Graham J Mann

List of Publications by Year in descending order

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238 papers	20,855 citations	25034 57 h-index	11607 135 g-index
246 all docs	246 docs citations	246 times ranked	25978 citing authors

#	Article	IF	Citations
1	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	28.9	2,562
2	Genome-wide association study identifies novel breast cancer susceptibility loci. Nature, 2007, 447, 1087-1093.	27.8	2,165
3	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	27.8	1,966
4	Whole-genome landscapes of major melanoma subtypes. Nature, 2017, 545, 175-180.	27.8	1,068
5	Prognostic and Clinicopathologic Associations of Oncogenic BRAF in Metastatic Melanoma. Journal of Clinical Oncology, 2011, 29, 1239-1246.	1.6	942
6	Geographical Variation in the Penetrance of CDKN2A Mutations for Melanoma. Journal of the National Cancer Institute, 2002, 94, 894-903.	6.3	435
7	Genome-wide association study identifies three loci associated with melanoma risk. Nature Genetics, 2009, 41, 920-925.	21.4	422
8	A novel recurrent mutation in MITF predisposes to familial and sporadic melanoma. Nature, 2011, 480, 99-103.	27.8	413
9	High-risk Melanoma Susceptibility Genes and Pancreatic Cancer, Neural System Tumors, and Uveal Melanoma across GenoMEL. Cancer Research, 2006, 66, 9818-9828.	0.9	373
10	Features associated with germline CDKN2A mutations: a GenoMEL study of melanoma-prone families from three continents. Journal of Medical Genetics, 2006, 44, 99-106.	3.2	350
11	UV-Associated Mutations Underlie the Etiology of MCV-Negative Merkel Cell Carcinomas. Cancer Research, 2015, 75, 5228-5234.	0.9	270
12	Circulating tumour DNA predicts response to anti-PD1 antibodies in metastatic melanoma. Annals of Oncology, 2017, 28, 1130-1136.	1.2	253
13	Genome-wide association study identifies three new melanoma susceptibility loci. Nature Genetics, 2011, 43, 1108-1113.	21.4	230
14	Exome sequencing of desmoplastic melanoma identifies recurrent NFKBIE promoter mutations and diverse activating mutations in the MAPK pathway. Nature Genetics, 2015, 47, 1194-1199.	21.4	221
15	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. Nature Genetics, 2015, 47, 987-995.	21.4	218
16	Dominant Negative ATM Mutations in Breast Cancer Families. Journal of the National Cancer Institute, 2002, 94, 205-215.	6.3	217
17	Common sequence variants on 20q11.22 confer melanoma susceptibility. Nature Genetics, 2008, 40, 838-840.	21.4	209
18	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. Nature Communications, 2019, 10, 3163.	12.8	205

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19	Sunbed use during adolescence and early adulthood is associated with increased risk of earlyâ€onset melanoma. International Journal of Cancer, 2011, 128, 2425-2435.	5.1	194
20	Genome-wide association study identifies novel loci predisposing to cutaneous melanomaâ€. Human Molecular Genetics, 2011, 20, 5012-5023.	2.9	187
21	BRAF Mutation, NRAS Mutation, and the Absence of an Immune-Related Expressed Gene Profile Predict Poor Outcome in Patients with Stage III Melanoma. Journal of Investigative Dermatology, 2013, 133, 509-517.	0.7	156
22	Selection criteria for genetic assessment of patients with familial melanoma. Journal of the American Academy of Dermatology, 2009, 61, 677.e1-677.e14.	1.2	154
23	Purification and characterization of recombinant mouse and herpes simplex virus ribonucleotide reductase R2 subunit. Biochemistry, 1991, 30, 1939-1947.	2.5	146
24	Phylogenetic analyses of melanoma reveal complex patterns of metastatic dissemination. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10995-11000.	7.1	146
25	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. Nature Genetics, 2011, 43, 1114-1118.	21.4	140
26	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
