Richard A Sturm

List of Publications by Year
in descending order

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166 papers	9,453 citations	38742 50 h-index	43889 91 g-index
172 all docs	172 docs citations	172 times ranked	10046 citing authors

#	Article	IF	Citations
1	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.	6.2	472
2	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.	6.2	334
3	Human pigmentation genes: identification, structure and consequences of polymorphic variation. Gene, 2001, 277, 49-62.	2.2	330
4	Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. Nature, 2014, 507, 225-228.	27.8	328
5	Molecular genetics of human pigmentation diversity. Human Molecular Genetics, 2009, 18, R9-R17.	2.9	311
6	The POU domain is a bipartite DNA-binding structure. Nature, 1988, 336, 601-604.	27.8	301
7	MC1R Genotype Modifies Risk of Melanoma in Families Segregating CDKN2A Mutations. American Journal of Human Genetics, 2001, 69, 765-773.	6.2	292
8	Interactive effects of MC1R and OCA2 on melanoma risk phenotypes. Human Molecular Genetics, 2003, 13, 447-461.	2.9	228
9	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.	6.2	199
10	A Polymorphism in IRF4 Affects Human Pigmentation through a Tyrosinase-Dependent MITF/TFAP2A Pathway. Cell, 2013, 155, 1022-1033.	28.9	184
11	Characterization of the Melanoma miRNAome by Deep Sequencing. PLoS ONE, 2010, 5, e9685.	2.5	181
12	Multiple Pigmentation Gene Polymorphisms Account for a Substantial Proportion of Risk of Cutaneous Malignant Melanoma. Journal of Investigative Dermatology, 2010, 130, 520-528.	0.7	174
13	Brn-2 Represses Microphthalmia-Associated Transcription Factor Expression and Marks a Distinct Subpopulation of Microphthalmia-Associated Transcription Factorâ€“Negative Melanoma Cells. Cancer Research, 2008, 68, 7788-7794.	0.9	173
14	Genetics of human iris colour and patterns. Pigment Cell and Melanoma Research, 2009, 22, 544-562.	3.3	171
15	Receptor function, dominant negative activity and phenotype correlations for MC1R variant alleles. Human Molecular Genetics, 2007, 16, 2249-2260.	2.9	164
16	Melanocortin-1 Receptor Genotype is a Risk Factor for Basal and Squamous Cell Carcinoma. Journal of Investigative Dermatology, 2001, 116, 224-229.	0.7	162
17	Human pigmentation genes under environmental selection. Genome Biology, 2012, 13, 248.	9.6	162
18	Melanoma cell invasiveness is regulated by miRâ€211 suppression of the BRN2 transcription factor. Pigment Cell and Melanoma Research, 2011, 24, 525-537.	3.3	158

