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	Excision Margins in High-Risk Malignant Melanoma. New England Journal of Medicine, 2004, 350, 757-766.	13.9	424
2	Genome-wide association study identifies three loci associated with melanoma risk. Nature Genetics, 2009, 41, 920-925.	9.4	422
3	A novel recurrent mutation in MITF predisposes to familial and sporadic melanoma. Nature, 2011, 480, 99-103.	13.7	413
4	Diagnosis and treatment of melanoma. European consensus-based interdisciplinary guideline â€“ Update 2012. European Journal of Cancer, 2012, 48, 2375-2390.	1.3	407
5	Diagnosis and treatment of melanoma. European consensus-based interdisciplinary guideline â€“ Update 2016. European Journal of Cancer, 2016, 63, 201-217.	1.3	330
6	POT1 loss-of-function variants predispose to familial melanoma. Nature Genetics, 2014, 46, 478-481.	9.4	319
7	Diagnosis and treatment of melanoma: European consensus-based interdisciplinary guideline. European Journal of Cancer, 2010, 46, 270-283.	1.3	284
8	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
9	A road map for efficient and reliable human genome epidemiology. Nature Genetics, 2006, 38, 3-5.	9.4	244
10	Genome-wide association study identifies three new melanoma susceptibility loci. Nature Genetics, 2011, 43, 1108-1113.	9.4	230
11	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
12	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. Nature Genetics, 2015, 47, 987-995.	9.4	218
13	Counseling and DNA Testing for Individuals Perceived to Be Genetically Predisposed to Melanoma: A Consensus Statement of the Melanoma Genetics Consortium. Journal of Clinical Oncology, 1999, 17, 3245-3251.	0.8	209
14	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
15	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
16	Effect of Pregnancy on Survival in Women With Cutaneous Malignant Melanoma. Journal of Clinical Oncology, 2004, 22, 4369-4375.	0.8	164
17	Comprehensive Study of the Clinical Phenotype of GermlineBAP1Variant-Carrying Families Worldwide. Journal of the National Cancer Institute, 2018, 110, 1328-1341.	3.0	164
18	Cross-cohort gut microbiome associations with immune checkpoint inhibitor response in advanced melanoma. Nature Medicine, 2022, 28, 535-544.	15.2	158

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19	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
20	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. Nature Genetics, 2011, 43, 1114-1118.	9.4	140
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	Nonsense Mutations in the Shelterin Complex Genes ACD and TERF2IP in Familial Melanoma. Journal of the National Cancer Institute, 2015, 107, .	3.0	134
23	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
24	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
25	Naevi and pigmentary characteristics as risk factors for melanoma in a high-risk population: A case-control study in new South Wales, Australia. , 1996, 67, 485-491.		114
26	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
27	Heritability and Geneâ€“Environment Interactions for Melanocytic Nevus Density Examined in a U.K. Adolescent Twin Study. Journal of Investigative Dermatology, 2001, 117, 348-352.	0.3	112
28	Biallelic Mutations in p16 INK4a Confer Resistance to Ras- and Ets-Induced Senescence in Human Diploid Fibroblasts. Molecular and Cellular Biology, 2002, 22, 8135-8143.	1.1	112
29	Melanoma prone families withCDK4germline mutation: phenotypic profile and associations withMC1Rvariants. Journal of Medical Genetics, 2013, 50, 264-270.	1.5	112
30	A variant in FTO shows association with melanoma risk not due to BMI. Nature Genetics, 2013, 45, 428-432.	9.4	111
31	The Effect on Melanoma Risk of Genes Previously Associated With Telomere Length. Journal of the National Cancer Institute, 2014, 106, .	3.0	109
32	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
33	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
34	A Network of Investigator Networks in Human Genome Epidemiology. American Journal of Epidemiology, 2005, 162, 302-304.	1.6	104
35	Genotype/Phenotype and Penetrance Studies in Melanoma Families with Germline CDKN2A Mutations. Journal of Investigative Dermatology, 2000, 114, 28-33.	0.3	102
36	The Emergence of Networks in Human Genome Epidemiology. Epidemiology, 2007, 18, 1-8.	1.2	102

