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List of Publications by Year
in descending order

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132 papers	8,270 citations	71102 41 h-index	49909 87 g-index
135 all docs	135 docs citations	135 times ranked	8635 citing authors

#	Article	IF	Citations
1	Geographical Variation in the Penetrance of CDKN2A Mutations for Melanoma. Journal of the National Cancer Institute, 2002, 94, 894-903.	6.3	435
2	Genome-wide association study identifies three loci associated with melanoma risk. Nature Genetics, 2009, 41, 920-925.	21.4	422
3	High-risk Melanoma Susceptibility Genes and Pancreatic Cancer, Neural System Tumors, and Uveal Melanoma across GenoMEL. Cancer Research, 2006, 66, 9818-9828.	0.9	373
4	Risk of developing pancreatic cancer in families with familial atypical multiple mole melanoma associated with a specific 19 deletion ofp16 (p16-Leiden). International Journal of Cancer, 2000, 87, 809-811.	5.1	362
5	Melanocortin 1 Receptor (MC1R) Gene Variants are Associated with an Increased Risk for Cutaneous Melanoma Which is Largely Independent of Skin Type and Hair Color. Journal of Investigative Dermatology, 2001, 117, 294-300.	0.7	351
6	Features associated with germline CDKN2A mutations: a GenoMEL study of melanoma-prone families from three continents. Journal of Medical Genetics, 2006, 44, 99-106.	3.2	350
7	POT1 loss-of-function variants predispose to familial melanoma. Nature Genetics, 2014, 46, 478-481.	21.4	319
8	Homozygotes for CDKN2 (p16) germline mutation in Dutch familial melanoma kindreds. Nature Genetics, 1995, 10, 351-353.	21.4	288
9	A road map for efficient and reliable human genome epidemiology. Nature Genetics, 2006, 38, 3-5.	21.4	244
10	Genome-wide association study identifies three new melanoma susceptibility loci. Nature Genetics, 2011, 43, 1108-1113.	21.4	230
11	Melanocortin-1 Receptor Gene Variants Determine the Risk of Nonmelanoma Skin Cancer Independently of Fair Skin and Red Hair. American Journal of Human Genetics, 2001, 68, 884-894.	6.2	221
12	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.	1.9	219
13	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. Nature Genetics, 2015, 47, 987-995.	21.4	218
14	Common sequence variants on 20q11.22 confer melanoma susceptibility. Nature Genetics, 2008, 40, 838-840.	21.4	209
15	INK4a-deficient human diploid fibroblasts are resistant to RAS-induced senescence. EMBO Journal, 2002, 21, 2936-2945.	7.8	173
16	Melanocortin-1 Receptor Variant R151C Modifies Melanoma Risk in Dutch Families with Melanoma. American Journal of Human Genetics, 2001, 69, 774-779.	6.2	162
17	Increased Risk of Cancer Other Than Melanoma in CDKN2A Founder Mutation (p16-Leiden)-Positive Melanoma Families. Clinical Cancer Research, 2008, 14, 7151-7157.	7.0	161
18	Magnetic Resonance Imaging Surveillance Detects Early-Stage Pancreatic Cancer in Carriers of a p16-Leiden Mutation. Gastroenterology, 2011, 140, 850-856.	1.3	148

