Irene Orlow

List of Publications by Year
in descending order

151	8,575	57719	49868
papers	citations	44 h-index	87 g-index

154	154	154	13753
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The Ink4a Tumor Suppressor Gene Product, p19Arf, Interacts with MDM2 and Neutralizes MDM2's Inhibition of p53. Cell, 1998, 92, 713-723.	13.5	1,412
2	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nature Genetics, 2013, 45, 371-384.	9.4	493
3	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	9.4	326
4	Tumor-Infiltrating Lymphocyte Grade in Primary Melanomas Is Independently Associated With Melanoma-Specific Survival in the Population-Based Genes, Environment and Melanoma Study. Journal of Clinical Oncology, 2013, 31, 4252-4259.	0.8	232
5	Common variation at 2p13.3, 3q29, 7p13 and 17q25.1 associated with susceptibility to pancreatic cancer. Nature Genetics, 2015, 47, 911-916.	9.4	224
6	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
7	Lifetime Risk of Melanoma in CDKN2A Mutation Carriers in a Population-Based Sample. Journal of the National Cancer Institute, 2005, 97, 1507-1515.	3.0	200
8	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. Nature Communications, 2018, 9, 556.	5.8	188
9	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	5.8	178
10	Association BetweenNRASandBRAFMutational Status and Melanoma-Specific Survival Among Patients With Higher-Risk Primary Melanoma. JAMA Oncology, 2015, 1, 359.	3.4	164
11	Deletions of the INK4A Gene Occur in Malignant Peripheral Nerve Sheath Tumors but not in Neurofibromas. American Journal of Pathology, 1999, 155, 1855-1860.	1.9	161
12	Previous Lung Diseases and Lung Cancer Risk: A Pooled Analysis From the International Lung Cancer Consortium. American Journal of Epidemiology, 2012, 176, 573-585.	1.6	160
13	Genomic and Mutational Profiling to Assess Clonal Relationships Between Multiple Nonâ€“Small Cell Lung Cancers. Clinical Cancer Research, 2009, 15, 5184-5190.	3.2	151
14	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628.	5.8	144
15	Increased risk of lung cancer in individuals with a family history of the disease: A pooled analysis from the International Lung Cancer Consortium. European Journal of Cancer, 2012, 48, 1957-1968.	1.3	143
16	Comparison of Clinicopathologic Features and Survival of Histopathologically Amelanotic and Pigmented Melanomas. JAMA Dermatology, 2014, 150, 1306.	2.0	142
17	Cannabis smoking and lung cancer risk: Pooled analysis in the <scp>I</scp>nternational <scp>L</scp>ung <scp>C</scp>ancer <scp>C</scp>onsortium. International Journal of Cancer, 2015, 136, 894-903.	2.3	131
18	Deletions of the INK4A Gene in Superficial Bladder Tumors. American Journal of Pathology, 1999, 155, 105-113.	1.9	121

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19	The Prevalence of CDKN2A Germ-Line Mutations and Relative Risk for Cutaneous Malignant Melanoma: An International Population-Based Study. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 1520-1525.	1.1	105
20	Variants in Estrogen Biosynthesis Genes, Sex Steroid Hormone Levels, and Endometrial Cancer: A HuGE Review. American Journal of Epidemiology, 2007, 165, 235-245.	1.6	102
21	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	2.6	101
22	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 2013, 4, 1627.	5.8	98
23	Molecular analyses of the mitotic checkpoint componentshsMAD2, hBUB1 andhBUB3 in human cancer. International Journal of Cancer, 2001, 95, 223-227.	2.3	92
24	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	5.8	86
25	Analysis of Genetic Variants in Never-Smokers with Lung Cancer Facilitated by an Internet-Based Blood Collection Protocol: A Preliminary Report. Clinical Cancer Research, 2010, 16, 755-763.	3.2	82
26	Genome-wide significant risk associations for mucinous ovarian carcinoma. Nature Genetics, 2015, 47, 888-897.	9.4	78
27	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
28	Asthma and lung cancer risk: a systematic investigation by the International Lung Cancer Consortium. Carcinogenesis, 2012, 33, 587-597.	1.3	69
29	The oral microbiota in patients with pancreatic cancer, patients with IPMNs, and controls: a pilot study. Cancer Causes and Control, 2017, 28, 959-969.	0.8	69
30	Phase II Study of Extended-Dose Temozolomide in Patients With Melanoma. Journal of Clinical Oncology, 2008, 26, 2299-2304.	0.8	66
31	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	5.8	63
32	Vitamin D receptor polymorphisms in patients with cutaneous melanoma. International Journal of Cancer, 2012, 130, 405-418.	2.3	61
33	A Transcriptome-Wide Association Study Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer. Journal of the National Cancer Institute, 2020, 112, 1003-1012.	3.0	59
34	Allergies, variants in IL-4 and IL-4RÎ± genes, and risk of pancreatic cancer. Cancer Detection and Prevention, 2007, 31, 345-351.	2.1	58
35	The Obesity-Associated Polymorphisms FTO rs9939609 and MC4R rs17782313 and Endometrial Cancer Risk in Non-Hispanic White Women. PLoS ONE, 2011, 6, e16756.	1.1	58
36	DNA Damage and Repair Capacity in Patients With Lung Cancer: Prediction of Multiple Primary Tumors. Journal of Clinical Oncology, 2008, 26, 3560-3566.	0.8	56

