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	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
2	Independent evaluation of melanoma polygenic risk scores in <scp>UK</scp> and Australian prospective cohorts*. British Journal of Dermatology, 2022, 186, 823-834.	1.5	10
3	Anatomic position determines oncogenic specificity in melanoma. Nature, 2022, 604, 354-361.	27.8	44
4	Development of melanoma clinical quality indicators for the Australian melanoma clinical outcomes registry (<scp>MelCOR</scp>): A modified Delphi study. Australasian Journal of Dermatology, 2022, , .	0.7	2
5	Cross-Platform Omics Prediction procedure: a statistical machine learning framework for wider implementation of precision medicine. Npj Digital Medicine, 2022, 5, .	10.9	3
6	FRAMe: Familial Risk Assessment of Melanomaâ€”a risk prediction tool to guide CDKN2A germline mutation testing in Australian familial melanoma. Familial Cancer, 2021, 20, 231-239.	1.9	6
7	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
8	Risk factors for melanoma by anatomical site: an evaluation of aetiological heterogeneity*. British Journal of Dermatology, 2021, 184, 1085-1093.	1.5	13
9	An independent external validation of melanoma risk prediction models using the Australian Melanoma Family Study. British Journal of Dermatology, 2021, 184, 957-960.	1.5	3
10	Knowledge and attitudes of Australian dermatologists towards sentinel lymph node biopsy for melanoma: a mixed methods study. Australasian Journal of Dermatology, 2021, 62, 168-176.	0.7	3
11	Prevalence of asymptomatic SARSâ€CoV â€2 infection in elective surgical patients in Australia: a prospective surveillance study. ANZ Journal of Surgery, 2021, 91, 27-32.	0.7	8
12	Implementation of patient-reported outcome measures and patient-reported experience measures in melanoma clinical quality registries: a systematic review. BMJ Open, 2021, 11, e040751.	1.9	13
13	Evolution of late-stage metastatic melanoma is dominated by aneuploidy and whole genome doubling. Nature Communications, 2021, 12, 1434.	12.8	46
14	Birth cohort-specific trends of sun-related behaviors among individuals from an international consortium of melanoma-prone families. BMC Public Health, 2021, 21, 692.	2.9	4
15	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
16	Identifying the â€˜Active Ingredients' of an Effective Psychological Intervention to Reduce Fear of Cancer Recurrence: A Process Evaluation. Frontiers in Psychology, 2021, 12, 661190.	2.1	4
17	Specialised skin cancer spectral library for use in dataâ€independent mass spectrometry. Proteomics, 2021, 21, e2100128.	2.2	3
18	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	6.4	9

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19	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
20	Irregular Sleep/Wake Patterns Are Associated With Reduced Quality of Life in Post-treatment Cancer Patients: A Study Across Three Cancer Cohorts. Frontiers in Neuroscience, 2021, 15, 700923.	2.8	6
21	Association Between Melanoma Detected During Routine Skin Checks and Mortality. JAMA Dermatology, 2021, 157, 1425.	4.1	27
22	Germline variants are associated with increased primary melanoma tumor thickness at diagnosis. Human Molecular Genetics, 2021, 29, 3578-3587.	2.9	3
23	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
24	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
25	Development and external validation study of a melanoma risk prediction model incorporating clinically assessed naevi and solar lentigines. British Journal of Dermatology, 2020, 182, 1262-1268.	1.5	12
26	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
27	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. Nature Communications, 2020, 11, 5259.	12.8	102
28	Multiplex melanoma families are enriched for polygenic risk. Human Molecular Genetics, 2020, 29, 2976-2985.	2.9	9
29	Equitable Expanded Carrier Screening Needs Indigenous Clinical and Population Genomic Data. American Journal of Human Genetics, 2020, 107, 175-182.	6.2	24
30	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	6.2	39
31	Tumor Mutation Burden and Structural Chromosomal Aberrations Are Not Associated with T-cell Density or Patient Survival in Acral, Mucosal, and Cutaneous Melanomas. Cancer Immunology Research, 2020, 8, 1346-1353.	3.4	13