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19	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. Nature Genetics, 2011, 43, 1114-1118.	21.4	140
20	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
21	Nonsense Mutations in the Shelterin Complex Genes ACD and TERF2IP in Familial Melanoma. Journal of the National Cancer Institute, 2015, 107, .	6.3	134
22	Localization of a Novel Melanoma Susceptibility Locus to 1p22. American Journal of Human Genetics, 2003, 73, 301-313.	6.2	113
23	A variant in FTO shows association with melanoma risk not due to BMI. Nature Genetics, 2013, 45, 428-432.	21.4	111
24	The Effect on Melanoma Risk of Genes Previously Associated With Telomere Length. Journal of the National Cancer Institute, 2014, 106, .	6.3	109
25	Predictors of Sun Protection Behaviors and Severe Sunburn in an International Online Study. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2199-2210.	2.5	106
26	The Emergence of Networks in Human Genome Epidemiology. Epidemiology, 2007, 18, 1-8.	2.7	102
27	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.	5.1	92
28	Expression profiling reveals that methylation of TIMP3 is involved in uveal melanoma development. International Journal of Cancer, 2003, 106, 472-479.	5.1	86
29	A pooled analysis of melanocytic nevus phenotype and the risk of cutaneous melanoma at different latitudes. International Journal of Cancer, 2009, 124, 420-428.	5.1	84
30	A mutation hotspot at the p14ARF splice site. Oncogene, 2005, 24, 4604-4608.	5.9	70
31	Aberrant DNA Methylation in Cutaneous Malignancies. Seminars in Oncology, 2005, 32, 479-487.	2.2	69
32	Epigenetic Inactivation of RASSF1a in Uveal Melanoma. , 2007, 48, 486.		67
33	Risk of developing pancreatic cancer in families with familial atypical multiple mole melanoma associated with a specific 19 deletion of p16 p16Leiden. International Journal of Cancer, 2000, 87, 809-811.	5.1	67
34	PCR-based microsatellite polymorphisms in the detection of loss of heterozygosity in fresh and archival tumour tissue. British Journal of Cancer, 1993, 68, 308-313.	6.4	63
35	Haplotype analysis of two recurrentCDKN2A mutations in 10 melanoma families: Evidence for common founders and independent mutations. , 1998, 11, 424-431.		61
36	Inherited variants in the MC1R gene and survival from cutaneous melanoma: a BioGenoMEL study. Pigment Cell and Melanoma Research, 2012, 25, 384-394.	3.3	61

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37	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.	1.9	57
38	Localization of the 9p Melanoma Susceptibility Locus (MLM) to a 2-cM Region between D9S736 and D9S171. Genomics, 1994, 23, 265-268.	2.9	55
39	Genomeâ€wide promoter methylation analysis identifies epigenetic silencing of <scp>MAPK</scp>13 in primary cutaneous melanoma. Pigment Cell and Melanoma Research, 2013, 26, 542-554.	3.3	52
40	Germline TERT promoter mutations are rare in familial melanoma. Familial Cancer, 2016, 15, 139-144.	1.9	51
41	Melanoma risk factors, perceived threat and intentional tanning: an international online survey. European Journal of Cancer Prevention, 2010, 19, 216-226.	1.3	47
42	Clinical and histologic characteristics of malignant melanoma in families with a germline mutation in CDKN2A. Journal of the American Academy of Dermatology, 2011, 65, 281-288.	1.2	45
43	Affected members of melanoma-prone families with linkage to 9p21 but lacking mutations in CDKN2A do not harbor mutations in the coding regions of either CDKN2B or p19ARF. Genes Chromosomes and Cancer, 1997, 19, 52-54.	2.8	43
44	Epigenetic Regulation IdentifiesRASEFas a Tumor-Suppressor Gene in Uveal Melanoma. , 2008, 49, 1291.		43
45	Excess Cancer Mortality in Six Dutch Pedigrees with the Familial Atypical Multiple Mole-Melanoma Syndrome from 1830 to 1994. Journal of Investigative Dermatology, 1998, 110, 788-792.	0.7	42
46	Cutaneous squamous cell carcinoma andp53 codon 72 polymorphism: A need for screening?. Molecular Carcinogenesis, 2001, 30, 56-61.	2.7	41
47	Familial melanoma: a complex disorder leading to controversy on DNA testing. Familial Cancer, 2003, 2, 109-116.	1.9	41
48	Pyrophosphorolysis DetectsB-RAFMutations in Primary Uveal Melanoma. , 2008, 49, 23.		41
49	Promoter CpG Island Hypermethylation in Dysplastic Nevus and Melanoma: CLDN11 as an Epigenetic Biomarker for Malignancy. Journal of Investigative Dermatology, 2014, 134, 2957-2966.	0.7	38
50	Infrequent CDKN2 (MTS1/p16) gene alterations in human primary breast cancer. British Journal of Cancer, 1995, 72, 964-967.	6.4	36
51	Skin Examination Behavior. Archives of Dermatology, 2012, 148, 1142.	1.4	36
52	Gene-specific fluorescence in-situ hybridization analysis on tissue microarray to refine the region of chromosome 20q amplification in melanoma. Melanoma Research, 2007, 17, 37-41.	1.2	33
53	Multigene panel sequencing of established and candidate melanoma susceptibility genes in a large cohort of Dutch nonâ€CDKN2A/CDK4 melanoma families. International Journal of Cancer, 2019, 144, 2453-2464.	5.1	33
54	Proteomic Analysis of Uveal Melanoma Reveals Novel Potential Markers Involved in Tumor Progression. , 2006, 47, 786.		32

