Margaret A Tucker

List of Publications by Year
in descending order

123	9,820	76294	37183
papers	citations	40 h-index	96 g-index

124	124	124	11257
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The Risk of Cancer Associated with Specific Mutations ofBRCA1andBRCA2among Ashkenazi Jews. New England Journal of Medicine, 1997, 336, 1401-1408.	13.9	2,135
2	Germline p16 mutations in familial melanoma. Nature Genetics, 1994, 8, 15-21.	9.4	1,170
3	Germline mutations in the p16INK4a binding domain of CDK4 in familial melanoma. Nature Genetics, 1996, 12, 97-99.	9.4	756
4	Risk of New Cancers After Radiotherapy in Long-Term Survivors of Retinoblastoma: An Extended Follow-Up. Journal of Clinical Oncology, 2005, 23, 2272-2279.	0.8	453
5	Acquired Precursors of Cutaneous Malignant Melanoma. New England Journal of Medicine, 1985, 312, 91-97.	13.9	342
6	Rare missense variants in POT1 predispose to familial cutaneous malignant melanoma. Nature Genetics, 2014, 46, 482-486.	9.4	283
7	Mutations associated with familial melanoma impair p16INK4 function. Nature Genetics, 1995, 10, 114-116.	9.4	273
8	The Prevalence of Common BRCA1 and BRCA2 Mutations among Ashkenazi Jews. American Journal of Human Genetics, 1999, 64, 963-970.	2.6	204
9	The APC I1307K allele and cancer risk in a community-based study of Ashkenazi Jews. Nature Genetics, 1998, 20, 62-65.	9.4	176
10	Genotype-Phenotype Relationships in U.S. Melanoma-Prone Families With CDKN2A and CDK4 Mutations. Journal of the National Cancer Institute, 2000, 92, 1006-1010.	3.0	172
11	Second Malignancy Risks After Non-Hodgkin's Lymphoma and Chronic Lymphocytic Leukemia: Differences by Lymphoma Subtype. Journal of Clinical Oncology, 2010, 28, 4935-4944.	0.8	161
12	Joint analysis of three genome-wide association studies of esophageal squamous cell carcinoma in Chinese populations. Nature Genetics, 2014, 46, 1001-1006.	9.4	148
13	Frequency of Pathogenic Germline Variants in Cancer-Susceptibility Genes in Patients With Osteosarcoma. JAMA Oncology, 2020, 6, 724.	3.4	139
14	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.	9.4	138
15	A natural history of melanomas and dysplastic nevi. Cancer, 2002, 94, 3192-3209.	2.0	137
16	Mosaic loss of chromosome Y is associated with common variation near TCL1A. Nature Genetics, 2016, 48, 563-568.	9.4	134
17	Characterizing the genetic basis of methylome diversity in histologically normal human lung tissue. Nature Communications, 2014, 5, 3365.	5.8	123
18	Association of Chemotherapy for Solid Tumors With Development of Therapy-Related Myelodysplastic Syndrome or Acute Myeloid Leukemia in the Modern Era. JAMA Oncology, 2019, 5, 318.	3.4	116

