

Julia A Newton-Bishop

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

175 papers	8,609 citations	50 h-index	87 g-index
202 ext. papers	9,994 ext. citations	8.3 avg, IF	5.06 L-index

#	Paper	IF	Citations
175	Genome-wide association study identifies three loci associated with melanoma risk. <i>Nature Genetics</i> , 2009 , 41, 920-5	36.3	360
174	Excision margins in high-risk malignant melanoma. <i>New England Journal of Medicine</i> , 2004 , 350, 757-66	59.2	341
173	A novel recurrent mutation in MITF predisposes to familial and sporadic melanoma. <i>Nature</i> , 2011 , 480, 99-103	50.4	335
172	Diagnosis and treatment of melanoma. European consensus-based interdisciplinary guideline - Update 2016. <i>European Journal of Cancer</i> , 2016 , 63, 201-17	7.5	265
171	POT1 loss-of-function variants predispose to familial melanoma. <i>Nature Genetics</i> , 2014 , 46, 478-481	36.3	241
170	Diagnosis and treatment of melanoma: European consensus-based interdisciplinary guideline. <i>European Journal of Cancer</i> , 2010 , 46, 270-83	7.5	230
169	Serum 25-hydroxyvitamin D3 levels are associated with breslow thickness at presentation and survival from melanoma. <i>Journal of Clinical Oncology</i> , 2009 , 27, 5439-44	2.2	212
168	Genome-wide association study identifies three new melanoma susceptibility loci. <i>Nature Genetics</i> , 2011 , 43, 1108-13	36.3	203
167	Diagnosis and treatment of melanoma. European consensus-based interdisciplinary guideline--Update 2012. <i>European Journal of Cancer</i> , 2012 , 48, 2375-90	7.5	199
166	A road map for efficient and reliable human genome epidemiology. <i>Nature Genetics</i> , 2006 , 38, 3-5	36.3	198
165	Sun exposure and melanoma risk at different latitudes: a pooled analysis of 5700 cases and 7216 controls. <i>International Journal of Epidemiology</i> , 2009 , 38, 814-30	7.8	187
164	Genome-wide association study identifies variants at 9p21 and 22q13 associated with development of cutaneous nevi. <i>Nature Genetics</i> , 2009 , 41, 915-9	36.3	186
163	Counseling and DNA testing for individuals perceived to be genetically predisposed to melanoma: A consensus statement of the Melanoma Genetics Consortium. <i>Journal of Clinical Oncology</i> , 1999 , 17, 3245-51	2.2	185
162	Prognosis in patients with sentinel node-positive melanoma is accurately defined by the combined Rotterdam tumor load and Dewar topography criteria. <i>Journal of Clinical Oncology</i> , 2011 , 29, 2206-14	2.2	164
161	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. <i>Nature Genetics</i> , 2015 , 47, 987-995	36.3	162
160	Effect of pregnancy on survival in women with cutaneous malignant melanoma. <i>Journal of Clinical Oncology</i> , 2004 , 22, 4369-75	2.2	130
159	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. <i>Nature Genetics</i> , 2011 , 43, 1114-8	36.3	126