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55	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.	5.1	30
56	From sporadic atypical nevi to familial melanoma: Risk analysis for melanoma in sporadic atypical nevus patients. Journal of the American Academy of Dermatology, 2007, 56, 748-752.	1.2	28
57	Genetic Linkage Between the Collagen VII (COL7A1) Gene and the Autosomal Dominant Form of Dystrophic Epidermolysis Bullosa in Two Dutch Kindreds. Journal of Investigative Dermatology, 1992, 99, 528-530.	0.7	27
58	Risk of cutaneous malignant melanoma in patients with nonfamilial atypical nevi from a pigmented lesions clinic. Journal of the American Academy of Dermatology, 1999, 40, 686-693.	1.2	27
59	A comparison of CDKN2A mutation detection within the Melanoma Genetics Consortium (GenoMEL). European Journal of Cancer, 2008, 44, 1269-1274.	2.8	26
60	The Dutch FAMMM family material: Clinical and genetic data. Cytogenetic and Genome Research, 1992, 59, 161-164.	1.1	25
61	Genetic testing in familial melanoma: uptake and implications. Psycho-Oncology, 2008, 17, 790-796.	2.3	25
62	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.	3.3	25
63	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.	2.5	25
64	Increased p21-activated kinase-1 expression is associated with invasive potential in uveal melanoma. Melanoma Research, 2006, 16, 285-296.	1.2	24
65	Multiple rare variants in high-risk pancreatic cancer-related genes may increase risk for pancreatic cancer in a subset of patients with and without germline CDKN2A mutations. Human Genetics, 2016, 135, 1241-1249.	3.8	24
66	Telomere length and survival in primary cutaneous melanoma patients. Scientific Reports, 2018, 8, 10947.	3.3	23
67	Pancreatic carcinoma in carriers of a specific 19 base pair deletion of CDKN2A/p16 (p16-leiden). Clinical Cancer Research, 2003, 9, 3598-605.	7.0	22
68	Genetics of Seven Dutch Familial Atypical Multiple Mole-Melanoma Syndrome Families: A Review of Linkage Results Including Chromosomes 1 and 9. Journal of Investigative Dermatology, 1994, 103, S122-S125.	0.7	21
69	Genetics: What Advice for Patients Who Present With a Family History of Melanoma?. Seminars in Oncology, 2007, 34, 452-459.	2.2	21
70	Homozygous germline mutation of CDKN2A/p16 and glucose-6-phosphate dehydrogenase deficiency in a multiple melanoma case. Melanoma Research, 2003, 13, 171-178.	1.2	20
71	Familial Melanoma; CDKN2A and Beyond. Journal of Investigative Dermatology Symposium Proceedings, 1999, 4, 50-54.	0.8	19
72	Histologic features of melanoma associated with CDKN2A genotype. Journal of the American Academy of Dermatology, 2015, 72, 496-507.e7.	1.2	19