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19	Melanoma Epidemiology. Hematology/Oncology Clinics of North America, 2009, 23, 383-395.	0.9	113
20	Thyroid Cancer Following Childhood Low-Dose Radiation Exposure: A Pooled Analysis of Nine Cohorts. Journal of Clinical Endocrinology and Metabolism, 2017, 102, 2575-2583.	1.8	112
21	Risk of Subsequent Malignant Neoplasms in Long-Term Hereditary Retinoblastoma Survivors After Chemotherapy and Radiotherapy. Journal of Clinical Oncology, 2014, 32, 3284-3290.	0.8	103
22	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	2.6	101
23	Second cancers after medulloblastoma: population-based results from the United States and Sweden. Cancer Causes and Control, 1997, 8, 865-871.	0.8	96
24	A Genome-Wide Scan Identifies Variants in NFIB Associated with Metastasis in Patients with Osteosarcoma. Cancer Discovery, 2015, 5, 920-931.	7.7	88
25	Two susceptibility loci identified for prostate cancer aggressiveness. Nature Communications, 2015, 6, 6889.	5.8	88
26	Lung Cancer Prognosis Before and After Recurrence in a Population-Based Setting. Journal of the National Cancer Institute, 2015, 107, djv059.	3.0	86
27	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	5.8	86
28	<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.	2.3	72
29	Retinoblastoma Incidence Patterns in the US Surveillance, Epidemiology, and End Results Program. JAMA Ophthalmology, 2014, 132, 478.	1.4	69
30	Genome-wide Scan of 29,141 African Americans Finds No Evidence of Directional Selection since Admixture. American Journal of Human Genetics, 2014, 95, 437-444.	2.6	69
31	Genetic polymorphisms in the 9p21 region associated with risk of multiple cancers. Carcinogenesis, 2014, 35, 2698-2705.	1.3	67
32	Genome-Wide Association Study to Identify Susceptibility Loci That Modify Radiation-Related Risk for Breast Cancer After Childhood Cancer. Journal of the National Cancer Institute, 2017, 109, .	3.0	66
33	Hereditary Retinoblastoma and Risk of Lung Cancer. Journal of the National Cancer Institute, 2000, 92, 2037-2039.	3.0	62
34	Italian and Austrian-German populations. International Journal of Cancer, 1997, 71, 9-13.	2.3	61
35	Haplotype analysis of two recurrentCDKN2A mutations in 10 melanoma families: Evidence for common founders and independent mutations. , 1998, 11, 424-431.		61
36	Mutation screening of theCDKN2A promoter in melanoma families. , 2000, 28, 45-57.		59

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37	Outdoor particulate matter (PM10) exposure and lung cancer risk in the EAGLE study. PLoS ONE, 2018, 13, e0203539.	1.1	57
38	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.	1.4	50
39	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.	1.4	50
40	Genome-wide association study identifies multiple new loci associated with Ewing sarcoma susceptibility. Nature Communications, 2018, 9, 3184.	5.8	50
41	Genome-wide association study confirms lung cancer susceptibility loci on chromosomes 5p15 and 15q25 in an African-American population. Lung Cancer, 2016, 98, 33-42.	0.9	49
42	Melanoma burden and recent trends among non-Hispanic whites aged 15â€“49 years, United States. Preventive Medicine, 2016, 91, 294-298.	1.6	49
43	Germline mutations in Protection of Telomeres 1 in two families with Hodgkin lymphoma. British Journal of Haematology, 2018, 181, 372-377.	1.2	48
44	Whole exome sequencing in families at high risk for Hodgkin lymphoma: identification of a predisposing mutation in the KDR gene. Haematologica, 2016, 101, 853-860.	1.7	40
45	Rare germline variants in known melanoma susceptibility genes in familial melanoma. Human Molecular Genetics, 2017, 26, 4886-4895.	1.4	37
46	Familial eosinophilia: Clinical and laboratory results on a U.S. Kindred. American Journal of Medical Genetics Part A, 1998, 76, 229-237.	2.4	35
47	Genomeâ€wide association study identifies the GLDC/IL33 locus associated with survival of osteosarcoma patients. International Journal of Cancer, 2018, 142, 1594-1601.	2.3	31
48	Association and aggregation analysis using kin-cohort designs with applications to genotype and family history data from the Washington Ashkenazi Study. Genetic Epidemiology, 2001, 21, 123-138.	0.6	27
49	Risk Factors for Melanoma Among Survivors of Non-Hodgkin Lymphoma. Journal of Clinical Oncology, 2015, 33, 3096-3104.	0.8	26
50	Patterns of Cause-Specific Mortality Among 2053 Survivors of Retinoblastoma, 1914â€“2016. Journal of the National Cancer Institute, 2019, 111, 961-969.	3.0	26
51	Etiological heterogeneity in Hodgkin's disease: HLA linked and unlinked determinants of susceptibility independent of histological concordance. Genetic Epidemiology, 1986, 3, 407-415.	0.6	25
52	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.	1.8	24
53	Reproductive factors, exogenous hormone use and incidence of melanoma among women in the United States. British Journal of Cancer, 2019, 120, 754-760.	2.9	24
54	Recommendations for Long-Term Follow-up of Adults with Heritable Retinoblastoma. Ophthalmology, 2020, 127, 1549-1557.	2.5	24