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19	Human pigmentation genetics: the difference is only skin deep. BioEssays, 1998, 20, 712-721.	2.5	156
20	Altered cell surface expression of human MC1R variant receptor alleles associated with red hair and skin cancer risk. Human Molecular Genetics, 2005, 14, 2145-2154.	2.9	156
21	Eye colour: portals into pigmentation genes and ancestry. Trends in Genetics, 2004, 20, 327-332.	6.7	149
22	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
23	Rufous Oculocutaneous Albinism in Southern African Blacks Is Caused by Mutations in the TYRP1 Gene. American Journal of Human Genetics, 1997, 61, 1095-1101.	6.2	134
24	Genetics of skin color variation in Europeans: genome-wide association studies with functional follow-up. Human Genetics, 2015, 134, 823-835.	3.8	133
25	Melanocortin 1 receptorgenotype: an important determinant of the damage response of melanocytes to ultraviolet radiation. FASEB Journal, 2010, 24, 3850-3860.	0.5	118
26	Diversity of pigmentation in cultured human melanocytes is due to differences in the type as well as quantity of melanin. Pigment Cell & Melanoma Research, 2006, 19, 154-162.	3.6	115
27	IRF4 Variants Have Age-Specific Effects on Nevus Count and Predispose to Melanoma. American Journal of Human Genetics, 2010, 87, 6-16.	6.2	114
28	The Role of Melanocortin-1 Receptor Polymorphism in Skin Cancer Risk Phenotypes. Pigment Cell & Melanoma Research, 2003, 16, 266-272.	3.6	102
29	Post-Transcriptional Regulation of Melanin Biosynthetic Enzymes by cAMP and Resveratrol in Human Melanocytes. Journal of Investigative Dermatology, 2007, 127, 2216-2227.	0.7	100
30	The Genetics of Human Skin and Hair Pigmentation. Annual Review of Genomics and Human Genetics, 2019, 20, 41-72.	6.2	98
31	Analysis of Cultured Human Melanocytes Based on Polymorphisms within the SLC45A2/MATP, SLC24A5/NCKX5, and OCA2/P Loci. Journal of Investigative Dermatology, 2009, 129, 392-405.	0.7	96
32	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.	1.0	91
33	A golden age of human pigmentation genetics. Trends in Genetics, 2006, 22, 464-468.	6.7	91
34	Human Melanoblasts in Culture: Expression of BRN2 and Synergistic Regulation by Fibroblast Growth Factor-2, Stem Cell Factor, and Endothelin-3. Journal of Investigative Dermatology, 2003, 121, 1150-1159.	0.7	88
35	Melanocortin-1 Receptor Signaling Markedly Induces the Expression of the NR4A Nuclear Receptor Subgroup in Melanocytic Cells. Journal of Biological Chemistry, 2008, 283, 12564-12570.	3.4	87
36	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. Nature Communications, 2018, 9, 4774.	12.8	87

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37	Inverse expression states of the BRN2 and MITF transcription factors in melanoma spheres and tumour xenografts regulate the NOTCH pathway. Oncogene, 2011, 30, 3036-3048.	5.9	86
38	NFIB Mediates BRN2 Driven Melanoma Cell Migration and Invasion Through Regulation of EZH2 and MITF. EBioMedicine, 2017, 16, 63-75.	6.1	85
39	The Recycling Endosome Protein Rab17 Regulates Melanocytic Filopodia Formation and Melanosome Trafficking. Traffic, 2011, 12, 627-643.	2.7	83
40	Quantitative analysis of MC1R gene expression in human skin cell cultures. Pigment Cell & Melanoma Research, 2006, 19, 76-89.	3.6	75
41	Sunâ€induced freckling: ephelides and solar lentigines. Pigment Cell and Melanoma Research, 2014, 27, 339-350.	3.3	70
42	Red hair is the null phenotype of MC1R. Human Mutation, 2008, 29, E88-E94.	2.5	69
43	Proneural and proneuroendocrine transcription factor expression in cutaneous mechanoreceptor (Merkel) cells and Merkel cell carcinoma. International Journal of Cancer, 2002, 101, 103-110.	5.1	68
44	Phenotypic Characterization of Nevus and Tumor Patterns in MITF E318K Mutation Carrier Melanoma Patients. Journal of Investigative Dermatology, 2014, 134, 141-149.	0.7	68
45	Chromosomal Structure of the Human TYRP1 and TYRP2 Loci and Comparison of the Tyrosinase-Related Protein Gene Family. Genomics, 1995, 29, 24-34.	2.9	65
46	Co-expression of SOX9 and SOX10 during melanocytic differentiation in vitro. Experimental Cell Research, 2005, 308, 222-235.	2.6	62
47	POU domain transcription factors: BRN2 as a regulator of melanocytic growth and tumourigenesis. Pigment Cell and Melanoma Research, 2008, 21, 611-626.	3.3	62
48	Activation of the cAMP pathway by variant human MC1R alleles expressed in HEK and in melanoma cells. Peptides, 2005, 26, 1818-1824.	2.4	61
49	Human melanocytes expressing MC1R variant alleles show impaired activation of multiple signaling pathways. Peptides, 2007, 28, 2387-2396.	2.4	59
50	GWAS Findings for Human Iris Patterns: Associations with Variants in Genes that Influence Normal Neuronal Pattern Development. American Journal of Human Genetics, 2011, 89, 334-343.	6.2	59
51	Nestin and SOX9 and SOX10 transcription factors are coexpressed in melanoma. Experimental Dermatology, 2010, 19, e89-94.	2.9	56
52	Distinct histone modifications denote early stress-induced drug tolerance in cancer. Oncotarget, 2018, 9, 8206-8222.	1.8	54
53	Adriamycin-induced DNA Adducts Inhibit the DNA Interactions of Transcription Factors and RNA Polymerase. Journal of Biological Chemistry, 1996, 271, 5422-5429.	3.4	51
54	<scp>BRN</scp>2, a <scp>POU</scp>erful driver of melanoma phenotype switching and metastasis. Pigment Cell and Melanoma Research, 2019, 32, 9-24.	3.3	50

