Nicholas K Hayward

List of Publications by Year
in descending order

335 papers	32,237 citations	5558 82 h-index	5364 164 g-index
346 all docs	346 docs citations	346 times ranked	36092 citing authors

#	Article	IF	Citations
1	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	13.5	2,562
2	High frequency of BRAF mutations in nevi. Nature Genetics, 2003, 33, 19-20.	9.4	1,547
3	Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. Nature Genetics, 2011, 43, 246-252.	9.4	1,201
4	Whole-genome landscapes of major melanoma subtypes. Nature, 2017, 545, 175-180.	13.7	1,068
5	Exome sequencing identifies recurrent somatic RAC1 mutations in melanoma. Nature Genetics, 2012, 44, 1006-1014.	9.4	1,052
6	A Versatile Gene-Based Test for Genome-wide Association Studies. American Journal of Human Genetics, 2010, 87, 139-145.	2.6	809
7	Germline mutations in the p16INK4a binding domain of CDK4 in familial melanoma. Nature Genetics, 1996, 12, 97-99.	9.4	756
8	Menin Associates with a Trithorax Family Histone Methyltransferase Complex and with the Hoxc8 Locus. Molecular Cell, 2004, 13, 587-597.	4.5	568
9	Melanocortin-1 Receptor Polymorphisms and Risk of Melanoma: Is the Association Explained Solely by Pigmentation Phenotype?. American Journal of Human Genetics, 2000, 66, 176-186.	2.6	472
10	A Genome-Wide Association Study Identifies Novel Alleles Associated with Hair Color and Skin Pigmentation. PLoS Genetics, 2008, 4, e1000074.	1.5	439
11	Geographical Variation in the Penetrance of CDKN2A Mutations for Melanoma. Journal of the National Cancer Institute, 2002, 94, 894-903.	3.0	435
12	Genome-wide association study identifies three loci associated with melanoma risk. Nature Genetics, 2009, 41, 920-925.	9.4	422
13	A novel recurrent mutation in MITF predisposes to familial and sporadic melanoma. Nature, 2011, 480, 99-103.	13.7	413
14	Melanocytic Nevi, Solar Keratoses, and Divergent Pathways to Cutaneous Melanoma. Journal of the National Cancer Institute, 2003, 95, 806-812.	3.0	388
15	High-risk Melanoma Susceptibility Genes and Pancreatic Cancer, Neural System Tumors, and Uveal Melanoma across GenoMEL. Cancer Research, 2006, 66, 9818-9828.	0.4	373
16	Features associated with germline CDKN2A mutations: a GenoMEL study of melanoma-prone families from three continents. Journal of Medical Genetics, 2006, 44, 99-106.	1.5	350
17	A Single SNP in an Evolutionary Conserved Region within Intron 86 of the HERC2 Gene Determines Human Blue-Brown Eye Color. American Journal of Human Genetics, 2008, 82, 424-431.	2.6	334
18	POT1 loss-of-function variants predispose to familial melanoma. Nature Genetics, 2014, 46, 478-481.	9.4	319

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19	Increased MAPK reactivation in early resistance to dabrafenib/trametinib combination therapy of BRAF-mutant metastatic melanoma. Nature Communications, 2014, 5, 5694.	5.8	295
20	MC1R Genotype Modifies Risk of Melanoma in Families Segregating CDKN2A Mutations. American Journal of Human Genetics, 2001, 69, 765-773.	2.6	292
21	Genetics of melanoma predisposition. Oncogene, 2003, 22, 3053-3062.	2.6	283
22	ZEB1 drives epithelial-to-mesenchymal transition in lung cancer. Journal of Clinical Investigation, 2016, 126, 3219-3235.	3.9	256
23	Mice Lacking the Vascular Endothelial Growth Factor-B Gene (Vegfb) Have Smaller Hearts, Dysfunctional Coronary Vasculature, and Impaired Recovery From Cardiac Ischemia. Circulation Research, 2000, 86, E29-35.	2.0	250
24	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. Nature Communications, 2014, 5, 5224.	5.8	236
25	Deep sequencing of uveal melanoma identifies a recurrent mutation in PLCB4. Oncotarget, 2016, 7, 4624-4631.	0.8	235
26	Genome-wide association study identifies three new melanoma susceptibility loci. Nature Genetics, 2011, 43, 1108-1113.	9.4	230