32	Whole genome landscapes of uveal melanoma show an ultraviolet radiation signature in iris tumours. Nature Communications, 2020, 11, 2408.	12.8	86
33	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
34	Identifying challenges to implementation of clinical practice guidelines for sentinel lymph node biopsy in patients with melanoma in Australia: protocol paper for a mixed methods study. BMJ Open, 2020, 10, e032636.	1.9	6
35	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	27.8	1,966
36	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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37	Proteomics: An emerging approach for the diagnosis and classification of cutaneous squamous cell carcinoma and its precursors. Journal of Dermatological Science, 2020, 99, 9-16.	1.9	10
38	Australian general practitionersâ€™ attitudes and knowledge of sentinel lymph node biopsy in melanoma management. Australian Journal of General Practice, 2020, 49, 355-362.	0.8	3
39	Molecular Epidemiology of Melanoma. , 2020, , 451-469.		0
40	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. Nature Communications, 2019, 10, 3163.	12.8	205
41	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
42	Cost-Effectiveness of a Psycho-Educational Intervention Targeting Fear of Cancer Recurrence in People Treated for Early-Stage Melanoma. Applied Health Economics and Health Policy, 2019, 17, 669-681.	2.1	11
43	Molecular Genomic Profiling of MelanocyticÂNevi. Journal of Investigative Dermatology, 2019, 139, 1762-1768.	0.7	55
44	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
45	Melanoma Explorer: a web application to allow easy reanalysis of publicly available and clinically annotated melanoma omics data sets. Melanoma Research, 2019, 29, 342-344.	1.2	5
46	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
47	RAB27A promotes melanoma cell invasion and metastasis via regulation of proâ€invasive exosomes. International Journal of Cancer, 2019, 144, 3070-3085.	5.1	72
48	Distinct Molecular Profiles and Immunotherapy Treatment Outcomes of V600E and V600K BRAF-Mutant Melanoma. Clinical Cancer Research, 2019, 25, 1272-1279.	7.0	57
49	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
50	Tape Stripped Stratum Corneum Samples Prove to be Suitable for Comprehensive Proteomic Investigation of Actinic Keratosis. Proteomics - Clinical Applications, 2019, 13, 1800084.	1.6	10
51	Comprehensive molecular profiling of metastatic melanoma to predict response to monotherapy and combination immunotherapy.. Journal of Clinical Oncology, 2019, 37, 9511-9511.	1.6	3
52	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
53	Molecular Epidemiology of Melanoma. , 2019, , 1-19.		0
54	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

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55	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
56	A National Budget Impact Analysis of a Specialised Surveillance Programme for Individuals at Very High Risk of Melanoma in Australia. Applied Health Economics and Health Policy, 2018, 16, 235-242.	2.1	7
57	Telomere sequence content can be used to determine ALT activity in tumours. Nucleic Acids Research, 2018, 46, 4903-4918.	14.5	40
58	Sensitivity of Preference-Based Quality-of-Life Measures for Economic Evaluations in Early-Stage Melanoma. JAMA Dermatology, 2018, 154, 52.	4.1	11
59	A 14â€Protein Signature for Rapid Identification of Poor Prognosis Stage III Metastatic Melanoma. Proteomics - Clinical Applications, 2018, 12, 1700094.	1.6	0
60	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
61	Sunscreen Use and Melanoma Risk Among Young Australian Adults. JAMA Dermatology, 2018, 154, 1001.	4.1	40
62	Proteomic phenotyping of metastatic melanoma reveals putative signatures of MEK inhibitor response and prognosis. British Journal of Cancer, 2018, 119, 713-723.	6.4	9
63	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
64	The Prognostic Significance of Low-Frequency Somatic Mutations in Metastatic Cutaneous Melanoma. Frontiers in Oncology, 2018, 8, 584.	2.8	14