158	Selection criteria for genetic assessment of patients with familial melanoma. <i>Journal of the American Academy of Dermatology</i> , 2009 , 61, 677.e1-14	4.5	115
157	Vitamin D receptor gene polymorphisms, serum 25-hydroxyvitamin D levels, and melanoma: UK case-control comparisons and a meta-analysis of published VDR data. <i>European Journal of Cancer</i> , 2009 , 45, 3271-81	7.5	108
156	Biallelic mutations in p16(INK4a) confer resistance to Ras- and Ets-induced senescence in human diploid fibroblasts. <i>Molecular and Cellular Biology</i> , 2002 , 22, 8135-43	4.8	108
155	Nonsense mutations in the shelterin complex genes ACD and TERF2IP in familial melanoma. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	102
154	IRF4 variants have age-specific effects on nevus count and predispose to melanoma. <i>American Journal of Human Genetics</i> , 2010 , 87, 6-16	11	100
153	The effect on melanoma risk of genes previously associated with telomere length. <i>Journal of the National Cancer Institute</i> , 2014 , 106,	9.7	97
152	Comprehensive Study of the Clinical Phenotype of Germline BAP1 Variant-Carrying Families Worldwide. <i>Journal of the National Cancer Institute</i> , 2018 , 110, 1328-1341	9.7	97
151	A variant in FTO shows association with melanoma risk not due to BMI. <i>Nature Genetics</i> , 2013 , 45, 428-32, 432e1	36.3	95
150	The emergence of networks in human genome epidemiology: challenges and opportunities. <i>Epidemiology</i> , 2007 , 18, 1-8	3.1	93
149	A network of investigator networks in human genome epidemiology. <i>American Journal of Epidemiology</i> , 2005 , 162, 302-4	3.8	92
148	Heritability and gene-environment interactions for melanocytic nevus density examined in a U.K. adolescent twin study. <i>Journal of Investigative Dermatology</i> , 2001 , 117, 348-52	4.3	92
147	Predictors of sun protection behaviors and severe sunburn in an international online study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010 , 19, 2199-210	4	91
146	Objective assessment of blood and lymphatic vessel invasion and association with macrophage infiltration in cutaneous melanoma. <i>Modern Pathology</i> , 2012 , 25, 493-504	9.8	91
145	Naevi and pigmentary characteristics as risk factors for melanoma in a high-risk population: a case-control study in New South Wales, Australia. <i>International Journal of Cancer</i> , 1996 , 67, 485-91	7.5	90
144	Melanoma prone families with CDK4 germline mutation: phenotypic profile and associations with MC1R variants. <i>Journal of Medical Genetics</i> , 2013 , 50, 264-70	5.8	89
143	Melanocytic nevi, nevus genes, and melanoma risk in a large case-control study in the United Kingdom. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010 , 19, 2043-54	4	83
142	Gene expression profiling of paraffin-embedded primary melanoma using the DASL assay identifies increased osteopontin expression as predictive of reduced relapse-free survival. <i>Clinical Cancer Research</i> , 2009 , 15, 6939-46	12.9	83
141	Frequent p16-independent inactivation of p14ARF in human melanoma. <i>Journal of the National Cancer Institute</i> , 2008 , 100, 784-95	9.7	83

140	Genotype/phenotype and penetrance studies in melanoma families with germline CDKN2A mutations. <i>Journal of Investigative Dermatology</i> , 2000 , 114, 28-33	4.3	83
139	Wide versus narrow excision margins for high-risk, primary cutaneous melanomas: long-term follow-up of survival in a randomised trial. <i>Lancet Oncology</i> , 2016 , 17, 184-192	21.7	82
138	Relationship between sun exposure and melanoma risk for tumours in different body sites in a large case-control study in a temperate climate. <i>European Journal of Cancer</i> , 2011 , 47, 732-41	7.5	80
137	Surgical excision methods for skin cancer involving the nail unit. <i>The Cochrane Library</i> ,	5.2	78
136	A pooled analysis of melanocytic nevus phenotype and the risk of cutaneous melanoma at different latitudes. <i>International Journal of Cancer</i> , 2009 , 124, 420-8	7.5	72
135	MC1R variants increased the risk of sporadic cutaneous melanoma in darker-pigmented Caucasians: a pooled-analysis from the M-SKIP project. <i>International Journal of Cancer</i> , 2015 , 136, 618-31	7.5	67
134	A mutation hotspot at the p14ARF splice site. <i>Oncogene</i> , 2005 , 24, 4604-8	9.2	67
133	Genetic heterogeneity in familial malignant melanoma. <i>Human Molecular Genetics</i> , 1994 , 3, 2195-200	5.6	63
132	UK guidelines for the management of cutaneous melanoma. <i>Journal of Plastic, Reconstructive and Aesthetic Surgery</i> , 2002 , 55, 46-54		60
131	Risk of ocular melanoma in relation to cutaneous and iris naevi. <i>International Journal of Cancer</i> , 1995 , 60, 622-6	7.5	55
130	The effect of sun exposure in determining nevus density in UK adolescent twins. <i>Journal of Investigative Dermatology</i> , 2005 , 124, 56-62	4.3	53
129	Excision margins in the treatment of primary cutaneous melanoma: a systematic review of randomized controlled trials comparing narrow vs wide excision. <i>Archives of Surgery</i> , 2002 , 137, 1101-5		52
128	Inherited variants in the MC1R gene and survival from cutaneous melanoma: a BioGenoMEL study. <i>Pigment Cell and Melanoma Research</i> , 2012 , 25, 384-94	4.5	50
127	Melanoma and vitamin D. <i>Molecular Oncology</i> , 2011 , 5, 197-214	7.9	50
126	Spontaneous involution of congenital melanocytic nevi of the scalp. <i>Journal of the American Academy of Dermatology</i> , 2008 , 58, 508-11	4.5	50
125	Haplotype analysis of two recurrent CDKN2A mutations in 10 melanoma families: evidence for common founders and independent mutations. <i>Human Mutation</i> , 1998 , 11, 424-31	4.7	49
124	Mutation testing in melanoma families: INK4A, CDK4 and INK4D. <i>British Journal of Cancer</i> , 1999 , 80, 295-300	8.0	49
123	Patterns of expression of DNA repair genes and relapse from melanoma. <i>Clinical Cancer Research</i> , 2010 , 16, 5211-21	12.9	48