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37	Prognostic Significance of Transcription Factor E2F-1 in Bladder Cancer: Genotypic and Phenotypic Characterization. Journal of the National Cancer Institute, 1999, 91, 874-881.	3.0	54
38	Vitamin D receptor polymorphisms and survival in patients with cutaneous melanoma: a population-based study. Carcinogenesis, 2016, 37, 30-38.	1.3	54
39	CDKN2A Germline Mutations in Individuals with Cutaneous Malignant Melanoma. Journal of Investigative Dermatology, 2007, 127, 1234-1243.	0.3	50
40	APOE polymorphisms and cognitive functions in patients with brain tumors. Neurology, 2014, 83, 320-327.	1.5	49
41	Functional Polymorphisms in the TERT Promoter Are Associated with Risk of Serous Epithelial Ovarian and Breast Cancers. PLoS ONE, 2011, 6, e24987.	1.1	48
42	Risk of Ovarian Cancer and the NF-Î²B Pathway: Genetic Association with IL1A and TNFSF10. Cancer Research, 2014, 74, 852-861.	0.4	48
43	Analysis of Heritability and Genetic Architecture of Pancreatic Cancer: A PanC4 Study. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 1238-1245.	1.1	48
44	Aspirin and NSAID use and lung cancer risk: a pooled analysis in the International Lung Cancer Consortium (ILCCO). Cancer Causes and Control, 2011, 22, 1709-1720.	0.8	47
45	A metastasis or a second independent cancer? Evaluating the clonal origin of tumors using array copy number data. Statistics in Medicine, 2010, 29, 1608-1621.	0.8	46
46	Associations of Cumulative Sun Exposure and Phenotypic Characteristics with Histologic Solar Elastosis. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2932-2941.	1.1	45
47	Clinicopathologic Features of Incident and Subsequent Tumors in Patients with Multiple Primary Cutaneous Melanomas. Annals of Surgical Oncology, 2012, 19, 1024-1033.	0.7	45
48	COMT,BDNF, andDTNBP1polymorphisms and cognitive functions in patients with brain tumors. Neuro-Oncology, 2016, 18, 1425-1433.	0.6	45
49	The hCOMET project: International database comparison of results with the comet assay in human biomonitoring. Baseline frequency of DNA damage and effect of main confounders. Mutation Research - Reviews in Mutation Research, 2021, 787, 108371.	2.4	45
50	Matrix Metalloproteinase-9 (MMP-9) polymorphisms in patients with cutaneous malignant melanoma. BMC Medical Genetics, 2007, 8, 10.	2.1	44
51	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	1.1	44
52	Risk of Non-Melanoma Cancers in First-Degree Relatives of CDKN2A Mutation Carriers. Journal of the National Cancer Institute, 2012, 104, 953-956.	3.0	42
53	Genome-wide association study of endometrial cancer in E2C2. Human Genetics, 2014, 133, 211-224.	1.8	42
54	A Replication Study and Genome-Wide Scan of Single-Nucleotide Polymorphisms Associated with Pancreatic Cancer Risk and Overall Survival. Clinical Cancer Research, 2012, 18, 3942-3951.	3.2	40