27	The CDKN2A (p16) Gene and Human Cancer. Molecular Medicine, 1997, 3, 5-20.	1.9	228
28	A Major Quantitative-Trait Locus for Mole Density Is Linked to the Familial Melanoma Gene CDKN2A: A Maximum-Likelihood Combined Linkage and Association Analysis in Twins and Their Sibs. American Journal of Human Genetics, 1999, 65, 483-492.	2.6	228
29	Interactive effects of MC1R and OCA2 on melanoma risk phenotypes. Human Molecular Genetics, 2003, 13, 447-461.	1.4	228
30	Transcriptional Pathway Signatures Predict MEK Addiction and Response to Selumetinib (AZD6244). Cancer Research, 2010, 70, 2264-2273.	0.4	222
31	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. Nature Genetics, 2015, 47, 987-995.	9.4	218
32	Genome-Wide Loss of Heterozygosity and Copy Number Analysis in Melanoma Using High-Density Single-Nucleotide Polymorphism Arrays. Cancer Research, 2007, 67, 2632-2642.	0.4	212
33	Common sequence variants on 20q11.22 confer melanoma susceptibility. Nature Genetics, 2008, 40, 838-840.	9.4	209
34	A combined analysis of D22S278 marker alleles in affected sib-pairs: Support for a susceptibility locus for schizophrenia at chromosome 22q12. , 1996, 67, 40-45.		205
35	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. Nature Communications, 2019, 10, 3163.	5.8	205
36	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

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37	A Threeâ€“Single-Nucleotide Polymorphism Haplotype in Intron 1 of OCA2 Explains Most Human Eye-Color Variation. American Journal of Human Genetics, 2007, 80, 241-252.	2.6	199
38	Genome-wide association study identifies novel loci predisposing to cutaneous melanomaâ€. Human Molecular Genetics, 2011, 20, 5012-5023.	1.4	187
39	Characterization of the Melanoma miRNAome by Deep Sequencing. PLoS ONE, 2010, 5, e9685.	1.1	181
40	Multiple Pigmentation Gene Polymorphisms Account for a Substantial Proportion of Risk of Cutaneous Malignant Melanoma. Journal of Investigative Dermatology, 2010, 130, 520-528.	0.3	174
41	A genome-wide association study identifies new susceptibility loci for esophageal adenocarcinoma and Barrett's esophagus. Nature Genetics, 2013, 45, 1487-1493.	9.4	174
42	Melanoma genetics. Journal of Medical Genetics, 2016, 53, 1-14.	1.5	173
43	Frequent somatic mutations in MAP3K5 and MAP3K9 in metastatic melanoma identified by exome sequencing. Nature Genetics, 2012, 44, 165-169.	9.4	170
44	Microarray expression profiling in melanoma reveals a BRAF mutation signature. Oncogene, 2004, 23, 4060-4067.	2.6	169
45	Additional support for schizophrenia linkage on chromosomes 6 and 8: A multicenter study. , 1996, 67, 580-594.		166
46	Loss of <scp>CDKN</scp>2A expression is a frequent event in primary invasive melanoma and correlates with sensitivity to the <scp>CDK</scp>4/6 inhibitor <scp>PD</scp>0332991 in melanoma cell lines. Pigment Cell and Melanoma Research, 2014, 27, 590-600.	1.5	165
47	Comprehensive Study of the Clinical Phenotype of GermlineBAP1Variant-Carrying Families Worldwide. Journal of the National Cancer Institute, 2018, 110, 1328-1341.	3.0	164
48	Nuclear PTEN expression and clinicopathologic features in a population-based series of primary cutaneous melanoma. International Journal of Cancer, 2002, 99, 63-67.	2.3	162
49	Melanoma cell invasiveness is regulated by miRâ€211 suppression of the BRN2 transcription factor. Pigment Cell and Melanoma Research, 2011, 24, 525-537.	1.5	158
50	Compilation of somatic mutations of theCDKN2 gene in human cancers: Non-random distribution of base substitutions. , 1996, 15, 77-88.		155
51	Whole-genome sequencing identifies a recurrent functional synonymous mutation in melanoma. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 13481-13486.	3.3	147