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37	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
38	Frequent p16-Independent Inactivation of p14ARF in Human Melanoma. Journal of the National Cancer Institute, 2008, 100, 784-795.	3.0	94
39	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
40	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
41	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
42	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. Nature Communications, 2018, 9, 4774.	5.8	87
43	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
44	UK guidelines for the management of cutaneous melanoma. Journal of Plastic, Reconstructive and Aesthetic Surgery, 2002, 55, 46-54.	1.1	80
45	Excision Margins in the Treatment of Primary Cutaneous Melanoma. Archives of Surgery, 2002, 137, 1101-5.	2.3	73
46	Î²-Cateninâ€“mediated immune evasion pathway frequently operates in primary cutaneous melanomas. Journal of Clinical Investigation, 2018, 128, 2048-2063.	3.9	71
47	A mutation hotspot at the p14ARF splice site. Oncogene, 2005, 24, 4604-4608.	2.6	70
48	Genetic heterogeneity in familial malignant melanoma. Human Molecular Genetics, 1994, 3, 2195-2200.	1.4	66
49	Vitamin Dâ€“VDR Signaling Inhibits Wnt/Î²-Cateninâ€“Mediated Melanoma Progression and Promotes Antitumor Immunity. Cancer Research, 2019, 79, 5986-5998.	0.4	65
50	The Effect of Sun Exposure in Determining Nevus Density in UK Adolescent Twins. Journal of Investigative Dermatology, 2005, 124, 56-62.	0.3	62
51	Haplotype analysis of two recurrentCDKN2A mutations in 10 melanoma families: Evidence for common founders and independent mutations. , 1998, 11, 424-431.		61
52	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
53	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
54	Risk of ocular melanoma in relation to cutaneous and IRIS naevi. International Journal of Cancer, 1995, 60, 622-626.	2.3	58

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55	Spontaneous involution of congenital melanocytic nevi of the scalp. Journal of the American Academy of Dermatology, 2008, 58, 508-511.	0.6	58
56	Melanoma and vitamin D. Molecular Oncology, 2011, 5, 197-214.	2.1	58
57	Mutation testing in melanoma families: INK4A, CDK4 and INK4D. British Journal of Cancer, 1999, 80, 295-300.	2.9	57
58	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
59	Melanoma sentinel node biopsy and prediction models for relapse and overall survival. British Journal of Cancer, 2010, 103, 1229-1236.	2.9	54
60	Patterns of Expression of DNA Repair Genes and Relapse From Melanoma. Clinical Cancer Research, 2010, 16, 5211-5221.	3.2	53
61	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
62	Germline TERT promoter mutations are rare in familial melanoma. Familial Cancer, 2016, 15, 139-144.	0.9	51
63	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
64	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
65	Melanoma risk factors, perceived threat and intentional tanning: an international online survey. European Journal of Cancer Prevention, 2010, 19, 216-226.	0.6	47
66	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
67	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
68	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
69	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
70	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
71	Genetic and Environmental Determinants of Immune Response to Cutaneous Melanoma. Cancer Research, 2019, 79, 2684-2696.	0.4	45
72	Gain-of-Function Genetic Alterations of G9a Drive Oncogenesis. Cancer Discovery, 2020, 10, 980-997.	7.7	44