27	Analysis of cancer risk and BRCA1 and BRCA2mutation prevalence in the kConFab familial breast cancer resource. Breast Cancer Research, 2006, 8, R12.	5.0	135
28	Imatinib Disposition and ABCB1 (MDR1, P-Glycoprotein) Genotype. Clinical Pharmacology and Therapeutics, 2007, 82, 33-40.	4.7	135
29	Nonsense Mutations in the Shelterin Complex Genes ACD and TERF2IP in Familial Melanoma. Journal of the National Cancer Institute, 2015, 107, .	6.3	134
30	Detection of Primary Melanoma in Individuals at Extreme High Risk. JAMA Dermatology, 2014, 150, 819.	4.1	118
31	BRAF/NRAS Wild-Type Melanomas Have a High Mutation Load Correlating with Histologic and Molecular Signatures of UV Damage. Clinical Cancer Research, 2013, 19, 4589-4598.	7.0	115
32	Clinical practice guidelines for identification, screening and follow-up of individuals at high risk of primary cutaneous melanoma: a systematic review. British Journal of Dermatology, 2015, 172, 33-47.	1.5	115
33	Localization of a Novel Melanoma Susceptibility Locus to 1p22. American Journal of Human Genetics, 2003, 73, 301-313.	6.2	113
34	Loss-of-Function Fibroblast Growth Factor Receptor-2 Mutations in Melanoma. Molecular Cancer Research, 2009, 7, 41-54.	3.4	112
35	A genome wide linkage search for breast cancer susceptibility genes. Genes Chromosomes and Cancer, 2006, 45, 646-655.	2.8	111
36	A variant in FTO shows association with melanoma risk not due to BMI. Nature Genetics, 2013, 45, 428-432.	21.4	111

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37	The Effect on Melanoma Risk of Genes Previously Associated With Telomere Length. Journal of the National Cancer Institute, 2014, 106, .	6.3	109
38	Association of MC1R Variants and Host Phenotypes With Melanoma Risk in CDKN2A Mutation Carriers: A GenoMEL Study. Journal of the National Cancer Institute, 2010, 102, 1568-1583.	6.3	108
39	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. Nature Communications, 2020, 11, 5259.	12.8	102
40	Mutations in the INK4a/ARF Melanoma Susceptibility Locus Functionally Impair p14ARF. Journal of Biological Chemistry, 2001, 276, 41424-41434.	3.4	99
41	CDKN2A (P16INK4a) andCDK4 mutation analysis in 131 Australian melanoma probands: Effect of family history and multiple primary melanomas. , 1999, 25, 339-348.		96
42	EDD, the human orthologue of the hyperplastic discs tumour suppressor gene, is amplified and overexpressed in cancer. Oncogene, 2003, 22, 5070-5081.	5.9	95
43	Diagnosis of cutaneous melanocytic tumours by four-colour fluorescence in situ hybridisation. Pathology, 2009, 41, 383-387.	0.6	92
44	Two arginine rich domains in the p14ARF tumour suppressor mediate nucleolar localization. Oncogene, 2000, 19, 2978-2985.	5.9	91
45	Psychoeducational Intervention to Reduce Fear of Cancer Recurrence in People at High Risk of Developing Another Primary Melanoma: Results of a Randomized Controlled Trial. Journal of Clinical Oncology, 2016, 34, 4405-4414.	1.6	91
46	PD-L1 Negative Status is Associated with Lower Mutation Burden, Differential Expression of Immune-Related Genes, and Worse Survival in Stage III Melanoma. Clinical Cancer Research, 2016, 22, 3915-3923.	7.0	91
47	Recurrent inactivating RASA2 mutations in melanoma. Nature Genetics, 2015, 47, 1408-1410.	21.4	90
48	The Prognostic and Predictive Value of Melanoma-related MicroRNAs Using Tissue and Serum: A MicroRNA Expression Analysis. EBioMedicine, 2015, 2, 671-680.	6.1	86
49	Whole genome landscapes of uveal melanoma show an ultraviolet radiation signature in iris tumours. Nature Communications, 2020, 11, 2408.	12.8	86
50	Improved Risk Prediction Calculator for Sentinel Node Positivity in Patients With Melanoma: The Melanoma Institute Australia Nomogram. Journal of Clinical Oncology, 2020, 38, 2719-2727.	1.6	84
51	Genetic testing for melanoma risk: a prospective cohort study of uptake and outcomes among Australian families. Genetics in Medicine, 2009, 11, 265-278.	2.4	83