52	Mutations of the CDKN2/p16INK4 gene in Australian melanoma kindreds. Human Molecular Genetics, 1995, 4, 1845-1852.	1.4	146
53	The genomic landscape of cutaneous melanoma. Pigment Cell and Melanoma Research, 2016, 29, 266-283.	1.5	144
54	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. Nature Genetics, 2011, 43, 1114-1118.	9.4	140

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55	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
56	Nonsense Mutations in the Shelterin Complex Genes ACD and TERF2IP in Familial Melanoma. Journal of the National Cancer Institute, 2015, 107, .	3.0	134
57	Characterization of the mouse Men1 gene and its expression during development. Oncogene, 1998, 17, 2485-2493.	2.6	133
58	Conditional Inactivation of the Men1 Gene Leads to Pancreatic and Pituitary Tumorigenesis but Does Not Affect Normal Development of These Tissues. Molecular and Cellular Biology, 2004, 24, 3125-3131.	1.1	129
59	MC1R Is a Potent Regulator of PTEN after UV Exposure in Melanocytes. Molecular Cell, 2013, 51, 409-422.	4.5	122
60	Novel Variants in Growth Differentiation Factor 9 in Mothers of Dizygotic Twins. Journal of Clinical Endocrinology and Metabolism, 2006, 91, 4713-4716.	1.8	121
61	Genetics of familial melanoma: 20Âyears after <scp>CDKN</scp>2<scp>A</scp>. Pigment Cell and Melanoma Research, 2015, 28, 148-160.	1.5	121
62	Vegfb gene knockout mice display reduced pathology and synovial angiogenesis in both antigen-induced and collagen-induced models of arthritis. Arthritis and Rheumatism, 2003, 48, 2660-2669.	6.7	118
63	Cell cycle alterations in biopsied olfactory neuroepithelium in schizophrenia and bipolar I disorder using cell culture and gene expression analyses. Schizophrenia Research, 2006, 82, 163-173.	1.1	118
64	Melanocortin 1 receptor and risk of cutaneous melanoma: A metaâ€analysis and estimates of population burden. International Journal of Cancer, 2011, 129, 1730-1740.	2.3	118
65	Analysis of gene amplification in head-and-neck squamous-cell carcinomas. International Journal of Cancer, 1991, 48, 511-515.	2.3	115
66	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
67	Association of Helicobacter pylori Infection With Reduced Risk for Esophageal Cancer Is Independent of Environmental and Genetic Modifiers. Gastroenterology, 2010, 139, 73-83.	0.6	114
68	Localization of a Novel Melanoma Susceptibility Locus to 1p22. American Journal of Human Genetics, 2003, 73, 301-313.	2.6	113
69	Melanoma prone families withCDK4germline mutation: phenotypic profile and associations withMC1Rvariants. Journal of Medical Genetics, 2013, 50, 264-270.	1.5	112
70	<scp>NF</scp>1â€mutated melanoma tumors harbor distinct clinical and biological characteristics. Molecular Oncology, 2017, 11, 438-451.	2.1	112
71	A variant in FTO shows association with melanoma risk not due to BMI. Nature Genetics, 2013, 45, 428-432.	9.4	111
72	A cryptic <scp>BAP1</scp> splice mutation in a family with uveal and cutaneous melanoma, and paraganglioma. Pigment Cell and Melanoma Research, 2012, 25, 815-818.	1.5	109

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73	The Effect on Melanoma Risk of Genes Previously Associated With Telomere Length. Journal of the National Cancer Institute, 2014, 106, .	3.0	109
74	Gene Expression Signature Predicts Recurrence in Lung Adenocarcinoma. Clinical Cancer Research, 2007, 13, 2946-2954.	3.2	107
75	Genetic testing for melanoma. Lancet Oncology, The, 2002, 3, 653-654.	5.1	106
76	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
77	Melanoma in adolescents: A case-control study of risk factors in Queensland, Australia. International Journal of Cancer, 2002, 98, 92-98.	2.3	105
78	Cutaneous melanoma susceptibility and progression genes. Cancer Letters, 2005, 230, 153-186.	3.2	102