65	Sustained long-term benefits of a psycho-educational intervention targeting fear of cancer recurrence in people at high risk of developing another melanoma: A randomised controlled trial.. Journal of Clinical Oncology, 2018, 36, 10082-10082.	1.6	1
66	Unexpected UVR and non-UVR mutation burden in some acral and cutaneous melanomas. Laboratory Investigation, 2017, 97, 130-145.	3.7	40
67	Whole-genome landscapes of major melanoma subtypes. Nature, 2017, 545, 175-180.	27.8	1,068
68	GermlineCDKN2A/P16INK4A mutations contribute to genetic determinism of sarcoma. Journal of Medical Genetics, 2017, 54, 607-612.	3.2	19
69	Rare Variant, Gene-Based Association Study of Hereditary Melanoma Using Whole-Exome Sequencing. Journal of the National Cancer Institute, 2017, 109, .	6.3	32
70	Circulating tumour DNA predicts response to anti-PD1 antibodies in metastatic melanoma. Annals of Oncology, 2017, 28, 1130-1136.	1.2	253
71	Mutation load in melanoma is affected by <scp>MC</scp>1R genotype. Pigment Cell and Melanoma Research, 2017, 30, 255-258.	3.3	19
72	Germline Variation at CDKN2A and Associations with Nevus Phenotypes amongÂMembers of Melanoma Families. Journal of Investigative Dermatology, 2017, 137, 2606-2612.	0.7	18

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73	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
74	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
75	Clinical Features Associated With Individuals at Higher Risk of Melanoma. JAMA Dermatology, 2017, 153, 23.	4.1	43
76	Diagnosis and clinical management of melanoma patients at higher risk of a new primary melanoma: A populationâ€based study in New South Wales, Australia. Australasian Journal of Dermatology, 2017, 58, 278-285.	0.7	12
77	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
78	Advantages of whole-genome sequencing for identification of tumor etiology and clinically actionable genomic aberrations: lessons from the Australian Melanoma Genome Project. Melanoma Management, 2017, 4, 147-149.	0.5	1
79	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
80	Psychoeducational intervention for people at high risk of developing another melanoma: a pilot randomised controlled trial. BMJ Open, 2017, 7, e015195.	1.9	8
81	Distinct gene expression, mutational profile and clinical outcomes of V600E and V600K/R BRAF-mutant metastatic melanoma (MM).. Journal of Clinical Oncology, 2017, 35, 9541-9541.	1.6	2
82	A multi-step classifier addressing cohort heterogeneity improves performance of prognostic biomarkers in three cancer types. Oncotarget, 2017, 8, 2807-2815.	1.8	10
83	Economic evaluations of psychosocial interventions in cancer: a systematic review. Psycho-Oncology, 2016, 25, 1380-1392.	2.3	53
84	Protocol for a within-trial economic evaluation of a psychoeducational intervention tailored to people at high risk of developing a second or subsequent melanoma. BMJ Open, 2016, 6, e012153.	1.9	6
85	The molecular profile of metastatic melanoma in Australia. Pathology, 2016, 48, 188-193.	0.6	26
86	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
87	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
88	Doctorsâ€™ recognition and management of melanoma patientsâ€™ risk: An Australian population-based study. Cancer Epidemiology, 2016, 45, 32-39.	1.9	1
89	Development and External Validation of a Melanoma Risk Prediction Model Based on Self-assessed Risk Factors. JAMA Dermatology, 2016, 152, 889.	4.1	53
90	Differential distribution improves gene selection stability and has competitive classification performance for patient survival. Nucleic Acids Research, 2016, 44, e119-e119.	14.5	16

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91	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
92	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
93	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
94	Identification, Review, and Systematic Cross-Validation of microRNA Prognostic Signatures in Metastatic Melanoma. Journal of Investigative Dermatology, 2016, 136, 245-254.	0.7	82
95	Randomised controlled trial of a psycho-educational intervention to reduce fear of cancer recurrence in people at high risk of developing another primary melanoma.. Journal of Clinical Oncology, 2016, 34, 10068-10068.	1.6	1
96	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