52	Targeting activating mutations of EZH2 leads to potent cell growth inhibition in human melanoma by derepression of tumor suppressor genes. Oncotarget, 2015, 6, 27023-27036.	1.8	83
53	Identification, Review, and Systematic Cross-Validation of microRNA Prognostic Signatures in Metastatic Melanoma. Journal of Investigative Dermatology, 2016, 136, 245-254.	0.7	82
54	Evaluation of linkage of breast cancer to the putative BRCA3 locus on chromosome 13q21 in 128 multiple case families from the Breast Cancer Linkage Consortium. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 827-831.	7.1	73

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55	RAB27A promotes melanoma cell invasion and metastasis via regulation of proâ€invasive exosomes. International Journal of Cancer, 2019, 144, 3070-3085.	5.1	72
56	Determination of prognosis in metastatic melanoma through integration of clinicoâ€pathologic, mutation, mRNA, microRNA, and protein information. International Journal of Cancer, 2015, 136, 863-874.	5.1	67
57	Cost-Effectiveness of Skin Surveillance Through a Specialized Clinic for Patients at High Risk of Melanoma. Journal of Clinical Oncology, 2017, 35, 63-71.	1.6	66
58	Multiomic profiling of checkpoint inhibitor-treated melanoma: Identifying predictors of response and resistance, and markers of biological discordance. Cancer Cell, 2022, 40, 88-102.e7.	16.8	64
59	IGFBP7 Is Not Required for B-RAF-Induced Melanocyte Senescence. Cell, 2010, 141, 717-727.	28.9	60
60	Mutant B-RAF-Mcl-1 survival signaling depends on the STAT3 transcription factor. Oncogene, 2014, 33, 1158-1166.	5.9	60
61	A highly recurrent RPS27 5'UTR mutation in melanoma. Oncotarget, 2014, 5, 2912-2917.	1.8	60
62	Mutation screening of theCDKN2A promoter in melanoma families. , 2000, 28, 45-57.		59
63	MicroRNA and mRNA expression profiling in metastatic melanoma reveal associations with BRAF mutation and patient prognosis. Pigment Cell and Melanoma Research, 2015, 28, 254-266.	3.3	59
64	Predictors of Vinorelbine Pharmacokinetics and Pharmacodynamics in Patients With Cancer. Journal of Clinical Oncology, 2006, 24, 2448-2455.	1.6	58
65	Paracetamol inhibits replicative DNA synthesis and induces sister chromatid exchange and chromosomal aberrations by inhibition of ribonucleotide reductase. Mutagenesis, 1990, 5, 475-480.	2.6	57
66	Distinct Molecular Profiles and Immunotherapy Treatment Outcomes of V600E and V600K BRAF-Mutant Melanoma. Clinical Cancer Research, 2019, 25, 1272-1279.	7.0	57
67	The chromatin remodelling factor BRG1 is a novel binding partner of the tumor suppressor p16INK4a. Molecular Cancer, 2009, 8, 4.	19.2	55
68	Molecular Genomic Profiling of MelanocyticÂNevi. Journal of Investigative Dermatology, 2019, 139, 1762-1768.	0.7	55
69	Whole genome sequencing of melanomas in adolescent and young adults reveals distinct mutation landscapes and the potential role of germline variants in disease susceptibility. International Journal of Cancer, 2019, 144, 1049-1060.	5.1	54
70	Economic evaluations of psychosocial interventions in cancer: a systematic review. Psycho-Oncology, 2016, 25, 1380-1392.	2.3	53
71	Development and External Validation of a Melanoma Risk Prediction Model Based on Self-assessed Risk Factors. JAMA Dermatology, 2016, 152, 889.	4.1	53
72	Hepatic technetium Tc 99m?labeled sestamibi elimination rate and () genotype as indicators of ABCB1 (P-glycoprotein) activity in patients with cancer. Clinical Pharmacology and Therapeutics, 2005, 77, 33-42.	4.7	52

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73	Review and Cross-Validation of Gene Expression Signatures and Melanoma Prognosis. Journal of Investigative Dermatology, 2012, 132, 274-283.	0.7	52
74	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
75	Loss of heterozygosity in malignant melanoma at loci on chromosomes 11 and 17 implicated in the pathogenesis of other cancers. Genes Chromosomes and Cancer, 1993, 7, 169-172.	2.8	51