122	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. <i>Nature Communications</i> , 2018 , 9, 4774	17.4	47
121	ECatenin-mediated immune evasion pathway frequently operates in primary cutaneous melanomas. <i>Journal of Clinical Investigation</i> , 2018 , 128, 2048-2063	15.9	46
120	Melanoma sentinel node biopsy and prediction models for relapse and overall survival. <i>British Journal of Cancer</i> , 2010 , 103, 1229-36	8.7	43
119	25-Hydroxyvitamin D2 /D3 levels and factors associated with systemic inflammation and melanoma survival in the Leeds Melanoma Cohort. <i>International Journal of Cancer</i> , 2015 , 136, 2890-9	7.5	42
118	Melanoma risk factors, perceived threat and intentional tanning: an international online survey. <i>European Journal of Cancer Prevention</i> , 2010 , 19, 216-26	2	41
117	Deletion at chromosome arm 9p in relation to BRAF/NRAS mutations and prognostic significance for primary melanoma. <i>Genes Chromosomes and Cancer</i> , 2010 , 49, 425-38	5	40
116	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. <i>Nature Genetics</i> , 2020 , 52, 494-504	36.3	39
115	MGMT promoter methylation is associated with temozolomide response and prolonged progression-free survival in disseminated cutaneous melanoma. <i>International Journal of Cancer</i> , 2015 , 136, 2844-53	7.5	39
114	Identification of a melanoma susceptibility locus and somatic mutation in TET2. <i>Carcinogenesis</i> , 2014 , 35, 2097-101	4.6	38
113	Trends in prognostic factors and survival from cutaneous melanoma in Yorkshire, UK and New South Wales, Australia between 1993 and 2003. <i>International Journal of Cancer</i> , 2008 , 123, 861-6	7.5	37
112	Targeting human apurinic/apyrimidinic endonuclease 1 (APE1) in phosphatase and tensin homolog (PTEN) deficient melanoma cells for personalized therapy. <i>Oncotarget</i> , 2014 , 5, 3273-86	3.3	37
111	Assessing the Incremental Contribution of Common Genomic Variants to Melanoma Risk Prediction in Two Population-Based Studies. <i>Journal of Investigative Dermatology</i> , 2018 , 138, 2617-2624	4.3	36
110	A common intronic variant of PARP1 confers melanoma risk and mediates melanocyte growth via regulation of MITF. <i>Nature Genetics</i> , 2017 , 49, 1326-1335	36.3	36
109	A quality-of-life study in high-risk (thickness \geq or 2 mm) cutaneous melanoma patients in a randomized trial of 1-cm versus 3-cm surgical excision margins. <i>Journal of Investigative Dermatology Symposium Proceedings</i> , 2004 , 9, 152-9	1.1	35
108	Prevalence of 9p21 deletions in UK melanoma families. <i>Genes Chromosomes and Cancer</i> , 2005 , 44, 292-300	30	35
107	The atypical-mole syndrome and predisposition to melanoma. <i>New England Journal of Medicine</i> , 1998 , 339, 348-9	59.2	35
106	Germline TERT promoter mutations are rare in familial melanoma. <i>Familial Cancer</i> , 2016 , 15, 139-44	3	34
105	Overseas sun exposure, nevus counts, and premature skin aging in young English women: a population-based survey. <i>Journal of Investigative Dermatology</i> , 2009 , 129, 50-9	4.3	34

