Julia A Newton-Bishop

List of Publications by Year
in descending order

191 papers	11,171 citations	28242 55 h-index	34964 98 g-index
202 all docs	202 docs citations	202 times ranked	12275 citing authors

#	Article	IF	Citations
1	ROR2 promotes epithelial-mesenchymal transition by hyperactivating ERK in melanoma. Journal of Cell Communication and Signaling, 2023, 17, 75-88.	1.8	3
2	Ulcerated melanoma: Systems biology evidence of inflammatory imbalance towards proâ€tumourigenicity. Pigment Cell and Melanoma Research, 2022, 35, 252-267.	1.5	4
3	Genes regulated by DNA methylation are involved in distinct phenotypes during melanoma progression and are prognostic factors for patients. Molecular Oncology, 2022, 16, 1913-1930.	2.1	1
4	Cross-cohort gut microbiome associations with immune checkpoint inhibitor response in advanced melanoma. Nature Medicine, 2022, 28, 535-544.	15.2	158
5	Defining novel causal SNPs and linked phenotypes at melanoma-associated loci. Human Molecular Genetics, 2022, 31, 2845-2856.	1.4	3
6	Multiple Primary Melanoma Incidence Trends Over Five Decades: A Nationwide Population-Based Study. Journal of the National Cancer Institute, 2021, 113, 318-328.	3.0	19
7	MX2 mediates establishment of interferon response profile, regulates XAF1, and can sensitize melanoma cells to targeted therapy. Cancer Medicine, 2021, 10, 2840-2854.	1.3	6
8	Birth cohort-specific trends of sun-related behaviors among individuals from an international consortium of melanoma-prone families. BMC Public Health, 2021, 21, 692.	1.2	4
9	Transcriptional signatures underlying dynamic phenotypic switching and novel disease biomarkers in a linear cellular model of melanoma progression. Neoplasia, 2021, 23, 439-455.	2.3	5
10	Inherited duplications of PPP2R3B predispose to nevi and melanoma via a C21orf91-driven proliferative phenotype. Genetics in Medicine, 2021, 23, 1636-1647.	1.1	5
11	Road to Metastasis: The TWEAK Pathway as a Discriminant between Metastasizing and Non-Metastasizing Thick Melanomas. International Journal of Molecular Sciences, 2021, 22, 10568.	1.8	0
12	Cooperation between melanoma cell states promotes metastasis through heterotypic cluster formation. Developmental Cell, 2021, 56, 2808-2825.e10.	3.1	37
13	Tumour gene expression signature in primary melanoma predicts long-term outcomes. Nature Communications, 2021, 12, 1137.	5.8	33
14	ROR2 has a protective role in melanoma by inhibiting Akt activity, cell-cycle progression, and proliferation. Journal of Biomedical Science, 2021, 28, 76.	2.6	8
15	Environmental Exposures Such as Smoking and Low Vitamin D Are Predictive of Poor Outcome in Cutaneous Melanoma rather than Other Deprivation Measures. Journal of Investigative Dermatology, 2020, 140, 327-337.e2.	0.3	14
16	MX 2 is a novel regulator of cell cycle in melanoma cells. Pigment Cell and Melanoma Research, 2020, 33, 446-457.	1.5	11
17	Study of the Female Sex Survival Advantage in Melanomaâ€"A Focus on X-Linked Epigenetic Regulators and Immune Responses in Two Cohorts. Cancers, 2020, 12, 2082.	1.7	16
18	Gene co-expression and histone modification signatures are associated with melanoma progression, epithelial-to-mesenchymal transition, and metastasis. Clinical Epigenetics, 2020, 12, 127.	1.8	9

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19	MC1R variants and cutaneous melanoma risk according to histological type, body site, and Breslow thickness: a pooled analysis from the M-SKIP project. Melanoma Research, 2020, 30, 500-510.	0.6	6
20	Factors Affecting Sentinel Node Metastasis in Thin (T1) Cutaneous Melanomas: Development and External Validation of a Predictive Nomogram. Journal of Clinical Oncology, 2020, 38, 1591-1601.	0.8	50
21	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