79	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. Nature Communications, 2020, 11, 5259.	5.8	102
80	MicroRNA-218 Is Deleted and Downregulated in Lung Squamous Cell Carcinoma. PLoS ONE, 2010, 5, e12560.	1.1	100
81	A large Norwegian family with inherited malignant melanoma, multiple atypical nevi, andCDK4 mutation. Genes Chromosomes and Cancer, 2005, 44, 10-18.	1.5	94
82	A Genome Scan for Eye Color in 502 Twin Families: Most Variation is due to a QTL on Chromosome 15q. Twin Research and Human Genetics, 2004, 7, 197-210.	1.5	91
83	Recurrent inactivating RASA2 mutations in melanoma. Nature Genetics, 2015, 47, 1408-1410.	9.4	90
84	A genetic model of melanoma tumorigenesis based on allelic losses. Genes Chromosomes and Cancer, 1995, 12, 134-141.	1.5	88
85	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. Nature Communications, 2018, 9, 4774.	5.8	87
86	The Prognostic and Predictive Value of Melanoma-related MicroRNAs Using Tissue and Serum: A MicroRNA Expression Analysis. EBioMedicine, 2015, 2, 671-680.	2.7	86
87	Whole genome landscapes of uveal melanoma show an ultraviolet radiation signature in iris tumours. Nature Communications, 2020, 11, 2408.	5.8	86
88	Most common â€˜sporadicâ€™ cancers have a significant germline genetic component. Human Molecular Genetics, 2014, 23, 6112-6118.	1.4	85
89	Broad tumor spectrum in a mouse model of multiple endocrine neoplasia type 1. International Journal of Cancer, 2007, 120, 259-267.	2.3	83
90	Targeting activating mutations of EZH2 leads to potent cell growth inhibition in human melanoma by derepression of tumor suppressor genes. Oncotarget, 2015, 6, 27023-27036.	0.8	83

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91	A recurrent germline <scp>BAP1</scp> mutation and extension of the <scp>BAP1</scp> tumor predisposition spectrum to include basal cell carcinoma. Clinical Genetics, 2015, 88, 267-272.	1.0	81
92	miR-514a regulates the tumour suppressor NF1 and modulates BRAFi sensitivity in melanoma. Oncotarget, 2015, 6, 17753-17763.	0.8	81
93	High-Risk Human Papillomavirus in Esophageal Squamous Cell Carcinoma. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2080-2087.	1.1	80
94	ATG16L1 T300A Shows Strong Associations With Disease Subgroups in a Large Australian IBD Population: Further Support for Significant Disease Heterogeneity. American Journal of Gastroenterology, 2008, 103, 2519-2526.	0.2	79
95	Genome-Wide Copy Number Analysis in Esophageal Adenocarcinoma Using High-Density Single-Nucleotide Polymorphism Arrays. Cancer Research, 2008, 68, 4163-4172.	0.4	79
96	Analysis of the CDKN2A, CDKN2B and CDK4 genes in 48 Australian melanoma kindreds. Oncogene, 1997, 15, 2999-3005.	2.6	78
97	Molecular Pathways: Mitogen-Activated Protein Kinase Pathway Mutations and Drug Resistance. Clinical Cancer Research, 2013, 19, 2301-2309.	3.2	77
98	Confirmation of a BRAF mutation-associated gene expression signature in melanoma. Pigment Cell & Melanoma Research, 2007, 20, 216-221.	4.0	76
99	The Association between MC1R Genotype and BRAF Mutation Status in Cutaneous Melanoma: Findings from an Australian Population. Journal of Investigative Dermatology, 2010, 130, 241-248.	0.3	76
100	MicroRNA-34c is associated with emphysema severity and modulates SERPINE1 expression. BMC Genomics, 2014, 15, 88.	1.2	76
101	A genome-wide scan for naevus count: linkage to CDKN2A and to other chromosome regions. European Journal of Human Genetics, 2007, 15, 94-102.	1.4	73
102	Cross-Platform Array Screening Identifies COL1A2, THBS1, TNFRSF10D and UCHL1 as Genes Frequently Silenced by Methylation in Melanoma. PLoS ONE, 2011, 6, e26121.	1.1	73
103	Melanoma Genetics: Recent Findings Take Us Beyond Well-Traveled Pathways. Journal of Investigative Dermatology, 2012, 132, 1763-1774.	0.3	72