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73	GermlineCDKN2A/P16INK4A mutations contribute to genetic determinism of sarcoma. Journal of Medical Genetics, 2017, 54, 607-612.	3.2	19
74	A Locus Linked to p16 Modifies Melanoma Risk in Dutch Familial Atypical Multiple Mole Melanoma (FAMMM) Syndrome Families. Genome Research, 1999, 9, 575-580.	5.5	19
75	Class III Î²-tubulin, a novel biomarker in the human melanocyte lineage. Differentiation, 2013, 85, 173-181.	1.9	18
76	Somatic BRAF and NRAS Mutations in Familial Melanomas with Known Germline CDKN2A Status: A GenoMEL Study. Journal of Investigative Dermatology, 2014, 134, 287-290.	0.7	18
77	Germline Variation at CDKN2A and Associations with Nevus Phenotypes amongÂMembers of Melanoma Families. Journal of Investigative Dermatology, 2017, 137, 2606-2612.	0.7	18
78	Genome-wide linkage scan for atypical nevi in p16-Leiden melanoma families. European Journal of Human Genetics, 2008, 16, 1135-1141.	2.8	17
79	Melanocortin 1 Receptor (MC1R) Variants in High Melanoma Risk Patients are Associated with Specific Dermoscopic ABCD Features. Acta Dermato-Venereologica, 2012, 92, 587-592.	1.3	17
80	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.	2.8	17
81	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
82	Effectiveness and causes for failure of surveillance of CDKN2A-mutated melanoma families. Journal of the American Academy of Dermatology, 2011, 65, 289-296.	1.2	16
83	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.	0.7	16
84	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.	5.6	16
85	Interplay between TERT promoter mutations and methylation culminates in chromatin accessibility and TERT expression. PLoS ONE, 2020, 15, e0231418.	2.5	15
86	MICA Gene Polymorphism is Not Associated With an Increased Risk for Skin Cancer. Journal of Investigative Dermatology, 2002, 118, 686-691.	0.7	14
87	Prognostic Significance of Promoter Hypermethylation and Diminished Gene Expression of SYNPO2 in Melanoma. Journal of Investigative Dermatology, 2015, 135, 2328-2331.	0.7	13
88	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
89	CM-Score: a validated scoring system to predict CDKN2A germline mutations in melanoma families from Northern Europe. Journal of Medical Genetics, 2018, 55, 661-668.	3.2	13
90	Genetics of Seven Dutch Familial Atypcial Multiple Mole-Menaloma Syndrome Families: A Review of Linkage Results Including Chromosomes 1 and 9.. Journal of Investigative Dermatology, 1994, 103, 122S-125S.	0.7	12

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91	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.	3.1	12
92	Genomic analysis and clinical management of adolescent cutaneous melanoma. Pigment Cell and Melanoma Research, 2017, 30, 307-316.	3.3	12
93	A Flexible Multiplex Bead-Based Assay for Detecting Germline CDKN2A and CDK4 Variants in Melanoma-Prone Kindreds. Journal of Investigative Dermatology, 2011, 131, 480-486.	0.7	11
94	Acquired Melanocytic Nevi in Childhood and Familial Melanoma. JAMA Dermatology, 2014, 150, 35.	4.1	11
95	Loss of Wild-Type CDKN2A Is an Early Event in the Development of Melanoma in FAMMM Syndrome. Journal of Investigative Dermatology, 2020, 140, 2298-2301.e3.	0.7	11
96	Association of HERV-K and LINE-1 hypomethylation with reduced disease-free survival in melanoma patients. Epigenomics, 2020, 12, 1689-1706.	2.1	11
97	Increased C-MYC copy numbers on the background of CDKN2A loss is associated with improved survival in nodular melanoma. Journal of Cancer Research and Clinical Oncology, 2007, 133, 117-123.	2.5	9
98	NEK11 as a candidate high-penetrance melanoma susceptibility gene. Journal of Medical Genetics, 2020, 57, 203-210.	3.2	9
99	Dinucleotide repeat polymorphism at the D17S513 locus. Nucleic Acids Research, 1991, 19, 4794-4794.	14.5	8
100	Genome-Wide Analysis of Gene and Protein Expression of Dysplastic Naevus Cells. Journal of Skin Cancer, 2012, 2012, 1-13.	1.2	8
101	In-vitro melanoma models. Melanoma Research, 2014, 24, 305-314.	1.2	8
102	Cutaneous melanoma: Medical specialists' opinions onÂfollow-up and sentinel lymph node biopsy. European Journal of Surgical Oncology, 2014, 40, 1276-1283.	1.0	8
103	Primary Melanoma Tumors from CDKN2A Mutation Carriers Do Not Belong to a Distinct Molecular Subclass. Journal of Investigative Dermatology, 2014, 134, 3000-3003.	0.7	8
104	Association between a 46-SNP Polygenic Risk Score and melanoma risk in Dutch patients with familial melanoma. Journal of Medical Genetics, 2021, 58, 760-766.	3.2	8
105	Genomeâ€wide characterization of 5â€hydoxymethylcytosine in melanoma reveals major differences with nevus. Genes Chromosomes and Cancer, 2020, 59, 366-374.	2.8	8
106	Absence of Germline Epimutation of the CDKN2A Gene in Familial Melanoma. Journal of Investigative Dermatology, 2009, 129, 781-784.	0.7	7
107	A novel germline variant in the DOT1L gene co-segregating in a Dutch family with a history of melanoma. Melanoma Research, 2019, 29, 582-589.	1.2	7
108	p16INK4A-independence of Epsteinâ€“Barr virus-induced cell proliferation and virus latency. Journal of General Virology, 2004, 85, 1381-1386.	2.9	6