22	Gain-of-Function Genetic Alterations of G9a Drive Oncogenesis. Cancer Discovery, 2020, 10, 980-997.	7.7	44
23	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
24	Transcriptomic Analysis Reveals Prognostic Molecular Signatures of Stage I Melanoma. Clinical Cancer Research, 2019, 25, 7424-7435.	3.2	27
25	High-Resolution Copy Number Patterns From Clinically Relevant FFPE Material. Scientific Reports, 2019, 9, 8908.	1.6	6
26	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
27	Genetic and Environmental Determinants of Immune Response to Cutaneous Melanoma. Cancer Research, 2019, 79, 2684-2696.	0.4	45
28	Vitamin Dâ€“VDR Signaling Inhibits Wnt/Î²-Cateninâ€“Mediated Melanoma Progression and Promotes Antitumor Immunity. Cancer Research, 2019, 79, 5986-5998.	0.4	65
29	Application of Circulating Cell-Free Tumor DNA Profiles for Therapeutic Monitoring and Outcome Prediction in Genetically Heterogeneous Metastatic Melanoma. JCO Precision Oncology, 2019, 3, 1-10.	1.5	25
30	Association of the POT1 Germline Missense Variant p.I78T With Familial Melanoma. JAMA Dermatology, 2019, 155, 604.	2.0	34
31	ctDNA as a noninvasive monitoring tool in metastatic melanoma.. Journal of Clinical Oncology, 2019, 37, 9548-9548.	0.8	0
32	Comparative genomics reveals that loss of lunatic fringe (LFNG) promotes melanoma metastasis. Molecular Oncology, 2018, 12, 239-255.	2.1	20
33	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. Nature Communications, 2018, 9, 4774.	5.8	87
34	Comprehensive Study of the Clinical Phenotype of GermlineBAP1Variant-Carrying Families Worldwide. Journal of the National Cancer Institute, 2018, 110, 1328-1341.	3.0	164
35	Somatic cancer genetics in the UK: real-world data from phase I of the Cancer Research UK Stratified Medicine Programme. ESMO Open, 2018, 3, e000408.	2.0	4
36	25-hydroxyvitamin D serum levels in patients with high risk resected melanoma treated in an adjuvant bevacizumab trial. British Journal of Cancer, 2018, 119, 793-800.	2.9	11

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37	Amelanotic melanoma. BMJ: British Medical Journal, 2018, 360, k826.	2.4	9
38	MC1R variants as melanoma risk factors independent of at-risk phenotypic characteristics: a pooled analysis from the M-SKIP project. Cancer Management and Research, 2018, Volume 10, 1143-1154.	0.9	57
39	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.	0.3	52
40	Î²-Cateninâ€“mediated immune evasion pathway frequently operates in primary cutaneous melanomas. Journal of Clinical Investigation, 2018, 128, 2048-2063.	3.9	71
41	Abstract 5204:MYCexpression and smoking as drivers of failure of immune response to melanoma. , 2018, , .		0
42	Abstract 5205: Primary melanoma expression of the vitamin D receptor (VDR) is protective for melanoma survival and is associated with increased tumor immune response, decreased Wnt/B-catenin signaling and tumor proliferation. , 2018, , .		0
43	Abstract 228: Association analysis across different populations identifies 26 new cutaneous melanoma risk loci. , 2018, , .		0
44	Abstract 234: Understanding melanoma susceptibility through GWAS of risk phenotypes. , 2018, , .		0
45	Abstract 5372: The mutational landscape of primary cutaneous melanoma. , 2018, , .		0
46	A population-based analysis of germline BAP1 mutations in melanoma. Human Molecular Genetics, 2017, 26, ddw403.	1.4	31
47	Functional characterization of a multi-cancer risk locus on chr5p15.33 reveals regulation of TERT by ZNF148. Nature Communications, 2017, 8, 15034.	5.8	40
48	GermlineCDKN2A/P16INK4A mutations contribute to genetic determinism of sarcoma. Journal of Medical Genetics, 2017, 54, 607-612.	1.5	19