104	The relationship between the epidermal growth factor (EGF) 5'UTR variant A61G and melanoma/nevus susceptibility. <i>Journal of Investigative Dermatology</i> , 2004 , 123, 755-9	4.3	34
103	Independent replication of a melanoma subtype gene signature and evaluation of its prognostic value and biological correlates in a population cohort. <i>Oncotarget</i> , 2015 , 6, 11683-93	3.3	34
102	variants as melanoma risk factors independent of at-risk phenotypic characteristics: a pooled analysis from the M-SKIP project. <i>Cancer Management and Research</i> , 2018 , 10, 1143-1154	3.6	32
101	CDKN2A and CDK4 variants in Latvian melanoma patients: analysis of a clinic-based population. <i>Melanoma Research</i> , 2007 , 17, 185-91	3.3	32
100	Genetic and Environmental Determinants of Immune Response to Cutaneous Melanoma. <i>Cancer Research</i> , 2019 , 79, 2684-2696	10.1	31
99	Prevalence and predictors of germline CDKN2A mutations for melanoma cases from Australia, Spain and the United Kingdom. <i>Hereditary Cancer in Clinical Practice</i> , 2014 , 12, 20	2.3	31
98	Melanoma risk for CDKN2A mutation carriers who are relatives of population-based case carriers in Australia and the UK. <i>Journal of Medical Genetics</i> , 2011 , 48, 266-72	5.8	30
97	The genetics of susceptibility to cutaneous melanoma. <i>Drugs of Today</i> , 2005 , 41, 193-203		30
96	An assessment of the CDKN2A variant Ala148Thr as a nevus/melanoma susceptibility allele. <i>Journal of Investigative Dermatology</i> , 2002 , 119, 961-5	4.3	29
95	Intronic sequence variants of the CDKN2A gene in melanoma pedigrees. <i>Genes Chromosomes and Cancer</i> , 2005 , 43, 128-36	5	29
94	Loss-of-Function Mutations in the Cell-Cycle Control Gene CDKN2A Impact on Glucose Homeostasis in Humans. <i>Diabetes</i> , 2016 , 65, 527-33	0.9	28
93	Skin examination behavior: the role of melanoma history, skin type, psychosocial factors, and region of residence in determining clinical and self-conducted skin examination. <i>Archives of Dermatology</i> , 2012 , 148, 1142-51		28
92	High nevus counts confer a favorable prognosis in melanoma patients. <i>International Journal of Cancer</i> , 2015 , 137, 1691-8	7.5	27
91	The determinants of serum vitamin D levels in participants in a melanoma case-control study living in a temperate climate. <i>Cancer Causes and Control</i> , 2011 , 22, 1471-82	2.8	27
90	Functional characterization of a multi-cancer risk locus on chr5p15.33 reveals regulation of TERT by ZNF148. <i>Nature Communications</i> , 2017 , 8, 15034	17.4	26
89	Fine mapping of genetic susceptibility loci for melanoma reveals a mixture of single variant and multiple variant regions. <i>International Journal of Cancer</i> , 2015 , 136, 1351-60	7.5	26
88	Factors Affecting Sentinel Node Metastasis in Thin (T1) Cutaneous Melanomas: Development and External Validation of a Predictive Nomogram. <i>Journal of Clinical Oncology</i> , 2020 , 38, 1591-1601	2.2	26
87	A population-based analysis of germline BAP1 mutations in melanoma. <i>Human Molecular Genetics</i> , 2017 , 26, 717-728	5.6	24