104	Second stage of a genome scan of schizophrenia: Study of five positive regions in an expanded sample. American Journal of Medical Genetics Part A, 2000, 96, 864-869.	2.4	71
105	Identification of candidate tumor suppressor genes inactivated by promoter methylation in melanoma. Genes Chromosomes and Cancer, 2009, 48, 10-21.	1.5	71
106	InterSCOPE Study: Associations Between Esophageal Squamous Cell Carcinoma and Human Papillomavirus Serological Markers. Journal of the National Cancer Institute, 2012, 104, 147-158.	3.0	71
107	SOX10 Ablation Arrests Cell Cycle, Induces Senescence, and Suppresses Melanomagenesis. Cancer Research, 2013, 73, 5709-5718.	0.4	70
108	Schizophrenia susceptibility and chromosome 6p24â€“22. Nature Genetics, 1995, 11, 233-234.	9.4	69

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109	Secretome from senescent melanoma engages the STAT3 pathway to favor reprogramming of naive melanoma towards a tumor-initiating cell phenotype. Oncotarget, 2013, 4, 2212-2224.	0.8	69
110	Mixed lineage kinases activate MEK independently of RAF to mediate resistance to RAF inhibitors. Nature Communications, 2014, 5, 3901.	5.8	68
111	MicroRNA regulation of melanoma progression. Melanoma Research, 2012, 22, 101-113.	0.6	67
112	BRAF mutation status is an independent prognostic factor for resected stage IIIB and IIIC melanoma: Implications for melanoma staging and adjuvant therapy. European Journal of Cancer, 2014, 50, 2668-2676.	1.3	67
113	Pathways to Melanoma Development: Lessons from the Mouse. Journal of Investigative Dermatology, 2002, 119, 783-792.	0.3	66
114	Polymorphisms in MGMT and DNA repair genes and the risk of esophageal adenocarcinoma. International Journal of Cancer, 2008, 123, 174-180.	2.3	65
115	Loss of alleles on the short arm of chromosome 11 in a hepatoblastoma from a child with Beckwith-Wiedemann syndrome. Human Genetics, 1988, 79, 186-189.	1.8	64
116	Multiomic profiling of checkpoint inhibitor-treated melanoma: Identifying predictors of response and resistance, and markers of biological discordance. Cancer Cell, 2022, 40, 88-102.e7.	7.7	64
117	The protective role of DOT1L in UV-induced melanomagenesis. Nature Communications, 2018, 9, 259.	5.8	63
118	Genetic Heterogeneity of BRAF Fusion Kinases in Melanoma Affects Drug Responses. Cell Reports, 2019, 29, 573-588.e7.	2.9	62
119	A Genome Scan for Eye Color in 502 Twin Families: Most Variation is due to a QTL on Chromosome 15q. , 0, .		62
120	Haplotype analysis of two recurrentCDKN2A mutations in 10 melanoma families: Evidence for common founders and independent mutations. , 1998, 11, 424-431.		61
121	A linkage study of schizophrenia to markers within Xp11 near the MAOB gene. Psychiatry Research, 1997, 70, 131-143.	1.7	60
122	A highly recurrent RPS27 5'UTR mutation in melanoma. Oncotarget, 2014, 5, 2912-2917.	0.8	60
123	PI3-Kinase Subunits Are Infrequent Somatic Targets in Melanoma. Journal of Investigative Dermatology, 2006, 126, 1660-1663.	0.3	59
124	KCNN4 Gene Variant Is Associated With Ileal Crohn's Disease in the Australian and New Zealand Population. American Journal of Gastroenterology, 2010, 105, 2209-2217.	0.2	59
125	MicroRNA and mRNA expression profiling in metastatic melanoma reveal associations with BRAF mutation and patient prognosis. Pigment Cell and Melanoma Research, 2015, 28, 254-266.	1.5	59
126	High Intake of Folate from Food Sources Is Associated with Reduced Risk of Esophageal Cancer in an Australian Population ,. Journal of Nutrition, 2011, 141, 274-283.	1.3	56

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127	Somatic inactivating PTPRJ mutations and dysregulated pathways identified in canine malignant melanoma by integrated comparative genomic analysis. PLoS Genetics, 2018, 14, e1007589.	1.5	56