49	Rare Variant, Gene-Based Association Study of Hereditary Melanoma Using Whole-Exome Sequencing. Journal of the National Cancer Institute, 2017, 109, .	3.0	32
50	Tests to assist in the staging of cutaneous melanoma: a generic protocol. The Cochrane Library, 2017, , .	1.5	1
51	Germline Variation at CDKN2A and Associations with Nevus Phenotypes amongÂMembers of Melanoma Families. Journal of Investigative Dermatology, 2017, 137, 2606-2612.	0.3	18
52	A common intronic variant of PARP1 confers melanoma risk and mediates melanocyte growth via regulation of MITF. Nature Genetics, 2017, 49, 1326-1335.	9.4	51
53	Identification of a gene signature for discriminating metastatic from primary melanoma using a molecular interaction network approach. Scientific Reports, 2017, 7, 17314.	1.6	32
54	Which symptoms are linked to a delayed presentation among melanoma patients? A retrospective study. BMC Cancer, 2017, 17, 5.	1.1	5

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55	Genomic expression differences between cutaneous cells from red hair color individuals and black hair color individuals based on bioinformatic analysis. Oncotarget, 2017, 8, 11589-11599.	0.8	5
56	Abstract 4006: Immune cell profiles and Î²-catenin signaling in melanoma. , 2017, , .		1
57	Abstract 3717: New therapies for the treatment ofBRAF/NRASwild type melanoma. , 2017, , .		0
58	Abstract 1741: Whole-transcriptome characterisation ofNRASandBRAFmutated primary melanomas associated with immune cell infiltration signatures and differential survival benefit. , 2017, , .		0
59	Psychosocial, clinical and demographic features related to worry in patients with melanoma. Melanoma Research, 2016, 26, 497-504.	0.6	8
60	Diagnosis and treatment of melanoma. European consensus-based interdisciplinary guideline â€“ Update 2016. European Journal of Cancer, 2016, 63, 201-217.	1.3	330
61	Vitamin D, vitamin A, the primary melanoma transcriptome and survival. British Journal of Dermatology, 2016, 175, 30-34.	1.4	11
62	Histopathology of melanocytic lesions in a family with an inherited <scp>BAP1</scp> mutation. Journal of Cutaneous Pathology, 2016, 43, 287-289.	0.7	10
63	Association of Melanocortin-1 Receptor Variants with Pigmentary Traits in Humans: AÂPooled Analysis from the M-Skip Project. Journal of Investigative Dermatology, 2016, 136, 1914-1917.	0.3	16
64	The <scp>CDKN</scp>2A/p16<scp>^{INK}</scp>^{4a} 5â€²<scp>UTR</scp> sequence and translational regulation: impact of novel variants predisposing to melanoma. Pigment Cell and Melanoma Research, 2016, 29, 210-221.	1.5	9
65	Consensus of Melanoma Gene Expression Subtypes Converges on Biological Entities. Journal of Investigative Dermatology, 2016, 136, 2502-2505.	0.3	23
66	Wide versus narrow excision margins for high-risk, primary cutaneous melanomas: long-term follow-up of survival in a randomised trial. Lancet Oncology, The, 2016, 17, 184-192.	5.1	116
67	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
68	Loss-of-Function Mutations in the Cell-Cycle Control Gene CDKN2A Impact on Glucose Homeostasis in Humans. Diabetes, 2016, 65, 527-533.	0.3	38
69	Germline TERT promoter mutations are rare in familial melanoma. Familial Cancer, 2016, 15, 139-144.	0.9	51
70	MC1R variants increased the risk of sporadic cutaneous melanoma in darkerâ€pigmented <scp>C</scp>aucasians: A pooledâ€analysis from the Mâ€SKIP project. International Journal of Cancer, 2015, 136, 618-631.	2.3	92
71	25â€Hydroxyvitamin D₂/D₃ levels and factors associated with systemic inflammation and melanoma survival in the Leeds Melanoma Cohort. International Journal of Cancer, 2015, 136, 2890-2899.	2.3	61
72	Authors' reply to: High naevus counts confer a favourable prognosis in patients with melanoma. International Journal of Cancer, 2015, 137, 3008-3009.	2.3	0