86	MC1R genotype as a predictor of early-onset melanoma, compared with self-reported and physician-measured traditional risk factors: an Australian case-control-family study. <i>BMC Cancer</i> , 2013 , 13, 406	4.8	24
85	The clinicopathological and gene expression patterns associated with ulceration of primary melanoma. <i>Pigment Cell and Melanoma Research</i> , 2015 , 28, 94-104	4.5	23
84	Erythema nodosum-like panniculitis in patients with melanoma treated with vemurafenib. <i>Journal of Clinical Oncology</i> , 2013 , 31, e320-1	2.2	23
83	Molecular pathology of melanoma. <i>Cancer and Metastasis Reviews</i> , 1997 , 16, 141-54	9.6	23
82	No Evidence for BRAF as a melanoma/nevus susceptibility gene. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2005 , 14, 913-8	4	23
81	Vitamin D-VDR Signaling Inhibits Wnt/ECatenin-Mediated Melanoma Progression and Promotes Antitumor Immunity. <i>Cancer Research</i> , 2019 , 79, 5986-5998	10.1	23
80	Identification of a gene signature for discriminating metastatic from primary melanoma using a molecular interaction network approach. <i>Scientific Reports</i> , 2017 , 7, 17314	4.9	22
79	Inherited variation in the PARP1 gene and survival from melanoma. <i>International Journal of Cancer</i> , 2014 , 135, 1625-33	7.5	22
78	An inherited variant in the gene coding for vitamin D-binding protein and survival from cutaneous melanoma: a BioGenoMEL study. <i>Pigment Cell and Melanoma Research</i> , 2014 , 27, 234-43	4.5	21
77	Infliximab in the treatment of a child with cutaneous granulomas associated with ataxia telangiectasia. <i>Journal of the American Academy of Dermatology</i> , 2011 , 65, 676-677	4.5	21
76	An assessment of a variant of the DNA repair gene XRCC3 as a possible nevus or melanoma susceptibility genotype. <i>Journal of Investigative Dermatology</i> , 2004 , 122, 429-32	4.3	21
75	Vitamin D and melanoma. <i>Dermato-Endocrinology</i> , 2013 , 5, 121-9		20
74	Genetics: what advice for patients who present with a family history of melanoma?. <i>Seminars in Oncology</i> , 2007 , 34, 452-9	5.5	20
73	Consensus of Melanoma Gene Expression Subtypes Converges on Biological Entities. <i>Journal of Investigative Dermatology</i> , 2016 , 136, 2502-2505	4.3	18
72	Development and validation of a melanoma risk score based on pooled data from 16 case-control studies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 817-24	4	18
71	Cutaneous melanoma during pregnancy: is the controversy over?. <i>Journal of Clinical Oncology</i> , 2009 , 27, e11-2; author reply e13-4	2.2	17
70	Gain-of-Function Genetic Alterations of G9a Drive Oncogenesis. <i>Cancer Discovery</i> , 2020 , 10, 980-997	24.4	17
69	Rare Variant, Gene-Based Association Study of Hereditary Melanoma Using Whole-Exome Sequencing. <i>Journal of the National Cancer Institute</i> , 2017 , 109,	9.7	16

68	Transcriptomic Analysis Reveals Prognostic Molecular Signatures of Stage I Melanoma. <i>Clinical Cancer Research</i> , 2019 , 25, 7424-7435	12.9	16
67	Melanoma: summary of NICE guidance. <i>BMJ, The</i> , 2015 , 351, h3708	5.9	16
66	Histologic features of melanoma associated with CDKN2A genotype. <i>Journal of the American Academy of Dermatology</i> , 2015 , 72, 496-507.e7	4.5	16
65	Pathway-based analysis of a melanoma genome-wide association study: analysis of genes related to tumour-immunosuppression. <i>PLoS ONE</i> , 2011 , 6, e29451	3.7	16
64	Somatic BRAF and NRAS mutations in familial melanomas with known germline CDKN2A status: a GenoMEL study. <i>Journal of Investigative Dermatology</i> , 2014 , 134, 287-290	4.3	15
63	Malignant melanoma in pregnancy. <i>Obstetrics and Gynecology Clinics of North America</i> , 2005 , 32, 559-68	3.3	15
62	Association of the POT1 Germline Missense Variant p.I78T With Familial Melanoma. <i>JAMA Dermatology</i> , 2019 , 155, 604-609	5.1	15
61	Germline /P16INK4A mutations contribute to genetic determinism of sarcoma. <i>Journal of Medical Genetics</i> , 2017 , 54, 607-612	5.8	14
60	Perceptions of genetic research and testing among members of families with an increased risk of malignant melanoma. <i>European Journal of Cancer</i> , 2012 , 48, 3052-62	7.5	14
59	Clinicopathologic features of V600E and V600K melanoma--letter. <i>Clinical Cancer Research</i> , 2012 , 18, 6792; authorB reply p. 6793	12.9	14
58	Cross-cohort gut microbiome associations with immune checkpoint inhibitor response in advanced melanoma.. <i>Nature Medicine</i> , 2022 ,	50.5	14
57	The determinants of periorbital skin ageing in participants of a melanoma case-control study in the U.K. <i>British Journal of Dermatology</i> , 2011 , 165, 1011-21	4	13
56	Environmental risk factors for relapse of melanoma. <i>European Journal of Cancer</i> , 2008 , 44, 1717-25	7.5	13
55	Sun-protective behaviors in families at increased risk of melanoma. <i>Journal of Investigative Dermatology</i> , 2007 , 127, 1343-50	4.3	13
54	Association of Melanocortin-1 Receptor Variants with Pigmentary Traits in Humans: A Pooled Analysis from the M-Skip Project. <i>Journal of Investigative Dermatology</i> , 2016 , 136, 1914-1917	4.3	12
53	Relationship between sunbed use and melanoma risk in a large case-control study in the United Kingdom. <i>International Journal of Cancer</i> , 2012 , 130, 3011-3	7.5	12
52	Comparative genomics reveals that loss of lunatic fringe (LFNG) promotes melanoma metastasis. <i>Molecular Oncology</i> , 2018 , 12, 239-255	7.9	12
51	Prognostic Significance of Promoter Hypermethylation and Diminished Gene Expression of SYNPO2 in Melanoma. <i>Journal of Investigative Dermatology</i> , 2015 , 135, 2328-2331	4.3	10