128	Osteopontin is a downstream effector of the PI3-kinase pathway in melanomas that is inversely correlated with functional PTEN. Carcinogenesis, 2006, 27, 1778-1786.	1.3	55
129	Downregulation of the Ubiquitin Ligase RNF125 Underlies Resistance of Melanoma Cells to BRAF Inhibitors via JAK1 Deregulation. Cell Reports, 2015, 11, 1458-1473.	2.9	55
130	Molecular Genomic Profiling of MelanocyticÂNevi. Journal of Investigative Dermatology, 2019, 139, 1762-1768.	0.3	55
131	Whole genome sequencing of melanomas in adolescent and young adults reveals distinct mutation landscapes and the potential role of germline variants in disease susceptibility. International Journal of Cancer, 2019, 144, 1049-1060.	2.3	54
132	The phospholipase C Î²3 gene located in the MEN1 region shows loss of expression in endocrine tumours. Human Molecular Genetics, 1994, 3, 1775-1781.	1.4	53
133	Spontaneous and UV Radiationâ€“Induced Multiple Metastatic Melanomas in Cdk4R24C/R24C/TPras Mice. Cancer Research, 2006, 66, 2946-2952.	0.4	52
134	Similarity of aberrant DNA methylation in Barrett's esophagus and esophageal adenocarcinoma. Molecular Cancer, 2008, 7, 75.	7.9	52
135	Hâ€Cadherin expression reduces invasion of malignant melanoma. Pigment Cell and Melanoma Research, 2009, 22, 296-306.	1.5	52
136	Prevalence of germline <scp>BAP</scp>1 mutation in a populationâ€based sample of uveal melanoma cases. Pigment Cell and Melanoma Research, 2013, 26, 278-279.	1.5	52
137	Exclusion of the familial melanoma locus (MLM) from the PNDD1S47 and MYCL1 regions of chromosome arm 1p in 7 Australian pedigrees. Genomics, 1992, 12, 18-25.	1.3	51
138	Nevi, Family History, and Fair Skin Increase the Risk of Second Primary Melanoma. Journal of Investigative Dermatology, 2011, 131, 461-467.	0.3	51
139	Helicobacter pylori infection and the risks of Barrett's oesophagus: A populationâ€based caseâ€control study. International Journal of Cancer, 2012, 130, 2407-2416.	2.3	51
140	Germline TERT promoter mutations are rare in familial melanoma. Familial Cancer, 2016, 15, 139-144.	0.9	51
141	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
142	Prolonged stable disease in a uveal melanoma patient with germline MBD4 nonsense mutation treated with pembrolizumab and ipilimumab. Immunogenetics, 2019, 71, 433-436.	1.2	51
143	A BAP1 Mutation in a Danish Family Predisposes to Uveal Melanoma and Other Cancers. PLoS ONE, 2013, 8, e72144.	1.1	51
144	Hepatocellular carcinoma mutation. Nature, 1991, 352, 764-764.	13.7	50

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145	Exome Sequencing to Predict Neoantigens in Melanoma. Cancer Immunology Research, 2015, 3, 992-998.	1.6	50
146	Allelic losses on chromosome band 11q13 in aldosterone-producing adrenal tumors. Genes Chromosomes and Cancer, 1995, 12, 73-75.	1.5	49
147	New developments in melanoma genetics. Current Oncology Reports, 2000, 2, 300-306.	1.8	49
148	Expression and localization of mutant p16 proteins in melanocytic lesions from familial melanoma patients. Human Pathology, 2004, 35, 25-33.	1.1	49
149	<scp>BRAF</scp>/<scp>NRAS</scp> wildâ€type melanoma, <scp>NF</scp>1 status and sensitivity to trametinib. Pigment Cell and Melanoma Research, 2015, 28, 117-119.	1.5	49
150	Transgenic Overexpression of Vascular Endothelial Growth Factor-B Isoforms by Endothelial Cells Potentiates Postnatal Vessel Growth In Vivo and In Vitro. Circulation Research, 2005, 97, e60-70.	2.0	48
151	Melanomas of unknown primary have a mutation profile consistent with cutaneous sunâ€exposed melanoma. Pigment Cell and Melanoma Research, 2013, 26, 852-860.	1.5	48
152	Functional reassessment of P16 variants using a transfection-based assay. , 1999, 82, 305-312.		47
153	Vascular endothelial growth factor-B-deficient mice show impaired development of hypoxic pulmonary hypertension. Cardiovascular Research, 2002, 55, 361-368.	1.8	47