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55	Prescription Diuretic Use and Risk of Basal Cell Carcinoma in the Nationwide U.S. Radiologic Technologists Cohort. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1539-1545.	1.1	23
56	Is Sunlight Important to Melanoma Causation?. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 467-468.	1.1	21
57	Enhancing Career Paths for Tomorrow's Radiation Oncologists. International Journal of Radiation Oncology Biology Physics, 2019, 105, 52-63.	0.4	20
58	Inguinal hernia in patients with Ewing sarcoma: A clue to etiology. , 2000, 34, 195-199.		19
59	Histologic features of melanoma associated with CDKN2A genotype. Journal of the American Academy of Dermatology, 2015, 72, 496-507.e7.	0.6	19
60	Risks of Melanoma and Other Cancers in Melanoma-Prone Families over 4 Decades. Journal of Investigative Dermatology, 2018, 138, 1620-1626.	0.3	19
61	Bone and Softâ€Tissue Sarcoma Risk in Longâ€Term Survivors of Hereditary Retinoblastoma Treated With Radiation. Journal of Clinical Oncology, 2019, 37, 3436-3445.	0.8	19
62	Sebaceous Carcinoma Epidemiology and Genetics: Emerging Concepts and Clinical Implications for Screening, Prevention, and Treatment. Clinical Cancer Research, 2021, 27, 389-393.	3.2	19
63	Germline Variation at CDKN2A and Associations with Nevus Phenotypes amongÂMembers of Melanoma Families. Journal of Investigative Dermatology, 2017, 137, 2606-2612.	0.3	18
64	Genome-Wide Association Study in Irradiated Childhood Cancer Survivors Identifies HTR2A forÂSubsequent Basal Cell Carcinoma. Journal of Investigative Dermatology, 2019, 139, 2042-2045.e8.	0.3	18
65	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. American Journal of Human Genetics, 2021, 108, 564-582.	2.6	18
66	Estimating CDKN2A mutation carrier probability among global familial melanoma cases using GenoMELPREDICT. Journal of the American Academy of Dermatology, 2019, 81, 386-394.	0.6	17
67	Risk of therapy-related myelodysplastic syndrome/acute myeloid leukemia after childhood cancer: a population-based study. Leukemia, 2019, 33, 2947-2978.	3.3	17
68	Successful use of whole genome amplified DNA from multiple source types for high-density Illumina SNP microarrays. BMC Genomics, 2018, 19, 182.	1.2	16
69	Pediatric melanoma in melanomaâ€prone families. Cancer, 2018, 124, 3715-3723.	2.0	16
70	Long-term risk of subsequent cancer incidence among hereditary and nonhereditary retinoblastoma survivors. British Journal of Cancer, 2021, 124, 1312-1319.	2.9	16
71	Immune-Related Adverse Events After Immune Checkpoint Inhibitors for Melanoma Among Older Adults. JAMA Network Open, 2022, 5, e223461.	2.8	16
72	Constitutional promoter methylation and risk of familial melanoma. Epigenetics, 2014, 9, 685-692.	1.3	15