50	Germline Variation at CDKN2A and Associations with Nevus Phenotypes among Members of Melanoma Families. <i>Journal of Investigative Dermatology</i> , 2017 , 137, 2606-2612	4.3	10
49	Melanocortin-1 receptor, skin cancer and phenotypic characteristics (M-SKIP) project: study design and methods for pooling results of genetic epidemiological studies. <i>BMC Medical Research Methodology</i> , 2012 , 12, 116	4.7	10
48	Management of regional lymph nodes in patients with malignant melanoma: questionnaire survey of UK current practice. <i>Journal of Plastic, Reconstructive and Aesthetic Surgery</i> , 2002 , 55, 372-5		10
47	Application of Circulating Cell-Free Tumor DNA Profiles for Therapeutic Monitoring and Outcome Prediction in Genetically Heterogeneous Metastatic Melanoma. <i>JCO Precision Oncology</i> , 2020 , 3,	3.6	10
46	Phenotypic and Histopathological Tumor Characteristics According to CDKN2A Mutation Status among Affected Members of Melanoma Families. <i>Journal of Investigative Dermatology</i> , 2016 , 136, 1066-1069	4.3	9
45	Estimating CDKN2A mutation carrier probability among global familial melanoma cases using GenoMELPREDICT. <i>Journal of the American Academy of Dermatology</i> , 2019 , 81, 386-394	4.5	9
44	MC1R variants in childhood and adolescent melanoma: a retrospective pooled analysis of a multicentre cohort. <i>The Lancet Child and Adolescent Health</i> , 2019 , 3, 332-342	14.5	8
43	The CDKN2A/p16(INK) (4a) 5'UTR sequence and translational regulation: impact of novel variants predisposing to melanoma. <i>Pigment Cell and Melanoma Research</i> , 2016 , 29, 210-21	4.5	8
42	25-hydroxyvitamin D serum levels in patients with high risk resected melanoma treated in an adjuvant bevacizumab trial. <i>British Journal of Cancer</i> , 2018 , 119, 793-800	8.7	8
41	Histopathology of melanocytic lesions in a family with an inherited BAP1 mutation. <i>Journal of Cutaneous Pathology</i> , 2016 , 43, 287-9	1.7	8
40	Study of the Female Sex Survival Advantage in Melanoma-A Focus on X-Linked Epigenetic Regulators and Immune Responses in Two Cohorts. <i>Cancers</i> , 2020 , 12,	6.6	7
39	Environmental Exposures Such as Smoking and Low Vitamin D Are Predictive of Poor Outcome in Cutaneous Melanoma rather than Other Deprivation Measures. <i>Journal of Investigative Dermatology</i> , 2020 , 140, 327-337.e2	4.3	7
38	Do vitamin A serum levels moderate outcome or the protective effect of vitamin D on outcome from malignant melanoma?. <i>Clinical Nutrition</i> , 2013 , 32, 1012-6	5.9	6
37	Association between functional polymorphisms in genes involved in the MAPK signaling pathways and cutaneous melanoma risk. <i>Carcinogenesis</i> , 2013 , 34, 885-92	4.6	6
36	Laryngo-onycho-cutaneous syndrome. <i>Ophthalmology</i> , 2010 , 117, 1056-1056.e2	7.3	6
35	MX 2 is a novel regulator of cell cycle in melanoma cells. <i>Pigment Cell and Melanoma Research</i> , 2020 , 33, 446-457	4.5	6
34	Psychosocial, clinical and demographic features related to worry in patients with melanoma. <i>Melanoma Research</i> , 2016 , 26, 497-504	3.3	6
33	Vitamin D, vitamin A, the primary melanoma transcriptome and survival. <i>British Journal of Dermatology</i> , 2016 , 175 Suppl 2, 30-34	4	6