154	Melanoma risk factors, perceived threat and intentional tanning: an international online survey. European Journal of Cancer Prevention, 2010, 19, 216-226.	0.6	47
155	Reviewing the somatic genetics of melanoma: from current to future analytical approaches. Pigment Cell and Melanoma Research, 2012, 25, 144-154.	1.5	46
156	Identification of the CIMP-like subtype and aberrant methylation of members of the chromosomal segregation and spindle assembly pathways in esophageal adenocarcinoma. Carcinogenesis, 2016, 37, 356-365.	1.3	46
157	EZH2 Cooperates with DNA Methylation to Downregulate Key Tumor Suppressors and IFN Gene Signatures in Melanoma. Journal of Investigative Dermatology, 2020, 140, 2442-2454.e5.	0.3	46
158	Evolution of late-stage metastatic melanoma is dominated by aneuploidy and whole genome doubling. Nature Communications, 2021, 12, 1434.	5.8	46
159	Localization of Multiple Melanoma Tumorâ€“Suppressor Genes on Chromosome 11 by Use of Homozygosity Mapping-of-Deletions Analysis. American Journal of Human Genetics, 2000, 67, 417-431.	2.6	45
160	Fibroblast and Lymphoblast Gene Expression Profiles in Schizophrenia: Are Non-Neural Cells Informative?. PLoS ONE, 2008, 3, e2412.	1.1	45
161	Murine Neonatal Melanocytes Exhibit a Heightened Proliferative Response to Ultraviolet Radiation and Migrate to the Epidermal Basal Layer. Journal of Investigative Dermatology, 2009, 129, 184-193.	0.3	45
162	A High-Throughput Panel for Identifying Clinically Relevant Mutation Profiles in Melanoma. Molecular Cancer Therapeutics, 2012, 11, 888-897.	1.9	45

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163	Simple tandem repeat allelic deletions confirm the preferential loss of distal chromosome 6q in melanoma. International Journal of Cancer, 1994, 58, 203-206.	2.3	44
164	Epidermal Growth Factor Gene (EGF) Polymorphism and Risk of Melanocytic Neoplasia. Journal of Investigative Dermatology, 2004, 123, 760-762.	0.3	44
165	Expression of Wnt5a and its downstream effector Î²-catenin in uveal melanoma. Melanoma Research, 2007, 17, 380-386.	0.6	44
166	Locusâ€specific concordance of genomic alterations between tissue and plasma circulating tumor <scp>DNA</scp> in metastatic melanoma. Molecular Oncology, 2019, 13, 171-184.	2.1	44
167	Sensitive droplet digital PCR method for detection ofTERTpromoter mutations in cell free DNA from patients with metastatic melanoma. Oncotarget, 2017, 8, 78890-78900.	0.8	44
168	Anatomic position determines oncogenic specificity in melanoma. Nature, 2022, 604, 354-361.	13.7	44
169	Medical and Surgical Care of Patients With Mesothelioma and Their Relatives Carrying Germline BAP1 Mutations. Journal of Thoracic Oncology, 2022, 17, 873-889.	0.5	44
170	CDKN2A mutation in a non-FAMMM kindred with cancers at multiple sites results in a functionally abnormal protein. , 1997, 73, 531-536.		43
171	POLE mutations in families predisposed to cutaneous melanoma. Familial Cancer, 2015, 14, 621-628.	0.9	43
172	No evidence for the H133Y mutation in SONIC HEDGEHOG in a collection of common tumour types. Oncogene, 1998, 16, 1091-1093.	2.6	42
173	The Queensland Study of Melanoma: Environmental and Genetic Associations (Q-MEGA); Study Design, Baseline Characteristics, and Repeatability of Phenotype and Sun Exposure Measures. Twin Research and Human Genetics, 2008, 11, 183-196.	0.3	42
174	Analysis of the Promoter Region of the Human VEGF-Related Factor Gene. Biochemical and Biophysical Research Communications, 1997, 230, 413-418.	1.0	41
175	Single Nucleotide Polymorphisms in Obesity-Related Genes and the Risk of Esophageal Cancers. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 1007-1012.	1.1	41
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