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73	Whole exome sequencing in families with CLL detects a variant in Integrin Î² 2 associated with disease susceptibility. Blood, 2016, 128, 2261-2263.	0.6	15
74	Mutual Risks of Cutaneous Melanoma and Specific Lymphoid Neoplasms: Second Cancer Occurrence and Survival. Journal of the National Cancer Institute, 2018, 110, 1248-1258.	3.0	15
75	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.	3.6	15
76	Sebaceous Carcinoma Incidence and Survival Among Solid Organ Transplant Recipients in the United States, 1987-2017. JAMA Dermatology, 2020, 156, 1307.	2.0	14
77	Ambient Ultraviolet Radiation and Sebaceous Carcinoma Incidence in the United States, 2000â€“2016. JNCI Cancer Spectrum, 2020, 4, pkaa020.	1.4	14
78	Clinical and laboratory observations in a lymphoma-prone family. Cancer, 1987, 60, 864-869.	2.0	13
79	A 20 Year Clinical and Laboratory Study of Familial B-Chronic Lymphocytic Leukemia in a Single Kindred. Leukemia and Lymphoma, 1991, 3, 331-342.	0.6	13
80	Rare Germline Copy Number Variations and Disease Susceptibility in Familial Melanoma. Journal of Investigative Dermatology, 2016, 136, 2436-2443.	0.3	13
81	Phenotypic and Histopathological Tumor Characteristics According to CDKN2A Mutation Status among Affected Members ofÂMelanoma Families. Journal of Investigative Dermatology, 2016, 136, 1066-1069.	0.3	13
82	Risk for malignancies of infectious etiology among adult survivors of specific non-Hodgkin lymphoma subtypes. Blood Advances, 2019, 3, 1961-1969.	2.5	12
83	GWAS follow-up study of esophageal squamous cell carcinoma identifies potential genetic loci associated with family history of upper gastrointestinal cancer. Scientific Reports, 2017, 7, 4642.	1.6	11
84	Phenocopies in melanoma-prone families with germ-line CDKN2A mutations. Genetics in Medicine, 2018, 20, 1087-1090.	1.1	11
85	Variation in Cutaneous Patterns of Melanomagenesis According to Germline CDKN2A/CDK4 Status in Melanoma-Prone Families. Journal of Investigative Dermatology, 2020, 140, 174-181.e3.	0.3	11
86	Frequency of Pathogenic Germline Variants in Cancer-Susceptibility Genes in the Childhood Cancer Survivor Study. JNCI Cancer Spectrum, 2021, 5, pkab007.	1.4	11
87	Role of radiotherapy and chemotherapy in the risk of leukemia after childhood cancer: An international pooled analysis. International Journal of Cancer, 2021, 148, 2079-2089.	2.3	10
88	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.	1.3	9
89	Subsequent Neoplasm Risk Associated With Rare Variants in DNA Damage Response and Clinical Radiation Sensitivity Syndrome Genes in the Childhood Cancer Survivor Study. JCO Precision Oncology, 2020, 4, 926-936.	1.5	9
90	Treatment-related cancers after gynecologic malignancy. Cancer, 1987, 60, 2117-2122.	2.0	8