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55	TLR3 drives IRF6â€dependent ILâ€23p19 expression and p19/EBI3 heterodimer formation in keratinocytes. Immunology and Cell Biology, 2015, 93, 771-779.	2.3	49
56	Regulation of NR4A nuclear receptor expression by oncogenic BRAF in melanoma cells. Pigment Cell and Melanoma Research, 2011, 24, 551-563.	3.3	48
57	Genome-Wide Association Shows thatÂPigmentation Genes Play a Role in SkinÂAging. Journal of Investigative Dermatology, 2017, 137, 1887-1894.	0.7	48
58	Domains of Brn-2 that mediate homodimerization and interaction with general and melanocytic transcription factors. FEBS Journal, 2000, 267, 6413-6422.	0.2	47
59	Conservation of histone H2A/H2B intergene regions: a role for the H2B specific element in divergent transcription. Nucleic Acids Research, 1988, 16, 8571-8586.	14.5	44
60	SOX9 and SOX10 but Not BRN2 Are Required for Nestin Expression in Human Melanoma Cells. Journal of Investigative Dermatology, 2009, 129, 945-953.	0.7	43
61	Whole-Exome Sequencing of Acquired Nevi Identifies Mechanisms for Development and Maintenance of Benign Neoplasms. Journal of Investigative Dermatology, 2018, 138, 1636-1644.	0.7	43
62	Osteonectin downregulates Eâ€cadherin, induces Osteopontin and Focal adhesion kinase activity stimulating an invasive melanoma phenotype. International Journal of Cancer, 2007, 121, 2653-2660.	5.1	42
63	Tumor selectivity and transcriptional activation by azelaic bishydroxamic acid in human melanocytic cells. Biochemical Pharmacology, 1997, 53, 1719-1724.	4.4	41
64	Novel MC1R variants in Ligurian melanoma patients and controls. Human Mutation, 2004, 24, 103-103.	2.5	41
65	Melanocortin MC1 receptor in human genetics and model systems. European Journal of Pharmacology, 2011, 660, 103-110.	3.5	40
66	Screening of Human Primary Melanocytes of Defined Melanocortin-1 Receptor Genotype: Pigmentation Marker, Ultrastructural and UV-Survival Studies. Pigment Cell & Melanoma Research, 2003, 16, 198-207.	3.6	39
67	Osteonectin/SPARC induction by ectopic beta(3) integrin in human radial growth phase primary melanoma cells. Cancer Research, 2002, 62, 226-32.	0.9	39
68	The human melanocortin-1 receptor locus: analysis of transcription unit, locus polymorphism and haplotype evolution. Gene, 2001, 281, 81-94.	2.2	38
69	Molecular analysis of common polymorphisms within the human Tyrosinase locus and genetic association with pigmentation traits. Pigment Cell and Melanoma Research, 2014, 27, 552-564.	3.3	38
70	Human pigmentation genes and their response to solar UV radiation. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 1998, 422, 69-76.	1.0	36
71	The NR4A2 Nuclear Receptor Is Recruited to Novel Nuclear Foci in Response to UV Irradiation and Participates in Nucleotide Excision Repair. PLoS ONE, 2013, 8, e78075.	2.5	36
72	Broad binding-site specificity and affinity properties of octamer 1 and brain octamer-binding proteins. FEBS Journal, 1993, 217, 799-811.	0.2	35