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55	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	1.4	40
56	Contralateral breast cancers: Independent cancers or metastases?. International Journal of Cancer, 2018, 142, 347-356.	2.3	37
57	Inherited Genetic Variants Associated with Occurrence of Multiple Primary Melanoma. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 992-997.	1.1	36
58	Vitamin D Receptor Gene Haplotypes and Polymorphisms and Risk of Breast Cancer: A Nested Caseâ€“Control Study. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 1856-1867.	1.1	35
59	<scp>MITF</scp> E318K's effect on melanoma risk independent of, but modified by, other risk factors. Pigment Cell and Melanoma Research, 2014, 27, 485-488.	1.5	35
60	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.	2.3	35
61	Microsatellite instability and deletion analysis of chromosome 10 in human prostate cancer. , 1996, 69, 110-113.		34
62	Genome-wide Analysis Identifies Novel Loci Associated with Ovarian Cancer Outcomes: Findings from the Ovarian Cancer Association Consortium. Clinical Cancer Research, 2015, 21, 5264-5276.	3.2	33
63	Genotypic and phenotypic characterization of the histoblood group ABO(H) in primary bladder tumors. , 1998, 75, 819-824.		31
64	Genetic factors associated with naevus count and dermoscopic patterns: preliminary results from the Study of Nevi in Children (<scp>SONIC</scp>). British Journal of Dermatology, 2015, 172, 1081-1089.	1.4	31
65	Variants in hormone biosynthesis genes and risk of endometrial cancer. Cancer Causes and Control, 2008, 19, 955-963.	0.8	29
66	Vitamin D Metabolic Pathway Genes and Pancreatic Cancer Risk. PLoS ONE, 2015, 10, e0117574.	1.1	29
67	Association Between Aryl Hydrocarbon Receptor Genotype and Survival in Soft Tissue Sarcoma. Journal of Clinical Oncology, 2004, 22, 3997-4001.	0.8	28
68	Sun exposure, vitamin D receptor polymorphisms FokI and BsmI and risk of multiple primary melanoma. Cancer Epidemiology, 2011, 35, e105-e110.	0.8	28
69	Network-Based Integration of GWAS and Gene Expression Identifies a HOX-Centric Network Associated with Serous Ovarian Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1574-1584.	1.1	28
70	Association of Interferon Regulatory Factor-4 Polymorphism rs12203592 With Divergent Melanoma Pathways. Journal of the National Cancer Institute, 2016, 108, djw004.	3.0	28
71	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.	2.3	28
72	Evaluation of the Clonal Origin of Multiple Primary Melanomas Using Molecular Profiling. Journal of Investigative Dermatology, 2009, 129, 1972-1982.	0.3	27