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73	High nevus counts confer a favorable prognosis in melanoma patients. International Journal of Cancer, 2015, 137, 1691-1698.	2.3	37
74	Development and Validation of a Melanoma Risk Score Based on Pooled Data from 16 Caseâ€“Control Studies. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 817-824.	1.1	25
75	Histologic features of melanoma associated with CDKN2A genotype. Journal of the American Academy of Dermatology, 2015, 72, 496-507.e7.	0.6	19
76	MGMT promoter methylation is associated with temozolomide response and prolonged progressionâ€free survival in disseminated cutaneous melanoma. International Journal of Cancer, 2015, 136, 2844-2853.	2.3	45
77	The clinicopathological and gene expression patterns associated with ulceration of primary melanoma. Pigment Cell and Melanoma Research, 2015, 28, 94-104.	1.5	26
78	Nonsense Mutations in the Shelterin Complex Genes ACD and TERF2IP in Familial Melanoma. Journal of the National Cancer Institute, 2015, 107, .	3.0	134
79	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. Nature Genetics, 2015, 47, 987-995.	9.4	218
80	Fine mapping of genetic susceptibility loci for melanoma reveals a mixture of single variant and multiple variant regions. International Journal of Cancer, 2015, 136, 1351-1360.	2.3	30
81	Regressing Eruptive Disseminated Spitz Nevi. Pediatric Dermatology, 2015, 32, e181-3.	0.5	9
82	Melanoma: summary of NICE guidance. BMJ, The, 2015, 351, h3708.	3.0	23
83	Prognostic Significance of Promoter Hypermethylation and Diminished Gene Expression of SYNPO2 in Melanoma. Journal of Investigative Dermatology, 2015, 135, 2328-2331.	0.3	13
84	Independent replication of a melanoma subtype gene signature and evaluation of its prognostic value and biological correlates in a population cohort. Oncotarget, 2015, 6, 11683-11693.	0.8	44
85	Identification of a melanoma susceptibility locus and somatic mutation inTET2. Carcinogenesis, 2014, 35, 2097-2101.	1.3	41
86	Somatic BRAF and NRAS Mutations in Familial Melanomas with Known Germline CDKN2A Status: A GenoMEL Study. Journal of Investigative Dermatology, 2014, 134, 287-290.	0.3	18
87	Inherited variation in the PARP1 gene and survival from melanoma. International Journal of Cancer, 2014, 135, 1625-1633.	2.3	24
88	An inherited variant in the gene coding for vitamin <scp>D</scp>â€binding protein and survival from cutaneous melanoma: a <scp>B</scp>io<scp>G</scp>eno<scp>MEL</scp> study. Pigment Cell and Melanoma Research, 2014, 27, 234-243.	1.5	25
89	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.	0.6	45
90	The Effect on Melanoma Risk of Genes Previously Associated With Telomere Length. Journal of the National Cancer Institute, 2014, 106, .	3.0	109

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91	POT1 loss-of-function variants predispose to familial melanoma. Nature Genetics, 2014, 46, 478-481.	9.4	319
92	Primary Melanoma Tumors from CDKN2A Mutation Carriers Do Not Belong to a Distinct Molecular Subclass. Journal of Investigative Dermatology, 2014, 134, 3000-3003.	0.3	8
93	Targeting human apurinic/apyrimidinic endonuclease 1 (APE1) in phosphatase and tensin homolog (PTEN) deficient melanoma cells for personalized therapy. Oncotarget, 2014, 5, 3273-3286.	0.8	47
94	Abstract 20: POT1 mutations predispose to familial melanoma. , 2014, , .		0
95	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.	1.1	30
96	Do vitamin A serum levels moderate outcome or the protective effect of vitamin DÂon outcome from malignant melanoma?. Clinical Nutrition, 2013, 32, 1012-1016.	2.3	7
97	A variant in FTO shows association with melanoma risk not due to BMI. Nature Genetics, 2013, 45, 428-432.	9.4	111
98	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.	1.5	5