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73	Skin Pigmentation Genetics for the Clinic. Dermatology, 2017, 233, 1-15.	2.1	35
74	Spectrophotometric Methods for Quantifying Pigmentation in Human Hairâ€"Influence of MC1R Genotype and Environment. Photochemistry and Photobiology, 2008, 84, 719-726.	2.5	34
75	A polymorphism in the agouti signalling protein (ASIP) is associated with decreased levels of mRNA. Pigment Cell & Melanoma Research, 2006, 19, 226-231.	3.6	33
76	The marsupial MHC: The Tammar Wallaby, Macropus eugenii, contains an expressed DNA-like gene on chromosome 1. Journal of Molecular Evolution, 1994, 38, 496-505.	1.8	32
77	MC1R Variant Allele Effects on UVR-Induced Phosphorylation of p38, p53, and DDB2 Repair Protein Responses in Melanocytic Cells in Culture. Journal of Investigative Dermatology, 2012, 132, 1452-1461.	0.7	32
78	PPARÎ³ agonists attenuate proliferation and modulate Wnt/Î²-catenin signalling in melanoma cells. International Journal of Biochemistry and Cell Biology, 2009, 41, 844-852.	2.8	31
79	Chromosomal Structure and Expression of the Human OTF1 Locus Encoding the Oct-1 Protein. Genomics, 1993, 16, 333-341.	2.9	30
80	Complete sequence and polymorphism study of the human TYRP1 gene encoding tyrosinase-related protein 1. Mammalian Genome, 1998, 9, 50-53.	2.2	30
81	The <scp>BRAF</scp> and <scp>NRAS</scp> mutation prevalence in dermoscopic subtypes of acquired naevi reveals constitutive mitogenâ€activated protein kinase pathway activation. British Journal of Dermatology, 2018, 178, 191-197.	1.5	30
82	Chapter 4 The Melanocortinâ€1 Receptor Gene Polymorphism and Association with Human Skin Cancer. Progress in Molecular Biology and Translational Science, 2009, 88, 85-153.	1.7	29
83	High naevus count and <scp>MC</scp> 1R red hair alleles contribute synergistically to increased melanoma risk. British Journal of Dermatology, 2019, 181, 1009-1016.	1.5	29
84	Expression Studies of Pigmentation and POU-Domain Genes in Human Melanoma Cells. Pigment Cell & Melanoma Research, 1994, 7, 235-240.	3.6	26
85	BRAF^{V600E}Mutation Status of Involuting and Stable Nevi in Dabrafenib Therapy With or Without Trametinib. JAMA Dermatology, 2014, 150, 1079.	4.1	26
86	In Vivo and In Vitro Expression of Octamer Binding Proteins in Human Melanoma Metastases, Brain Tissue, and Fibroblasts. Pigment Cell & Melanoma Research, 1993, 6, 13-22.	3.6	25
87	Transcriptional regulation of differentiation, selective toxicity and ATGCAAAT binding of bisbenzimidazole derivatives in human melanoma cells. Biochemical Pharmacology, 1994, 47, 827-837.	4.4	25
88	The deacylase SIRT5 supports melanoma viability by influencing chromatin dynamics. Journal of Clinical Investigation, 2021, 131, .	8.2	23
89	Sequence of the human dopachrome tautomerase-encoding TRP-2 cDNA. Gene, 1994, 143, 295-298.	2.2	22
90	DNA elution from buccal cells stored on Whatman FTA Classic Cards using a modified methanol fixation method. BioTechniques, 2009, 46, 309-311.	1.8	22