97	A pilot randomised controlled trial examining the feasibility, acceptability and impact of giving information on personalised genomic risk of melanoma to the public, for motivating preventive behaviours.. Journal of Clinical Oncology, 2016, 34, 1556-1556.	1.6	0
98	Men's preferences and tradeâ€offs for prostate cancer screening: a discrete choice experiment. Health Expectations, 2015, 18, 3123-3135.	2.6	29
99	Tumour procurement, DNA extraction, coverage analysis and optimisation of mutation-detection algorithms for human melanoma genomes. Pathology, 2015, 47, 683-693.	0.6	9
100	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
101	Specialized Surveillance for Individuals at High Risk for Melanoma. JAMA Dermatology, 2015, 151, 178.	4.1	25
102	UV-Associated Mutations Underlie the Etiology of MCV-Negative Merkel Cell Carcinomas. Cancer Research, 2015, 75, 5228-5234.	0.9	270
103	Histologic features of melanoma associated with CDKN2A genotype. Journal of the American Academy of Dermatology, 2015, 72, 496-507.e7.	1.2	19
104	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
105	Nonsense Mutations in the Shelterin Complex Genes ACD and TERF2IP in Familial Melanoma. Journal of the National Cancer Institute, 2015, 107, .	6.3	134
106	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	28.9	2,562
107	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
108	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. Nature Genetics, 2015, 47, 987-995.	21.4	218

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109	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
110	ClassifyR: an R package for performance assessment of classification with applications to transcriptomics. Bioinformatics, 2015, 31, 1851-1853.	4.1	17
111	Recurrent inactivating RASA2 mutations in melanoma. Nature Genetics, 2015, 47, 1408-1410.	21.4	90
112	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
113	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
114	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
115	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
116	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
117	Identification of a melanoma susceptibility locus and somatic mutation inTET2. Carcinogenesis, 2014, 35, 2097-2101.	2.8	41
118	Occupational sun exposure and risk of melanoma according to anatomical site. International Journal of Cancer, 2014, 134, 2735-2741.	5.1	29
119	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
120	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
121	Detection of Primary Melanoma in Individuals at Extreme High Risk. JAMA Dermatology, 2014, 150, 819.	4.1	118
122	The Effect on Melanoma Risk of Genes Previously Associated With Telomere Length. Journal of the National Cancer Institute, 2014, 106, .	6.3	109
123	Protein signatures correspond to survival outcomes of AJCC stage III melanoma patients. Pigment Cell and Melanoma Research, 2014, 27, 1106-1116.	3.3	16
124	Surface antigen profiles of leukocytes and melanoma cells in lymph node metastases are associated with survival in AJCC stage III melanoma patients. Clinical and Experimental Metastasis, 2014, 31, 407-421.	3.3	6
125	Mutant B-RAF-Mcl-1 survival signaling depends on the STAT3 transcription factor. Oncogene, 2014, 33, 1158-1166.	5.9	60
126	Online prostate cancer screening decision aid for at-risk men: A randomized trial.. Health Psychology, 2014, 33, 986-997.	1.6	22

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127	Network-based biomarkers enhance classical approaches to prognostic gene expression signatures. BMC Systems Biology, 2014, 8, S5.	3.0	21
128	A highly recurrent RPS27 5'UTR mutation in melanoma. Oncotarget, 2014, 5, 2912-2917.	1.8	60
129	TRIM16 inhibits proliferation and migration through regulation of interferon beta 1 in melanoma cells. Oncotarget, 2014, 5, 10127-10139.	1.8	31
130	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
131	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
132	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
133	A variant in FTO shows association with melanoma risk not due to BMI. Nature Genetics, 2013, 45, 428-432.	21.4	111