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73	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
74	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
75	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
76	Identification of a melanoma susceptibility locus and somatic mutation inTET2. Carcinogenesis, 2014, 35, 2097-2101.	1.3	41
77	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
78	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
79	The Atypical-Mole Syndrome and Predisposition to Melanoma. New England Journal of Medicine, 1998, 339, 348-349.	13.9	39
80	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
81	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
82	High nevus counts confer a favorable prognosis in melanoma patients. International Journal of Cancer, 2015, 137, 1691-1698.	2.3	37
83	Cooperation between melanoma cell states promotes metastasis through heterotypic cluster formation. Developmental Cell, 2021, 56, 2808-2825.e10.	3.1	37
84	An Assessment of the CDKN2A Variant Ala148Thr as a Nevus/Melanoma Susceptibility Allele. Journal of Investigative Dermatology, 2002, 119, 961-965.	0.3	36
85	Prevalence of 9p21 deletions in UK melanoma families. Genes Chromosomes and Cancer, 2005, 44, 292-300.	1.5	36
86	Skin Examination Behavior. Archives of Dermatology, 2012, 148, 1142.	1.7	36
87	CDKN2A and CDK4 variants in Latvian melanoma patients: analysis of a clinic-based population. Melanoma Research, 2007, 17, 185-191.	0.6	34
88	Association of the POT1 Germline Missense Variant p.I78T With Familial Melanoma. JAMA Dermatology, 2019, 155, 604.	2.0	34
89	Tumour gene expression signature in primary melanoma predicts long-term outcomes. Nature Communications, 2021, 12, 1137.	5.8	33
90	The genetics of susceptibility to cutaneous melanoma. Drugs of Today, 2005, 41, 193.	2.4	33

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91	Intronic sequence variants of theCDKN2A gene in melanoma pedigrees. Genes Chromosomes and Cancer, 2005, 43, 128-136.	1.5	32
92	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
93	Rare Variant, Gene-Based Association Study of Hereditary Melanoma Using Whole-Exome Sequencing. Journal of the National Cancer Institute, 2017, 109, .	3.0	32
94	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
95	A population-based analysis of germline BAP1 mutations in melanoma. Human Molecular Genetics, 2017, 26, ddw403.	1.4	31
96	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
97	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
98	Erythema Nodosumâ€“Like Panniculitis in Patients With Melanoma Treated With Vemurafenib. Journal of Clinical Oncology, 2013, 31, e320-e321.	0.8	29
99	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
100	Vitamin D and melanoma. Dermato-Endocrinology, 2013, 5, 121-129.	1.9	28
101	Transcriptomic Analysis Reveals Prognostic Molecular Signatures of Stage I Melanoma. Clinical Cancer Research, 2019, 25, 7424-7435.	3.2	27
102	The clinicopathological and gene expression patterns associated with ulceration of primary melanoma. Pigment Cell and Melanoma Research, 2015, 28, 94-104.	1.5	26
103	Molecular pathology of melanoma. , 1997, 16, 141-154.		25
104	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
105	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
106	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
107	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
108	No Evidence for BRAF as a Melanoma/Nevus Susceptibility Gene. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 913-918.	1.1	24

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109	Inherited variation in the PARP1 gene and survival from melanoma. International Journal of Cancer, 2014, 135, 1625-1633.	2.3	24
110	Melanoma: summary of NICE guidance. BMJ, The, 2015, 351, h3708.	3.0	23
111	Consensus of Melanoma Gene Expression Subtypes Converges on Biological Entities. Journal of Investigative Dermatology, 2016, 136, 2502-2505.	0.3	23
112	Cutaneous Melanoma During Pregnancy: Is the Controversy Over?. Journal of Clinical Oncology, 2009, 27, e11-e12.	0.8	22
113	Genetics: What Advice for Patients Who Present With a Family History of Melanoma?. Seminars in Oncology, 2007, 34, 452-459.	0.8	21
114	Malignant Melanoma in Pregnancy. Obstetrics and Gynecology Clinics of North America, 2005, 32, 559-568.	0.7	20
115	Comparative genomics reveals that loss of lunatic fringe (LFNG) promotes melanoma metastasis. Molecular Oncology, 2018, 12, 239-255.	2.1	20
116	Histologic features of melanoma associated with CDKN2A genotype. Journal of the American Academy of Dermatology, 2015, 72, 496-507.e7.	0.6	19
117	GermlineCDKN2A/P16INK4A mutations contribute to genetic determinism of sarcoma. Journal of Medical Genetics, 2017, 54, 607-612.	1.5	19
118	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
119	Environmental risk factors for relapse of melanoma. European Journal of Cancer, 2008, 44, 1717-1725.	1.3	18
120	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
121	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
122	Germline Variation at CDKN2A and Associations with Nevus Phenotypes amongÂMembers of Melanoma Families. Journal of Investigative Dermatology, 2017, 137, 2606-2612.	0.3	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	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
125	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
126	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