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109	Surveillance of Second-Degree Relatives from Melanoma Families with a CDKN2A Germline Mutation. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 1771-1777.	2.5	6
110	The absence of multiple atypical nevi in germline CDKN2A mutations: Comment on â€œHereditary melanoma: Update on syndromes and management: Genetics of familial atypical multiple mole melanoma syndromeâ€• Journal of the American Academy of Dermatology, 2016, 75, e157.	1.2	6
111	Melanoma susceptibility genes. Melanoma Research, 2010, 20, 161-162.	1.2	5
112	Management of Melanoma Families. Cancers, 2010, 2, 549-566.	3.7	5
113	High Growth Rate of Pancreatic Ductal Adenocarcinoma in CDKN2A-p16-Leiden Mutation Carriers. Cancer Prevention Research, 2018, 11, 551-556.	1.5	5
114	Dinucleotide repeat polymorphism at the D17S514 locus. Nucleic Acids Research, 1991, 19, 4794-4794.	14.5	4
115	Melanocortin 1 Receptor Function: Shifting Gears from Determining Skin and Nevus Phenotype to Fetal Growth. Journal of Investigative Dermatology, 2012, 132, 1953-1955.	0.7	4
116	Progress report on the major clinical advances in patient-oriented research into familial melanoma (2013â€“2018). Familial Cancer, 2019, 18, 267-271.	1.9	4
117	Genome-wide analysis of constitutional DNA methylation in familial melanoma. Clinical Epigenetics, 2020, 12, 43.	4.1	4
118	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
119	The importance of motivation in selecting undergraduate medical students for extracurricular research programmes. PLoS ONE, 2021, 16, e0260193.	2.5	4
120	Increasing First Year Studentâ€™s Attitude and Understanding towards Biomedical Research. Medical Science Educator, 2013, 23, 148-153.	1.5	3
121	MC1R variants in relation to naevi in melanoma cases and controls: a pooled analysis from the Mâ€SKIP project. Journal of the European Academy of Dermatology and Venereology, 2021, 35, e135-e138.	2.4	3
122	Phenotypic Variation in Familial Melanoma. Archives of Dermatology, 2007, 143, 525-6.	1.4	2
123	Accurate Quantification of T Cells in Copy Number Stable and Unstable DNA Samples Using Multiplex Digital PCR. Journal of Molecular Diagnostics, 2022, 24, 88-100.	2.8	2
124	The risk of developing pancreatic cancer in families with familial atypical multiple mole melanoma (FAMMM) associated with a specific 19 BP deletion of P16 (P16 Leiden). Gastroenterology, 2000, 118, A641.	1.3	1
125	High and low penetrance genes in melanoma. Melanoma Research, 2010, 20, e7.	1.2	0
126	The emergence of networks in human genome epidemiology: challenges and opportunities. , 2009, , 120-134.		0

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127	Familial melanoma. Atlas of Genetics and Cytogenetics in Oncology and Haematology, 2011, , .	0.1	0
128	Abstract 20: POT1 mutations predispose to familial melanoma. , 2014, , .		0
129	Title is missing!. , 2020, 15, e0231418.		0
130	Title is missing!. , 2020, 15, e0231418.		0
131	Title is missing!. , 2020, 15, e0231418.		0
132	Title is missing!. , 2020, 15, e0231418.		0