76	Melanoma Prognosis: A REMARK-Based Systematic Review and Bioinformatic Analysis of Immunohistochemical and Gene Microarray Studies. Molecular Cancer Therapeutics, 2011, 10, 1520-1528.	4.1	50
77	Responses to ultraviolet-B in cell lines from hereditary melanoma kindreds. Melanoma Research, 2001, 11, 1-9.	1.2	48
78	Melanomas of unknown primary have a mutation profile consistent with cutaneous sunâ€exposed melanoma. Pigment Cell and Melanoma Research, 2013, 26, 852-860.	3.3	48
79	Population-based, Case-Control-Family Design to Investigate Genetic and Environmental Influences on Melanoma Risk: Australian Melanoma Family Study. American Journal of Epidemiology, 2009, 170, 1541-1554.	3.4	46
80	Evolution of late-stage metastatic melanoma is dominated by aneuploidy and whole genome doubling. Nature Communications, 2021, 12, 1434.	12.8	46
81	A High-Throughput Panel for Identifying Clinically Relevant Mutation Profiles in Melanoma. Molecular Cancer Therapeutics, 2012, 11, 888-897.	4.1	45
82	Prevalence and predictors of germline CDKN2A mutations for melanoma cases from Australia, Spain and the United Kingdom. Hereditary Cancer in Clinical Practice, 2014, 12, 20.	1.5	45
83	Mutation analysis of FANCD2, BRIP1/BACH1, LMO4 and SFN in familial breast cancer. Breast Cancer Research, 2005, 7, R1005-16.	5.0	44
84	Oncogenic B-RAFV600E Signaling Induces the T-Box3 Transcriptional Repressor to Repress E-Cadherin and Enhance Melanoma Cell Invasion. Journal of Investigative Dermatology, 2013, 133, 1269-1277.	0.7	44
85	A Pilot Randomized Controlled Trial of the Feasibility, Acceptability, and Impact of Giving Information on Personalized Genomic Risk of Melanoma to the Public. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 212-221.	2.5	44
86	Anatomic position determines oncogenic specificity in melanoma. Nature, 2022, 604, 354-361.	27.8	44
87	Early-life sun exposure and risk of melanoma before age 40Âyears. Cancer Causes and Control, 2011, 22, 885-897.	1.8	43
88	Clinical Features Associated With Individuals at Higher Risk of Melanoma. JAMA Dermatology, 2017, 153, 23.	4.1	43
89	Is there a role for genetic testing in patients with melanoma?. Current Opinion in Oncology, 2003, 15, 157-161.	2.4	42
90	Immunofluorescent quantification of ribonucleotide reductase M1 subunit and correlation with DNA content by flow cytometry. Cytometry, 1987, 8, 509-517.	1.8	41

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91	Melanoma risk for CDKN2A mutation carriers who are relatives of population-based case carriers in Australia and the UK. Journal of Medical Genetics, 2011, 48, 266-272.	3.2	41
92	Identification of a melanoma susceptibility locus and somatic mutation inTET2. Carcinogenesis, 2014, 35, 2097-2101.	2.8	41
93	Unexpected UVR and non-UVR mutation burden in some acral and cutaneous melanomas. Laboratory Investigation, 2017, 97, 130-145.	3.7	40
94	Telomere sequence content can be used to determine ALT activity in tumours. Nucleic Acids Research, 2018, 46, 4903-4918.	14.5	40
95	Sunscreen Use and Melanoma Risk Among Young Australian Adults. JAMA Dermatology, 2018, 154, 1001.	4.1	40
96	p16INK4a Expression and Absence of Activated B-RAF Are Independent Predictors of Chemosensitivity in Melanoma Tumors. Neoplasia, 2008, 10, 1231-1239.	5.3	39
97	Meta-Analysis Combining New and Existing Data Sets Confirms that the TERTâ€“CLPTM1L Locus Influences Melanoma Risk. Journal of Investigative Dermatology, 2012, 132, 485-487.	0.7	39
98	Comparison of whole-exome sequencing of matched fresh and formalin fixed paraffin embedded melanoma tumours: implications for clinical decision making. Pathology, 2016, 48, 261-266.	0.6	39
99	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	6.2	39
100	Deletion mapping suggests that the 1p22 melanoma susceptibility gene is a tumor suppressor localized to a 9-mb interval. Genes Chromosomes and Cancer, 2004, 41, 56-64.	2.8	37
