traits in Humans: Pooled Analysis from the M-Skip Project. <i>Journal of Investigative Dermatology</i> , 2016, 136, 1914-1917.	0.7	16
98	Functional variants in DCAF4 associated with lung cancer risk in European populations. <i>Carcinogenesis</i> , 2017, 38, 541-551.	2.8	16
99	MC1R variants in childhood and adolescent melanoma: a retrospective pooled analysis of a multicentre cohort. <i>The Lancet Child and Adolescent Health</i> , 2019, 3, 332-342.	5.6	16
100	Tracing Lung Cancer Risk Factors Through Mutational Signatures in Never-Smokers. <i>American Journal of Epidemiology</i> , 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. <i>Carcinogenesis</i> , 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. <i>Carcinogenesis</i> , 2015, 36, 1275-1283.	2.8	15
103	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.	2.8	15
104	Risk factors for keratinocyte skin cancer in patients diagnosed with melanoma, a large retrospective study. <i>European Journal of Cancer</i> , 2016, 53, 115-124.	2.8	15
105	Gene-set meta-analysis of lung cancer identifies pathway related to systemic lupus erythematosus. <i>PLoS ONE</i> , 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. <i>Genome Medicine</i> , 2018, 10, 99.	8.2	15
107	Phenotypic and Histopathological Tumor Characteristics According to CDKN2A Mutation Status among Affected Members of Melanoma Families. <i>Journal of Investigative Dermatology</i> , 2016, 136, 1066-1069.	0.7	13
108	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.	2.7	13

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109	A Penalized Regression Framework for Building Polygenic Risk Models Based on Summary Statistics From Genome-Wide Association Studies and Incorporating External Information. <i>Journal of the American Statistical Association</i> , 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. <i>Environment International</i> , 2021, 147, 105975.	10.0	12
111	Cell-type-specific meQTLs extend melanoma GWAS annotation beyond eQTLs and inform melanocyte gene-regulatory mechanisms. <i>American Journal of Human Genetics</i> , 2021, 108, 1631-1646.	6.2	12
112	An exposure-weighted score test for genetic associations integrating environmental risk factors. <i>Biometrics</i> , 2015, 71, 596-605.	1.4	11
113	Use of Big Data to Estimate Prevalence of Defective DNA Repair Variants in the US Population. <i>JAMA Dermatology</i> , 2019, 155, 72.	4.1	11
114	A multifactorial score including autophagy for prognosis and care of COVID-19 patients. <i>Autophagy</i> , 2020, 16, 2276-2281.	9.1	11
115	Lung cancer risk in painters: results from the SYNERGY pooled case-control study consortium. <i>Occupational and Environmental Medicine</i> , 2021, 78, 269-278.	2.8	11
116	Multi-Trait Genetic Analysis Identifies Autoimmune Loci Associated with Cutaneous Melanoma. <i>Journal of Investigative Dermatology</i> , 2022, 142, 1607-1616.	0.7	11
117	Autophagopathies: from autophagy gene polymorphisms to precision medicine for human diseases. <i>Autophagy</i> , 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. <i>Scientific Reports</i> , 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. <i>Scientific Reports</i> , 2017, 7, 44634.	3.3	10
120	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.	2.7	10
121	Novel genetic variants in the P38MAPK pathway gene <i>ZAK</i> and susceptibility to lung cancer. <i>Molecular Carcinogenesis</i> , 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. <i>Journal of the European Academy of Dermatology and Venereology</i> , 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. <i>PLoS ONE</i> , 2012, 7, e42945.	2.5	9
124	Glucocorticoid use and melanoma risk. <i>International Journal of Cancer</i> , 2001, 94, 302-303.	5.1	8
125	Using imputed genotype data in the joint score tests for genetic association and gene-environment interactions in case-control studies. <i>Genetic Epidemiology</i> , 2018, 42, 146-155.	1.3	8
126	Clinical Implications of Inter- and Intratumor Heterogeneity of Immune Cell Markers in Lung Cancer. <i>Journal of the National Cancer Institute</i> , 2022, 114, 280-289.	6.3	8

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127	Characterizing the tumor microenvironment in rare renal cancer histological types. <i>Journal of Pathology: Clinical Research</i> , 2022, 8, 88-98.	3.0	8
128	Polymorphisms of the centrosomal gene (<i>FGFR1OP</i>) and lung cancer risk: a meta-analysis of 14 463 cases and 44 188 controls. <i>Carcinogenesis</i> , 2016, 37, 280-289.	2.8	7
129	Genome-wide association study of INDELS identified four novel susceptibility loci associated with lung cancer risk. <i>International Journal of Cancer</i> , 2020, 146, 2855-2864.	5.1	7
130	Integration of multiomic annotation data to prioritize and characterize inflammation and immune-related risk variants in squamous cell lung cancer. <i>Genetic Epidemiology</i> , 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. <i>American Journal of Human Genetics</i> , 2021, 108, 1611-1630.	6.2	7
132	Common <i>TDP1</i> Polymorphisms in Relation to Survival among Small Cell Lung Cancer Patients: A Multicenter Study from the International Lung Cancer Consortium. <i>Clinical Cancer Research</i> , 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. <i>Melanoma Research</i> , 2020, 30, 500-510.	1.2	6
134	Large-scale cross-cancer fine-mapping of the 5p15.33 region reveals multiple independent signals. <i>Human Genetics and Genomics Advances</i> , 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. <i>Journal of the American Academy of Dermatology</i> , 2020, 83, 860-869.	1.2	5
136	Genetic Relationship Between Endometriosis and Melanoma. <i>Frontiers in Reproductive Health</i> , 2021, 3, .	1.9	5
137	Rare germline deleterious variants increase susceptibility for lung cancer. <i>Human Molecular Genetics</i> , 2022, 31, 3558-3565.	2.9	5
138	Genome-wide interaction analysis identified low-frequency variants with sex disparity in lung cancer risk. <i>Human Molecular Genetics</i> , 2022, 31, 2831-2843.	2.9	4
139	Assessment of HER2 Protein Overexpression and Gene Amplification in Renal Collecting Duct Carcinoma: Therapeutic Implication. <i>Cancers</i> , 2020, 12, 3345.	3.7	3
140	Identification of Genetic Risk Factors for Familial Urinary Bladder Cancer: An Exome Sequencing Study. <i>JCO Precision Oncology</i> , 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. <i>Frontiers in Genetics</i> , 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. <i>Clinical Genitourinary Cancer</i> , 2021, 19, e280-e285.	1.9	2
143	Novel MAPK/AKT-impairing germline NRAS variant identified in a melanoma-prone family. <i>Familial Cancer</i> , 2022, 21, 347-355.	1.9	1
144	A hybrid parametric and empirical likelihood model for evaluating interactions in case-control studies. <i>Statistics and Its Interface</i> , 2016, 9, 147-158.	0.3	1

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145	Accounting for <i>EGFR</i> Mutations in Epidemiologic Analyses of Non-Small Cell Lung Cancers: Examples Based on the International Lung Cancer Consortium Data. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, 31, 679-687.	2.5	1
146	Gene-gene interaction of AhR with and within the Wnt cascade affects susceptibility to lung cancer. <i>European Journal of Medical Research</i> , 2022, 27, 14.	2.2	1
147	SUITOR: Selecting the number of mutational signatures through cross-validation. <i>PLoS Computational Biology</i> , 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