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91	Using whole-exome sequencing and protein interaction networks to prioritize candidate genes for germline cutaneous melanoma susceptibility. Scientific Reports, 2020, 10, 17198.	1.6	8
92	Risk of Second Primary Bone and Softâ€“Tissue Sarcomas Among Young Adulthood Cancer Survivors. JNCI Cancer Spectrum, 2019, 3, pkz043.	1.4	7
93	Reply to â€˜Mosaic loss of chromosome Y in leukocytes mattersâ€™. Nature Genetics, 2019, 51, 7-9.	9.4	7
94	Risk factors for the development of cutaneous melanoma after allogeneic hematopoietic cell transplantation. Journal of the American Academy of Dermatology, 2020, 83, 762-772.	0.6	7
95	A Pragmatic Testing-Eligibility Framework for Population Mutation Screening: The Example of BRCA1/2. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 293-302.	1.1	6
96	Low-frequency variation near common germline susceptibility loci are associated with risk of Ewing sarcoma. PLoS ONE, 2020, 15, e0237792.	1.1	6
97	Increased Risk of Skin Cancer in 1,851 Long-Term Retinoblastoma Survivors. Journal of Investigative Dermatology, 2021, 141, 2849-2857.e3.	0.3	6
98	Constitutive Mitochondrial DNA Copy Number in Peripheral Blood of Melanoma Families with and without CDKN2A Mutations. Journal of Carcinogenesis & Mutagenesis, 2012, S4`, .	0.3	5
99	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.	0.6	5
100	Benign Tumors in Long-Term Survivors of Retinoblastoma. Cancers, 2021, 13, 1773.	1.7	5
101	Comparison of Radiation Dose Reconstruction Methods to Investigate Late Adverse Effects of Radiotherapy for Childhood Cancer: A Report from the Childhood Cancer Survivor Study. Radiation Research, 2019, 193, 95.	0.7	4
102	Integrated Analysis of Coexpression and Exome Sequencing to Prioritize Susceptibility Genes for Familial Cutaneous Melanoma. Journal of Investigative Dermatology, 2022, 142, 2464-2475.e5.	0.3	4
103	Mutation rate estimate in hereditary cutaneous malignant melanoma/dysplastic nevi. American Journal of Medical Genetics Part A, 1990, 35, 293-294.	2.4	3
104	Sun Exposure Measurements in Populations. Nutrition Reviews, 2007, 65, S84-S86.	2.6	3
105	The Impact of Longitudinal Surveillance on Tumor Thickness for Melanoma-Prone Families with and without Pathogenic Germline Variants of CDKN2A and CDK4. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 676-681.	1.1	3
106	Ambient ultraviolet radiation and major salivary gland cancer in the United States. Journal of the American Academy of Dermatology, 2020, 83, 1775-1777.	0.6	1
107	Novel MAPK/AKT-impairing germline NRAS variant identified in a melanoma-prone family. Familial Cancer, 2022, 21, 347-355.	0.9	1
108	Familial eosinophilia: Clinical and laboratory results on a U.S. Kindred. , 1998, 76, 229.		1

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109	Mutation screening of the CDKN2A promoter in melanoma families. Genes Chromosomes and Cancer, 2000, 28, 45.	1.5	1
110	Subsequent neoplasm risk associated with rare variants in DNA repair and clinical radiation sensitivity syndrome genes: A report from the Childhood Cancer Survivor Study.. Journal of Clinical Oncology, 2019, 37, 10028-10028.	0.8	1
111	Emerging Risks of AML/MDS and Other Myeloid Neoplasms Following Chemotherapy for First Primary Malignancy, 2000-2012. Blood, 2015, 126, 562-562.	0.6	1
112	Does radiotherapy dose correlate with incidence of thyroid cancer in survivors of childhood tumors?. Nature Clinical Practice Endocrinology and Metabolism, 2006, 2, 68-69.	2.9	0
113	Reply to Divergent cancer pathways for earlyâ€onset and lateâ€onset cutaneous malignant melanoma. Cancer, 2010, 116, 2500-2500.	2.0	0
114	Improved Imputation of Common and Uncommon Single Nucleotide Polymorphisms (SNPs) with a New Reference Set. Nature Precedings, 2011, , .	0.1	0
115	Genotypic vs Phenotypic Risk Assessment for Melanoma. Journal of the National Cancer Institute, 2021, 113, 1279-1280.	3.0	0
116	Spectrum of pediatric and young adult cancer survivors at risk of developing subsequent sarcomas.. Journal of Clinical Oncology, 2016, 34, 10572-10572.	0.8	0
117	Genome-wide association study of meningioma as a subsequent neoplasm: A report from the Childhood Cancer Survivor Study (CCSS) and St. Jude Lifetime Cohort (SJLIFE).. Journal of Clinical Oncology, 2016, 34, 10510-10510.	0.8	0
118	Novel loss-of-function variant in DENND5A impedes melanosomal cargo transport and predisposes to familial cutaneous melanoma. Genetics in Medicine, 2022, 24, 157-169.	1.1	0
119	OUP accepted manuscript. Human Reproduction, 2022, , .	0.4	0
120	Title is missing!. , 2020, 15, e0237792.		0
121	Title is missing!. , 2020, 15, e0237792.		0
122	Title is missing!. , 2020, 15, e0237792.		0
123	Title is missing!. , 2020, 15, e0237792.		0