99	Melanoma prone families withCDK4germline mutation: phenotypic profile and associations withMC1Rvariants. Journal of Medical Genetics, 2013, 50, 264-270.	1.5	112
100	Association between functional polymorphisms in genes involved in the MAPK signaling pathways and cutaneous melanoma risk. Carcinogenesis, 2013, 34, 885-892.	1.3	10
101	Erythema Nodosumâ€“Like Panniculitis in Patients With Melanoma Treated With Vemurafenib. Journal of Clinical Oncology, 2013, 31, e320-e321.	0.8	29
102	Evaluation of <scp>PAX</scp>3 genetic variants and nevus number. Pigment Cell and Melanoma Research, 2013, 26, 666-676.	1.5	7
103	Response to P. Autier and M. Boniol regarding our article-Relationship between sunbed use and melanoma risk in a large case-control study in the United Kingdom. International Journal of Cancer, 2013, 132, 1960-1961.	2.3	1
104	Vitamin D and melanoma. Dermato-Endocrinology, 2013, 5, 121-129.	1.9	28
105	Skin Examination Behavior. Archives of Dermatology, 2012, 148, 1142.	1.7	36
106	Objective assessment of blood and lymphatic vessel invasion and association with macrophage infiltration in cutaneous melanoma. Modern Pathology, 2012, 25, 493-504.	2.9	105
107	Clinicopathologic Features of V600E and V600K Melanomaâ€”Letter. Clinical Cancer Research, 2012, 18, 6792-6792.	3.2	14
108	Authors' reply to Bayley and Cave. BMJ, The, 2012, 345, e5417-e5417.	3.0	0

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109	Nick Hayward. Pigment Cell and Melanoma Research, 2012, 25, 116-116.	1.5	0
110	Identification of differentially expressed genes in matched formalinâ€fixed paraffinâ€embedded primary and metastatic melanoma tumor pairs. Pigment Cell and Melanoma Research, 2012, 25, 284-286.	1.5	5
111	Inherited variants in the MC1R gene and survival from cutaneous melanoma: a BioGenoMEL study. Pigment Cell and Melanoma Research, 2012, 25, 384-394.	1.5	61
112	Perceptions of genetic research and testing among members of families with an increased risk of malignant melanoma. European Journal of Cancer, 2012, 48, 3052-3062.	1.3	17
113	Diagnosis and treatment of melanoma. European consensus-based interdisciplinary guideline â€“ Update 2012. European Journal of Cancer, 2012, 48, 2375-2390.	1.3	407
114	EORTC Melanoma Group achievements. European Journal of Cancer, Supplement, 2012, 10, 112-119.	2.2	0
115	Melanocortin-1 receptor, skin cancer and phenotypic characteristics (M-SKIP) project: study design and methods for pooling results of genetic epidemiological studies. BMC Medical Research Methodology, 2012, 12, 116.	1.4	12
116	Identifying melanomas in primary care: can we do better?. BMJ, The, 2012, 345, e4244-e4244.	3.0	6
117	Relationship between sunbed use and melanoma risk in a large caseâ€control study in the United Kingdom. International Journal of Cancer, 2012, 130, 3011-3013.	2.3	17
118	Genome-wide association study identifies three new melanoma susceptibility loci. Nature Genetics, 2011, 43, 1108-1113.	9.4	230
119	Melanoma and vitamin D. Molecular Oncology, 2011, 5, 197-214.	2.1	58
120	Relationship between sun exposure and melanoma risk for tumours in different body sites in a large case-control study in a temperate climate. European Journal of Cancer, 2011, 47, 732-741.	1.3	90
121	Infliximab in the treatment of a child with cutaneous granulomas associated with ataxia telangiectasia. Journal of the American Academy of Dermatology, 2011, 65, 676-677.	0.6	28
122	Pathway-Based Analysis of a Melanoma Genome-Wide Association Study: Analysis of Genes Related to Tumour-Immunosuppression. PLoS ONE, 2011, 6, e29451.	1.1	18
123	The determinants of periorbital skin ageing in participants of a melanoma caseâ€“control study in the U.K.. British Journal of Dermatology, 2011, 165, 1011-1021.	1.4	17