101	Low prevalence of RAS-RAF-activating mutations in Spitz melanocytic nevi compared with other melanocytic lesions. Journal of Cutaneous Pathology, 2007, 34, 448-455.	1.3	37
102	A Model of Prostate-Specific Antigen Screening Outcomes for Low- to High-Risk Men. Archives of Internal Medicine, 2009, 169, 1603-10.	3.8	37
103	Predicting functional significance of cancer-associated p16INK4a mutations in CDKN2A. Human Mutation, 2010, 31, 692-701.	2.5	37
104	Neurotropic melanoma: an analysis of the clinicopathological features, management strategies and survival outcomes for 671 patients treated at a tertiary referral center. Modern Pathology, 2017, 30, 1538-1550.	5.5	33
105	Intronic sequence variants of theCDKN2A gene in melanoma pedigrees. Genes Chromosomes and Cancer, 2005, 43, 128-136.	2.8	32
106	MC1R genotypes and risk of melanoma before age 40 years: A populationâ€based caseâ€controlâ€family study. International Journal of Cancer, 2012, 131, E269-81.	5.1	32
107	Rare Variant, Gene-Based Association Study of Hereditary Melanoma Using Whole-Exome Sequencing. Journal of the National Cancer Institute, 2017, 109, .	6.3	32
108	Poor Adherence to National Clinical Management Guidelines: A Population-Based, Cross-Sectional Study of the Surgical Management of Melanoma in New South Wales, Australia. Annals of Surgical Oncology, 2017, 24, 2080-2088.	1.5	31

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109	TRIM16 inhibits proliferation and migration through regulation of interferon beta 1 in melanoma cells. Oncotarget, 2014, 5, 10127-10139.	1.8	31
110	Recurrent hotspot SF3B1 mutations at codon 625 in vulvovaginal mucosal melanoma identified in a study of 27 Australian mucosal melanomas. Oncotarget, 2019, 10, 930-941.	1.8	31
111	MC1Rgenotype as a predictor of early-onset melanoma, compared with self-reported and physician-measured traditional risk factors: an Australian case-control-family study. BMC Cancer, 2013, 13, 406.	2.6	30
112	Psychoâ€educational interventions for melanoma survivors: a systematic review. Psycho-Oncology, 2013, 22, 1444-1456.	2.3	29
113	Occupational sun exposure and risk of melanoma according to anatomical site. International Journal of Cancer, 2014, 134, 2735-2741.	5.1	29
114	Improving subjective perception of personal cancer risk: systematic review and metaâ€analysis of educational interventions for people with cancer or at high risk of cancer. Psycho-Oncology, 2014, 23, 613-625.	2.3	29
115	Men's preferences and tradeâ€offs for prostate cancer screening: a discrete choice experiment. Health Expectations, 2015, 18, 3123-3135.	2.6	29
116	Multiple abnormalities of the p16INK4a-pRb regulatory pathway in cultured melanoma cells. Melanoma Research, 1999, 9, 10-20.	1.2	27
117	Association Between Melanoma Detected During Routine Skin Checks and Mortality. JAMA Dermatology, 2021, 157, 1425.	4.1	27
118	A comparison of CDKN2A mutation detection within the Melanoma Genetics Consortium (GenoMEL). European Journal of Cancer, 2008, 44, 1269-1274.	2.8	26
119	The molecular profile of metastatic melanoma in Australia. Pathology, 2016, 48, 188-193.	0.6	26
120	Variation in the RAD51 gene and familial breast cancer. Breast Cancer Research, 2006, 8, R26.	5.0	25
121	Better the Devil You Know? High-Risk Individualsâ€™ Anticipated Psychological Responses to Genetic Testing for Melanoma Susceptibility. Journal of Genetic Counseling, 2006, 15, 433-447.	1.6	25
122	Development and pilot testing of an online screening decision aid for men with a family history of prostate cancer. Patient Education and Counseling, 2011, 83, 64-72.	2.2	25
123	Identification of TFG (TRKâ€fused gene) as a putative metastatic melanoma tumor suppressor gene. Genes Chromosomes and Cancer, 2012, 51, 452-461.	2.8	25
124	Specialized Surveillance for Individuals at High Risk for Melanoma. JAMA Dermatology, 2015, 151, 178.	4.1	25