32	Multiple Primary Melanoma Incidence Trends Over Five Decades: A Nationwide Population-Based Study. <i>Journal of the National Cancer Institute</i> , 2021 , 113, 318-328	9.7	6
31	Regressing Eruptive Disseminated Spitz Nevus. <i>Pediatric Dermatology</i> , 2015 , 32, e181-3	1.9	5
30	Amelanotic melanoma. <i>BMJ, The</i> , 2018 , 360, k826	5.9	5
29	Primary melanoma tumors from CDKN2A mutation carriers do not belong to a distinct molecular subclass. <i>Journal of Investigative Dermatology</i> , 2014 , 134, 3000-3003	4.3	5
28	Identification of differentially expressed genes in matched formalin-fixed paraffin-embedded primary and metastatic melanoma tumor pairs. <i>Pigment Cell and Melanoma Research</i> , 2012 , 25, 284-6	4.5	5
27	Evaluation of PAX3 genetic variants and nevus number. <i>Pigment Cell and Melanoma Research</i> , 2013 , 26, 666-76	4.5	5
26	Genomic expression differences between cutaneous cells from red hair color individuals and black hair color individuals based on bioinformatic analysis. <i>Oncotarget</i> , 2017 , 8, 11589-11599	3.3	5
25	Tumour gene expression signature in primary melanoma predicts long-term outcomes. <i>Nature Communications</i> , 2021 , 12, 1137	17.4	5
24	High-Resolution Copy Number Patterns From Clinically Relevant FFPE Material. <i>Scientific Reports</i> , 2019 , 9, 8908	4.9	4
23	Which symptoms are linked to a delayed presentation among melanoma patients? A retrospective study. <i>BMC Cancer</i> , 2017 , 17, 5	4.8	4
22	Association between putative functional variants in the PSMB9 gene and risk of melanoma—re-analysis of published melanoma genome-wide association studies. <i>Pigment Cell and Melanoma Research</i> , 2013 , 26, 392-401	4.5	4
21	Cooperation between melanoma cell states promotes metastasis through heterotypic cluster formation. <i>Developmental Cell</i> , 2021 , 56, 2808-2825.e10	10.2	4
20	ROR2 has a protective role in melanoma by inhibiting Akt activity, cell-cycle progression, and proliferation. <i>Journal of Biomedical Science</i> , 2021 , 28, 76	13.3	3
19	Surgical margins in cutaneous melanoma (2 cm versus 5 cm for lesions measuring less than 2.1-mm thick). <i>Cancer</i> , 2004 , 100, 433-4; author reply 434	6.4	2
18	Tumour gene expression signature in primary melanoma predicts long-term outcomes: A prospective multicentre study		2
17	Cell state diversity promotes metastasis through heterotypic cluster formation in melanoma		2
16	Gene co-expression and histone modification signatures are associated with melanoma progression, epithelial-to-mesenchymal transition, and metastasis. <i>Clinical Epigenetics</i> , 2020 , 12, 127	7.7	2
15	MC1R variants and cutaneous melanoma risk according to histological type, body site, and Breslow thickness: a pooled analysis from the M-SKIP project. <i>Melanoma Research</i> , 2020 , 30, 500-510	3.3	2

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8	MX2 mediates establishment of interferon response profile, regulates XAF1, and can sensitize melanoma cells to targeted therapy. <i>Cancer Medicine</i> , 2021 , 10, 2840-2854	4.8	0
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