124	The determinants of serum vitamin D levels in participants in a melanoma caseâ€“control study living in a temperate climate. Cancer Causes and Control, 2011, 22, 1471-1482.	0.8	32
125	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.	1.5	41
126	Prognosis in Patients With Sentinel Nodeâ€“Positive Melanoma Is Accurately Defined by the Combined Rotterdam Tumor Load and Dewar Topography Criteria. Journal of Clinical Oncology, 2011, 29, 2206-2214.	0.8	195

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127	A novel recurrent mutation in MITF predisposes to familial and sporadic melanoma. Nature, 2011, 480, 99-103.	13.7	413
128	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. Nature Genetics, 2011, 43, 1114-1118.	9.4	140
129	Melanoma susceptibility genes. Melanoma Research, 2010, 20, 161-162.	0.6	5
130	Melanoma risk factors, perceived threat and intentional tanning: an international online survey. European Journal of Cancer Prevention, 2010, 19, 216-226.	0.6	47
131	IRF4 Variants Have Age-Specific Effects on Nevus Count and Predispose to Melanoma. American Journal of Human Genetics, 2010, 87, 6-16.	2.6	114
132	Deletion at chromosome arm 9p in relation to BRAF/NRAS mutations and prognostic significance for primary melanoma. Genes Chromosomes and Cancer, 2010, 49, 425-438.	1.5	46
133	Predictors of Sun Protection Behaviors and Severe Sunburn in an International Online Study. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2199-2210.	1.1	106
134	Patterns of Expression of DNA Repair Genes and Relapse From Melanoma. Clinical Cancer Research, 2010, 16, 5211-5221.	3.2	53
135	Melanocytic Nevi, Nevus Genes, and Melanoma Risk in a Large Case-Control Study in the United Kingdom. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2043-2054.	1.1	102
136	Reply to P.E. Hutchinson et al. Journal of Clinical Oncology, 2010, 28, e494-e495.	0.8	0
137	Diagnosis and treatment of melanoma: European consensus-based interdisciplinary guideline. European Journal of Cancer, 2010, 46, 270-283.	1.3	284
138	Laryngo-Onycho-Cutaneous Syndrome. Ophthalmology, 2010, 117, 1056-1056.e2.	2.5	7
139	Melanoma sentinel node biopsy and prediction models for relapse and overall survival. British Journal of Cancer, 2010, 103, 1229-1236.	2.9	54
140	Sun exposure and melanoma risk at different latitudes: a pooled analysis of 5700 cases and 7216 controls. International Journal of Epidemiology, 2009, 38, 814-830.	0.9	219
141	Gene Expression Profiling of Paraffin-Embedded Primary Melanoma Using the DASL Assay Identifies Increased Osteopontin Expression as Predictive of Reduced Relapse-Free Survival. Clinical Cancer Research, 2009, 15, 6939-6946.	3.2	93
142	Serum 25-Hydroxyvitamin D₃ Levels Are Associated With Breslow Thickness at Presentation and Survival From Melanoma. Journal of Clinical Oncology, 2009, 27, 5439-5444.	0.8	263
143	Cutaneous Melanoma During Pregnancy: Is the Controversy Over?. Journal of Clinical Oncology, 2009, 27, e11-e12.	0.8	22
144	A pooled analysis of melanocytic nevus phenotype and the risk of cutaneous melanoma at different latitudes. International Journal of Cancer, 2009, 124, 420-428.	2.3	84

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145	Overseas Sun Exposure, Nevus Counts, and Premature Skin Aging in Young English Women: A Population-Based Survey. Journal of Investigative Dermatology, 2009, 129, 50-59.	0.3	40
146	Genome-wide association study identifies variants at 9p21 and 22q13 associated with development of cutaneous nevi. Nature Genetics, 2009, 41, 915-919.	9.4	204
147	Genome-wide association study identifies three loci associated with melanoma risk. Nature Genetics, 2009, 41, 920-925.	9.4	422