125	Efficiency of Detecting New Primary Melanoma Among Individuals Treated in a High-risk Clinic for Skin Surveillance. JAMA Dermatology, 2021, 157, 521.	4.1	25
126	Differential expression of p16INK4a and p16Î² transcripts in B-lymphoblastoid cells from members of hereditary melanoma families without CDKN2A exon mutations. Oncogene, 1997, 15, 515-523.	5.9	24

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127	Equitable Expanded Carrier Screening Needs Indigenous Clinical and Population Genomic Data. American Journal of Human Genetics, 2020, 107, 175-182.	6.2	24
128	Anticipated uptake of genetic testing for familial melanoma in an Australian sample: an exploratory study. Psycho-Oncology, 2007, 16, 69-78.	2.3	23
129	An extended antibody microarray for surface profiling metastatic melanoma. Journal of Immunological Methods, 2010, 358, 23-34.	1.4	22
130	Skin cancer screening behaviours among individuals with a strong family history of malignant melanoma. British Journal of Cancer, 2010, 103, 1502-1509.	6.4	22
131	Online prostate cancer screening decision aid for at-risk men: A randomized trial.. Health Psychology, 2014, 33, 986-997.	1.6	22
132	Data Independent Acquisition Proteomic Analysis Can Discriminate between Actinic Keratosis, Bowenâ€™s Disease, and Cutaneous Squamous Cell Carcinoma. Journal of Investigative Dermatology, 2020, 140, 212-222.e11.	0.7	22
133	Impact of personal genomic risk information on melanoma prevention behaviors and psychological outcomes: a randomized controlled trial. Genetics in Medicine, 2021, 23, 2394-2403.	2.4	22
134	Predictors of psychological distress among individuals with a strong family history of malignant melanoma. Clinical Genetics, 2008, 73, 121-131.	2.0	21
135	Network-based biomarkers enhance classical approaches to prognostic gene expression signatures. BMC Systems Biology, 2014, 8, S5.	3.0	21
136	The steadily growing problem of lentigo maligna and lentigo maligna melanoma in Australia: Populationâ€based data on diagnosis and management. Australasian Journal of Dermatology, 2019, 60, 118-125.	0.7	21
137	A Dual-Antigen Enzyme-Linked Immunosorbent Assay Allows the Assessment of Severe Acute Respiratory Syndrome Coronavirus 2 Antibody Seroprevalence in a Low-Transmission Setting. Journal of Infectious Diseases, 2021, 223, 10-14.	4.0	21
138	Deoxyadenosine triphosphate as a mediator of deoxyguanosine toxicity in cultured T lymphoblasts.. Journal of Clinical Investigation, 1986, 78, 1261-1269.	8.2	21
139	10q deletions in metastatic cutaneous melanoma. Cancer Genetics and Cytogenetics, 1998, 100, 68-71.	1.0	19
140	Highâ€•and averageâ€•risk individuals' beliefs about, and perceptions of, malignant melanoma: an Australian perspective. Psycho-Oncology, 2008, 17, 270-279.	2.3	19
141	Melanoma survivors at high risk of developing new primary disease: a qualitative examination of the factors that contribute to patient satisfaction with clinical care. Psycho-Oncology, 2013, 22, 1994-2000.	2.3	19
142	Histologic features of melanoma associated with CDKN2A genotype. Journal of the American Academy of Dermatology, 2015, 72, 496-507.e7.	1.2	19
143	â€œMelanoma: Questions and Answers.â€•Development and evaluation of a psycho-educational resource for people with a history of melanoma. Supportive Care in Cancer, 2016, 24, 4849-4859.	2.2	19
144	GermlineCDKN2A/P16INK4A mutations contribute to genetic determinism of sarcoma. Journal of Medical Genetics, 2017, 54, 607-612.	3.2	19

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145	Mutation load in melanoma is affected by <scp>MC</scp>1R genotype. Pigment Cell and Melanoma Research, 2017, 30, 255-258.	3.3	19
146	The melanoma genomics managing your risk study: A protocol for a randomized controlled trial evaluating the impact of personal genomic risk information on skin cancer prevention behaviors. Contemporary Clinical Trials, 2018, 70, 106-116.	1.8	19