134	Association between putative functional variants in the <scp>PSMB</scp>9 gene and risk of melanoma â€“ reâ€analysis of published melanoma genomeâ€wide association studies. Pigment Cell and Melanoma Research, 2013, 26, 392-401.	3.3	5
135	Psychoâ€educational interventions for melanoma survivors: a systematic review. Psycho-Oncology, 2013, 22, 1444-1456.	2.3	29
136	VAN: an R package for identifying biologically perturbed networks via differential variability analysis. BMC Research Notes, 2013, 6, 430.	1.4	9
137	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
138	Association between functional polymorphisms in genes involved in the MAPK signaling pathways and cutaneous melanoma risk. Carcinogenesis, 2013, 34, 885-892.	2.8	10
139	Molecular biomarkers of prognosis in melanoma. Melanoma Research, 2013, 23, 423-425.	1.2	3
140	Identification of new prognostic biomarkers for Stage III metastatic melanoma patients. OncoImmunology, 2013, 2, e25564.	4.6	6
141	Molecular interaction networks for the analysis of human disease: Utility, limitations, and considerations. Proteomics, 2013, 13, 3393-3405.	2.2	17
142	Disturbed proteinâ€“protein interaction networks in metastatic melanoma are associated with worse prognosis and increased functional mutation burden. Pigment Cell and Melanoma Research, 2013, 26, 708-722.	3.3	12
143	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
144	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

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145	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
146	Review and Cross-Validation of Gene Expression Signatures and Melanoma Prognosis. Journal of Investigative Dermatology, 2012, 132, 274-283.	0.7	52
147	The COMPASs Study: Community Preferences for Prostate cAncer Screening. Protocol for a quantitative preference study: Figure 1. BMJ Open, 2012, 2, e000587.	1.9	4
148	Cellular blue naevus involving the urinary bladder. Pathology, 2012, 44, 664-668.	0.6	5
149	The nature and structure of psychological distress in people at high risk for melanoma: a factor analytic study. Psycho-Oncology, 2012, 21, 845-856.	2.3	7
150	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
151	A High-Throughput Panel for Identifying Clinically Relevant Mutation Profiles in Melanoma. Molecular Cancer Therapeutics, 2012, 11, 888-897.	4.1	45
152	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
153	Genome-wide association study identifies novel loci predisposing to cutaneous melanomaâ€. Human Molecular Genetics, 2011, 20, 5012-5023.	2.9	187
154	Genome-wide association study identifies three new melanoma susceptibility loci. Nature Genetics, 2011, 43, 1108-1113.	21.4	230
155	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
156	Early-life sun exposure and risk of melanoma before age 40Âyears. Cancer Causes and Control, 2011, 22, 885-897.	1.8	43
157	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
158	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
159	Selective Loss of Wild-Type p16INK4a Expression in Human Nevi. Journal of Investigative Dermatology, 2011, 131, 2329-2332.	0.7	9
160	Prognostic and Clinicopathologic Associations of Oncogenic BRAF in Metastatic Melanoma. Journal of Clinical Oncology, 2011, 29, 1239-1246.	1.6	942
161	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
162	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

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163	A novel recurrent mutation in MITF predisposes to familial and sporadic melanoma. Nature, 2011, 480, 99-103.	27.8	413
164	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. Nature Genetics, 2011, 43, 1114-1118.	21.4	140
165	An extended antibody microarray for surface profiling metastatic melanoma. Journal of Immunological Methods, 2010, 358, 23-34.	1.4	22
166	Familial concordance of breast cancer pathology as an indicator of genotype in multipleâ€case families. Genes Chromosomes and Cancer, 2010, 49, 1082-1094.	2.8	6
167	Predicting functional significance of cancer-associated p16INK4a mutations in CDKN2A. Human Mutation, 2010, 31, 692-701.	2.5	37
168	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
169	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
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