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73	Inherited variation at MC1R and ASIP and association with melanomaâ€specific survival. International Journal of Cancer, 2015, 136, 2659-2667.	2.3	27
74	Lung Cancer Risk in Never-Smokers of European Descent is Associated With Genetic Variation in the 5p15.33 TERT-CLPTM1Ll Region. Journal of Thoracic Oncology, 2019, 14, 1360-1369.	0.5	27
75	Sun Exposure and Melanoma Survival: A GEM Study. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2145-2152.	1.1	26
76	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). Journal of Genetics and Genome Research, 2015, 2, .	0.3	25
77	Common variants at theCHEK2gene locus and risk of epithelial ovarian cancer. Carcinogenesis, 2015, 36, 1341-1353.	1.3	24
78	Patterns of Persistent DNA Damage Associated with Sun Exposure and the Glutathione Sâ€transferase M1 Genotype in Melanoma Patients. Photochemistry and Photobiology, 2009, 85, 379-386.	1.3	23
79	Genome-wide association study of subtype-specific epithelial ovarian cancer risk alleles using pooled DNA. Human Genetics, 2014, 133, 481-497.	1.8	23
80	Variants in autophagyâ€related genes and clinical characteristics in melanoma: a populationâ€based study. Cancer Medicine, 2016, 5, 3336-3345.	1.3	23
81	MRI background parenchymal enhancement, breast density and serum hormones in postmenopausal women. International Journal of Cancer, 2018, 143, 823-830.	2.3	23
82	Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	0.6	22
83	Inherited Variation at MC1R and Histological Characteristics of Primary Melanoma. PLoS ONE, 2015, 10, e0119920.	1.1	22
84	Body mass index, weight change, and risk of second primary breast cancer in the <scp>WECARE</scp> study: influence of estrogen receptor status of the first breast cancer. Cancer Medicine, 2016, 5, 3282-3291.	1.3	22
85	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.	0.8	22
86	Large-Scale Evaluation of Common Variation in Regulatory T Cellâ€“Related Genes and Ovarian Cancer Outcome. Cancer Immunology Research, 2014, 2, 332-340.	1.6	21
87	Genetic variants and cognitive functions in patients with brain tumors. Neuro-Oncology, 2019, 21, 1297-1309.	0.6	21
88	Agnostic Pathway/Gene Set Analysis of Genome-Wide Association Data Identifies Associations for Pancreatic Cancer. Journal of the National Cancer Institute, 2019, 111, 557-567.	3.0	21
89	The use of hierarchical models for estimating relative risks of individual genetic variants: An application to a study of melanoma. Statistics in Medicine, 2008, 27, 1973-1992.	0.8	20
90	Analysis of Over 10,000 Cases Finds No Association between Previously Reported Candidate Polymorphisms and Ovarian Cancer Outcome. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 987-992.	1.1	20

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91	Sun Exposure, Vitamin D Receptor Genetic Variants, and Risk of Breast Cancer in the Agricultural Health Study. Environmental Health Perspectives, 2014, 122, 165-171.	2.8	20
92	Gastrointestinal Stromal Tumors, Somatic Mutations and Candidate Genetic Risk Variants. PLoS ONE, 2013, 8, e62119.	1.1	19
93	GWAS meta-analysis of 16 852 women identifies new susceptibility locus for endometrial cancer. Human Molecular Genetics, 2016, 25, ddw092.	1.4	19
94	Association of Incident Amelanotic Melanoma With Phenotypic Characteristics, MC1R Status, and Prior Amelanotic Melanoma. JAMA Dermatology, 2017, 153, 1026.	2.0	19
95	Molecular analysis of the INK4A and INK4B gene loci in human breast cancer cell lines and primary carcinomas. Cancer Genetics and Cytogenetics, 2001, 125, 131-138.	1.0	18
96	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	0.6	18
97	Genetic analyses of gynecological disease identify genetic relationships between uterine fibroids and endometrial cancer, and a novel endometrial cancer genetic risk region at the WNT4 1p36.12 locus. Human Genetics, 2021, 140, 1353-1365.	1.8	18
98	Validation of Denaturing High Performance Liquid Chromatography as a Rapid Detection Method for the Identification of Human INK4A Gene Mutations. Journal of Molecular Diagnostics, 2001, 3, 158-163.	1.2	17
99	Including Additional Controls from Public Databases Improves the Power of a Genome-Wide Association Study. Human Heredity, 2011, 72, 21-34.	0.4	17
100	Exome genotyping arrays to identify rare and low frequency variants associated with epithelial ovarian cancer risk. Human Molecular Genetics, 2016, 25, 3600-3612.	1.4	17
101	Identification of gene expression levels in primary melanoma associated with clinically meaningful characteristics. Melanoma Research, 2018, 28, 380-389.	0.6	17
102	Consortium analysis of gene and geneâ€“folate interactions in purine and pyrimidine metabolism pathways with ovarian carcinoma risk. Molecular Nutrition and Food Research, 2014, 58, 2023-2035.	1.5	16
103	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.	2.7	16
104	Alterations of cell cycle regulators affecting the RB pathway in nonfamilial retinoblastoma. Human Pathology, 2001, 32, 537-544.	1.1	15
105	Identifying Etiologically Distinct Subâ€Types of Cancer: A Demonstration Project Involving Breast Cancer. Cancer Medicine, 2015, 4, 1432-1439.	1.3	15
106	Evaluating the ovarian cancer gonadotropin hypothesis: A candidate gene study. Gynecologic Oncology, 2015, 136, 542-548.	0.6	15
107	Identification of lung cancer histology-specific variants applying Bayesian framework variant prioritization approaches within the TRICL and ILCCO consortia. Carcinogenesis, 2015, 36, 1314-1326.	1.3	15
108	Personalized electro-acupuncture versus auricular-acupuncture comparative effectiveness (PEACE): A protocol of a randomized controlled trial for chronic musculoskeletal pain in cancer survivors. Medicine (United States), 2020, 99, e20085.	0.4	14