147	Pathway-Based Analysis of a Melanoma Genome-Wide Association Study: Analysis of Genes Related to Tumour-Immunosuppression. PLoS ONE, 2011, 6, e29451.	2.5	18
148	Germline Variation at CDKN2A and Associations with Nevus Phenotypes amongÂMembers of Melanoma Families. Journal of Investigative Dermatology, 2017, 137, 2606-2612.	0.7	18
149	Polyunsaturated fatty acids and risk of melanoma: A <scp>M</scp>endelian randomisation analysis. International Journal of Cancer, 2018, 143, 508-514.	5.1	18
150	Follow-Up Recommendations after Diagnosis of Primary Cutaneous Melanoma: A Population-Based Study in New South Wales, Australia. Annals of Surgical Oncology, 2018, 25, 617-625.	1.5	18
151	Patterns of metastases in familial and non-familial melanoma. Melanoma Research, 2003, 13, 105-109.	1.2	17
152	Molecular interaction networks for the analysis of human disease: Utility, limitations, and considerations. Proteomics, 2013, 13, 3393-3405.	2.2	17
153	ClassifyR: an R package for performance assessment of classification with applications to transcriptomics. Bioinformatics, 2015, 31, 1851-1853.	4.1	17
154	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
155	Protein signatures correspond to survival outcomes of AJCC stage III melanoma patients. Pigment Cell and Melanoma Research, 2014, 27, 1106-1116.	3.3	16
156	Differential distribution improves gene selection stability and has competitive classification performance for patient survival. Nucleic Acids Research, 2016, 44, e119-e119.	14.5	16
157	eMelanoBase: An online locus-specific variant database for familial melanoma. Human Mutation, 2003, 21, 2-7.	2.5	15
158	Expression Analysis of a Tyrosinase Promoter Sequence in Zebrafish. Pigment Cell & Melanoma Research, 2003, 16, 117-126.	3.6	15
159	Impaired inhibition of NF-Î¹B activity by melanoma-associated p16INK4a mutations. Biochemical and Biophysical Research Communications, 2005, 332, 873-879.	2.1	15
160	Accuracy of Self-Reported Nevus and Pigmentation Phenotype Compared with Clinical Assessment in a Population-Based Study of Young Australian Adults. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 736-743.	2.5	15
161	The Role of Personalised Choice in Decision Support: A Randomized Controlled Trial of an Online Decision Aid for Prostate Cancer Screening. PLoS ONE, 2016, 11, e0152999.	2.5	15
162	Mutation analysis of five candidate genes in familial breast cancer. Breast Cancer Research and Treatment, 2007, 105, 377-389.	2.5	14

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163	Functional impairment of p16INK4A due to CDKN2A p.Gly23Asp missense mutation. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2009, 671, 26-32.	1.0	14
164	The Melanoma care study: protocol of a randomised controlled trial of a psycho-educational intervention for melanoma survivors at high risk of developing new primary disease. BMC Psychology, 2015, 3, 23.	2.1	14
165	The Prognostic Significance of Low-Frequency Somatic Mutations in Metastatic Cutaneous Melanoma. Frontiers in Oncology, 2018, 8, 584.	2.8	14
166	Conjugated ternary doped carbon dots from vitamin B derivative: Multispectral nanoprobes for targeted melanoma bioimaging and photosensitization. Journal of Luminescence, 2020, 217, 116811.	3.1	14
167	The intronic G13964C variant in p53 is not a high-risk mutation in familial breast cancer in Australia. Breast Cancer Research, 2001, 3, 346-9.	5.0	13
168	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
169	Evaluation of the contribution of germline variants in BRCA1 and BRCA2 to uveal and cutaneous melanoma. Melanoma Research, 2019, 29, 483-490.	1.2	13
170	Benefits of a brief psychological intervention targeting fear of cancer recurrence in people at high risk of developing another melanoma: 12â€month followâ€up results of a randomized controlled trial. British Journal of Dermatology, 2020, 182, 860-868.	1.5	13
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