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127	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
128	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
129	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
130	Sun-Protective Behaviors in Families at Increased Risk of Melanoma. Journal of Investigative Dermatology, 2007, 127, 1343-1350.	0.3	14
131	Clinicopathologic Features of V600E and V600K Melanomaâ€"Letter. Clinical Cancer Research, 2012, 18, 6792-6792.	3.2	14
132	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
133	Management of regional lymph nodes in patients with malignant melanoma: questionnaire survey of UK current practice. Journal of Plastic, Reconstructive and Aesthetic Surgery, 2002, 55, 372-375.	1.1	13
134	Prognostic Significance of Promoter Hypermethylation and Diminished Gene Expression of SYNPO2 in Melanoma. Journal of Investigative Dermatology, 2015, 135, 2328-2331.	0.3	13
135	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
136	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
137	Vitamin D, vitamin A, the primary melanoma transcriptome and survival. British Journal of Dermatology, 2016, 175, 30-34.	1.4	11
138	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
139	MX 2 is a novel regulator of cell cycle in melanoma cells. Pigment Cell and Melanoma Research, 2020, 33, 446-457.	1.5	11
140	Association between functional polymorphisms in genes involved in the MAPK signaling pathways and cutaneous melanoma risk. Carcinogenesis, 2013, 34, 885-892.	1.3	10
141	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
142	Regressing Eruptive Disseminated Spitz Nevi. Pediatric Dermatology, 2015, 32, e181-3.	0.5	9
143	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
144	Amelanotic melanoma. BMJ: British Medical Journal, 2018, 360, k826.	2.4	9

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145	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
146	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
147	Psychosocial, clinical and demographic features related to worry in patients with melanoma. Melanoma Research, 2016, 26, 497-504.	0.6	8
148	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
149	Laryngo-Onycho-Cutaneous Syndrome. Ophthalmology, 2010, 117, 1056-1056.e2.	2.5	7
150	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
151	Evaluation of <scp>PAX</scp>3 genetic variants and nevus number. Pigment Cell and Melanoma Research, 2013, 26, 666-676.	1.5	7
152	Identifying melanomas in primary care: can we do better?. BMJ, The, 2012, 345, e4244-e4244.	3.0	6
153	High-Resolution Copy Number Patterns From Clinically Relevant FFPE Material. Scientific Reports, 2019, 9, 8908.	1.6	6
154	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
155	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
156	Melanoma susceptibility genes. Melanoma Research, 2010, 20, 161-162.	0.6	5
157	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
158	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
159	Which symptoms are linked to a delayed presentation among melanoma patients? A retrospective study. BMC Cancer, 2017, 17, 5.	1.1	5
160	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
161	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
162	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

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163	Surgical margins in cutaneous melanoma (2 cm versus 5 cm for lesions measuring less than 2.1-mm) Tj ETQq1 1 0.784314 rgBT /Over	2.0	4
164	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
165	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
166	Ulcerated melanoma: Systems biology evidence of inflammatory imbalance towards proâ€tumourigenicity. Pigment Cell and Melanoma Research, 2022, 35, 252-267.	1.5	4
167	Defining novel causal SNPs and linked phenotypes at melanoma-associated loci. Human Molecular Genetics, 2022, 31, 2845-2856.	1.4	3
168	ROR2 promotes epithelial-mesenchymal transition by hyperactivating ERK in melanoma. Journal of Cell Communication and Signaling, 2023, 17, 75-88.	1.8	3
169	Melanoma. British Journal of Hospital Medicine, 2000, 61, 103-107.	0.3	1
170	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
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