148	Vitamin D receptor gene polymorphisms, serum 25-hydroxyvitamin D levels, and melanoma: UK caseâ€“control comparisons and a meta-analysis of published VDR data. European Journal of Cancer, 2009, 45, 3271-3281.	1.3	127
149	Selection criteria for genetic assessment of patients with familial melanoma. Journal of the American Academy of Dermatology, 2009, 61, 677.e1-677.e14.	0.6	154
150	The emergence of networks in human genome epidemiology: challenges and opportunities. , 2009, , 120-134.		0
151	Trends in prognostic factors and survival from cutaneous melanoma in Yorkshire, UK and New South Wales, Australia between 1993 and 2003. International Journal of Cancer, 2008, 123, 861-866.	2.3	43
152	Spontaneous involution of congenital melanocytic nevi of the scalp. Journal of the American Academy of Dermatology, 2008, 58, 508-511.	0.6	58
153	Environmental risk factors for relapse of melanoma. European Journal of Cancer, 2008, 44, 1717-1725.	1.3	18
154	Frequent p16-Independent Inactivation of p14ARF in Human Melanoma. Journal of the National Cancer Institute, 2008, 100, 784-795.	3.0	94
155	CDKN2A and CDK4 variants in Latvian melanoma patients: analysis of a clinic-based population. Melanoma Research, 2007, 17, 185-191.	0.6	34
156	The Emergence of Networks in Human Genome Epidemiology. Epidemiology, 2007, 18, 1-8.	1.2	102
157	Sun-Protective Behaviors in Families at Increased Risk of Melanoma. Journal of Investigative Dermatology, 2007, 127, 1343-1350.	0.3	14
158	Genetics: What Advice for Patients Who Present With a Family History of Melanoma?. Seminars in Oncology, 2007, 34, 452-459.	0.8	21
159	A road map for efficient and reliable human genome epidemiology. Nature Genetics, 2006, 38, 3-5.	9.4	244
160	A mutation hotspot at the p14ARF splice site. Oncogene, 2005, 24, 4604-4608.	2.6	70
161	The Effect of Sun Exposure in Determining Nevus Density in UK Adolescent Twins. Journal of Investigative Dermatology, 2005, 124, 56-62.	0.3	62
162	Intronic sequence variants of theCDKN2A gene in melanoma pedigrees. Genes Chromosomes and Cancer, 2005, 43, 128-136.	1.5	32

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163	Prevalence of 9p21 deletions in UK melanoma families. Genes Chromosomes and Cancer, 2005, 44, 292-300.	1.5	36
164	A Network of Investigator Networks in Human Genome Epidemiology. American Journal of Epidemiology, 2005, 162, 302-304.	1.6	104
165	No Evidence for BRAF as a Melanoma/Nevus Susceptibility Gene. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 913-918.	1.1	24
166	Malignant Melanoma in Pregnancy. Obstetrics and Gynecology Clinics of North America, 2005, 32, 559-568.	0.7	20
167	The genetics of susceptibility to cutaneous melanoma. Drugs of Today, 2005, 41, 193.	2.4	33
168	Effect of Pregnancy on Survival in Women With Cutaneous Malignant Melanoma. Journal of Clinical Oncology, 2004, 22, 4369-4375.	0.8	164
169	The Relationship Between the Epidermal Growth Factor (EGF) 5â€²UTR Variant A61G and Melanoma/Nevus Susceptibility. Journal of Investigative Dermatology, 2004, 123, 755-759.	0.3	39
170	An Assessment of a Variant of the DNA Repair Gene XRCC3 as a Possible Nevus or Melanoma Susceptibility Genotype. Journal of Investigative Dermatology, 2004, 122, 429-432.	0.3	25
171	A Quality-of-Life Study in High-Risk (Thicknessâ‰¥2 mm) Cutaneous Melanoma Patients in a Randomized Trial of 1-cm versus 3-cm Surgical Excision Margins. Journal of Investigative Dermatology Symposium Proceedings, 2004, 9, 152-159.	0.8	45
172	Surgical margins in cutaneous melanoma (2 cm versus 5 cm for lesions measuring less than 2.1-mm) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.0	4
173	Excision Margins in High-Risk Malignant Melanoma. New England Journal of Medicine, 2004, 350, 757-766.	13.9	424
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