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109	Functional polymorphisms in the promoter regions of MMP2 and MMP3 are not associated with melanoma progression. Journal of Negative Results in BioMedicine, 2007, 6, 9.	1.4	13
110	Genome-wide analysis of the role of copy-number variation in pancreatic cancer risk. Frontiers in Genetics, 2014, 5, 29.	1.1	13
111	Variation in NF-Î²B Signaling Pathways and Survival in Invasive Epithelial Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1421-1427.	1.1	13
112	Sunburn, sun exposure, and sun sensitivity in the Study of Nevi in Children. Annals of Epidemiology, 2015, 25, 839-843.e4.	0.9	13
113	The interaction between vitamin D receptor polymorphisms and sun exposure around time of diagnosis influences melanoma survival. Pigment Cell and Melanoma Research, 2018, 31, 287-296.	1.5	13
114	Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility: results from a large-scale collaboration. Oncotarget, 2016, 7, 72381-72394.	0.8	13
115	Exome-Wide Association Study of Endometrial Cancer in a Multiethnic Population. PLoS ONE, 2014, 9, e97045.	1.1	12
116	Investigation of the Effect of MDM2 SNP309 and TP53 Arg72Pro Polymorphisms on the Age of Onset of Cutaneous Melanoma. Journal of Investigative Dermatology, 2012, 132, 1471-1478.	0.3	11
117	Nevus count associations with pigmentary phenotype, histopathological melanoma characteristics and survival from melanoma. International Journal of Cancer, 2016, 139, 1217-1222.	2.3	11
118	Associations of MC1R Genotype and Patient Phenotypes with BRAF and NRAS Mutations in Melanoma. Journal of Investigative Dermatology, 2017, 137, 2588-2598.	0.3	11
119	CYP2D6 phenotype, tamoxifen, and risk of contralateral breast cancer in the WECARE Study. Breast Cancer Research, 2018, 20, 149.	2.2	11
120	Alterations in the retinoblastoma pathway of cell cycle control in parathyroid tumors.. Oncology Reports, 2000, 7, 421-5.	1.2	10
121	Gastrointestinal stromal tumors: a case-only analysis of single nucleotide polymorphisms and somatic mutations. Clinical Sarcoma Research, 2013, 3, 12.	2.3	10
122	Investigation of Exomic Variants Associated with Overall Survival in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 446-454.	1.1	9
123	Inherited Genetic Variants Associated with Melanoma BRAF/NRAS Subtypes. Journal of Investigative Dermatology, 2018, 138, 2398-2404.	0.3	9
124	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. PLoS ONE, 2018, 13, e0197561.	1.1	9
125	Genome-Wide Association Study for Ovarian Cancer Susceptibility Using Pooled DNA. Twin Research and Human Genetics, 2012, 15, 615-623.	0.3	8
126	Accuracy of Self-reported Smoking Exposure Among Bladder Cancer Patients Undergoing Surveillance at a Tertiary Referral Center. European Urology Focus, 2016, 2, 441-444.	1.6	8

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127	No association between prediagnosis exercise and survival in patients with highâ€risk primary melanoma: A populationâ€based study. Pigment Cell and Melanoma Research, 2017, 30, 424-427.	1.5	8
128	Interaction of CDKN2A and Sun Exposure in the Etiology of Melanoma in the General Population. Journal of Investigative Dermatology, 2011, 131, 2500-2503.	0.3	7
129	No prognostic value added by vitamin D pathway SNPs to current prognostic system for melanoma survival. PLoS ONE, 2017, 12, e0174234.	1.1	7
130	Association of Known Melanoma Risk Factors with Primary Melanoma of the Scalp and Neck. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 2203-2210.	1.1	6
131	Effects of acupuncture versus cognitive behavioral therapy on brain-derived neurotrophic factor in cancer survivors with insomnia: an exploratory analysis. Acupuncture in Medicine, 2021, 39, 637-645.	0.4	6
132	Association of a Pathway-Specific Genetic Risk Score With Risk of Radiation-Associated Contralateral Breast Cancer. JAMA Network Open, 2019, 2, e1912259.	2.8	5
133	Genome-Wide Geneâ€“Diabetes and Geneâ€“Obesity Interaction Scan in 8,255 Cases and 11,900 Controls from PanScan and PanC4 Consortia. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1784-1791.	1.1	5
134	Genetic Predictors of Response to Acupuncture or Cognitive Behavioral Therapy for Insomnia in Cancer Survivors: An Exploratory Analysis. Journal of Pain and Symptom Management, 2021, 62, e192-e199.	0.6	5
135	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with risk of clear cell ovarian cancer. Oncotarget, 2016, 7, 69097-69110.	0.8	5
136	Prospective evaluation of functional brain activity and oxidative damage in breast cancer: changes in task-induced deactivation during a working memory task. Brain Imaging and Behavior, 2021, 15, 1364-1373.	1.1	4
137	Interpretation of Melanoma Risk Feedback in First-Degree Relatives of Melanoma Patients. Journal of Cancer Epidemiology, 2012, 2012, 1-7.	0.5	3
138	rs495139 in the TYMS-ENOSF1 Region and Risk of Ovarian Carcinoma of Mucinous Histology. International Journal of Molecular Sciences, 2018, 19, 2473.	1.8	3
139	Comparison of community pathologists with expert dermatopathologists evaluating Breslow thickness and histopathologic subtype in a large international population-based study of melanoma. JAAD International, 2021, 4, 25-27.	1.1	3
140	Genotypic and phenotypic characterization of the histoblood group ABO(H) in primary bladder tumors. International Journal of Cancer, 1998, 75, 819-824.	2.3	2
141	Disease-Associated Risk Variants in ANRIL Are Associated with Tumor-Infiltrating Lymphocyte Presence in Primary Melanomas in the Population-Based GEM Study. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 2309-2316.	1.1	2
142	Characterization of the tobacco glycoprotein surface binding property of heart and skeletal muscle cells. Archives of Toxicology, 1995, 69, 149-159.	1.9	1
143	Evaluation of Alterations in the Tumor Suppressor Genes INK4A and INK4B in Human Bladder Tumors. , 2002, 179, 043-059.		1
144	Inherited Melanoma Risk Variants Associated with Histopathologically Amelanotic Melanoma. Journal of Investigative Dermatology, 2020, 140, 918-922.e7.	0.3	1

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145	Differences in Melanoma Between Canada and New South Wales, Australia: A Population-Based Genes, Environment, and Melanoma (GEM) Study. JID Innovations, 2021, 1, 100002.	1.2	1
146	Association of Melanoma-Risk Variants with Primary Melanoma Tumor Prognostic Characteristics and Melanoma-Specific Survival in the GEM Study. Current Oncology, 2021, 28, 4756-4771.	0.9	1
147	Patterns and sources of information about family melanoma risk among melanoma survivors. Melanoma Management, 2016, 3, 105-111.	0.1	0
148	Relationship of Chromosome Arm 10q Variants toÂOccurrence of Multiple Primary Melanoma in theÂPopulation-Based Genes, Environment, andÂMelanoma (GEM) Study. Journal of Investigative Dermatology, 2019, 139, 1410-1412.	0.3	0
149	Human genes differ by their UV sensitivity estimated through analysis of UVâ€induced silent mutations in melanoma. Human Mutation, 2020, 41, 1751-1760.	1.1	0
150	The p.Ser64Leu and p.Pro104Leu missense variants of PALB2 identified in familial pancreatic cancer patients compromise the DNA damage response. Human Mutation, 2021, 42, 150-163.	1.1	0
151	Minimally invasive microbiopsy for genetic profiling of melanocytic lesions: A case series. Journal of the American Academy of Dermatology, 2021, , .	0.6	0