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91	â€œWhiteâ€•Nevi and â€œRedâ€•Melanomas: Association with the RHC Phenotype of the MC1R Gene. Journal of Investigative Dermatology, 2009, 129, 1305-1307.	0.7	22
92	Melanocortinâ€1 receptorâ€mediated signalling pathways activated by NDPâ€MSH and HBD3 ligands. Pigment Cell and Melanoma Research, 2012, 25, 370-374.	3.3	22
93	Melanocytes expressing MC1R polymorphisms associated with red hair color have altered MSHâ€ligand activated pigmentary responses in coculture with keratinocytes. Journal of Cellular Physiology, 2008, 215, 344-355.	4.1	21
94	<scp>MC</scp>1R and <scp>NR</scp>4A receptors in cellular stress and <scp>DNA</scp> repair: implications for <scp>UVR</scp> protection. Experimental Dermatology, 2014, 23, 449-452.	2.9	21
95	â€˜Mind your Molesâ€™ study: protocol of a prospective cohort study of melanocytic naevi. BMJ Open, 2018, 8, e025857.	1.9	21
96	Linkage and Association Analysis of Spectrophotometrically Quantified Hair Color in Australian Adolescents: the Effect of OCA2 and HERC2. Journal of Investigative Dermatology, 2008, 128, 2807-2814.	0.7	20
97	Osteopontin expression in plasma of melanoma patients and in melanocytic tumours. Journal of the European Academy of Dermatology and Venereology, 2012, 26, 1084-1091.	2.4	20
98	Iris pigmented lesions as a marker of cutaneous melanoma risk: an Australian case-control study. British Journal of Dermatology, 2018, 178, 1119-1127.	1.5	20
99	Genetic variation in <scp>IRF</scp>4 expression modulates growth characteristics, tyrosinase expression and interferonâ€gamma response in melanocytic cells. Pigment Cell and Melanoma Research, 2018, 31, 51-63.	3.3	19
100	A Gel Mobility Shift Assay for Probing the Effect of Drugâ€“DNA Adducts on DNA-Binding Proteins. , 1997, 90, 95-106.		18
101	Unexpectedly Severe Acute Radiotherapy Side Effects Are Associated With Single Nucleotide Polymorphisms of the Melanocortin-1 Receptor. International Journal of Radiation Oncology Biology Physics, 2010, 77, 1486-1492.	0.8	18
102	Heritability of naevus patterns in an adult twin cohort from the Brisbane Twin Registry: a cross-sectional study. British Journal of Dermatology, 2016, 174, 356-363.	1.5	18
103	<scp>DCT</scp> protects human melanocytic cells from <scp>UVR</scp> and <scp>ROS</scp> damage and increases cell viability. Experimental Dermatology, 2014, 23, 916-921.	2.9	17
104	The interplay of sun damage and genetic risk in Australian multiple and single primary melanoma cases and controls. British Journal of Dermatology, 2020, 183, 357-366.	1.5	17
105	A UVR-Induced G2-Phase Checkpoint Response to ssDNA Gaps Produced by Replication Fork Bypass of Unrepaired Lesions Is Defective in Melanoma. Journal of Investigative Dermatology, 2012, 132, 1681-1688.	0.7	16
106	Endogenous Replication Stress Marks Melanomas Sensitive to CHEK1 Inhibitors In Vivo. Clinical Cancer Research, 2018, 24, 2901-2912.	7.0	15
107	Dermoscopy, reflectance confocal microscopy and histopathology of an amelanotic melanoma from an individual heterozygous for MC1R and tyrosinase variant alleles. Australasian Journal of Dermatology, 2012, 53, 291-294.	0.7	14
108	Phenotypic and genotypic analysis of amelanotic and hypomelanotic melanoma patients. Journal of the European Academy of Dermatology and Venereology, 2019, 33, 1076-1083.	2.4	14

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109	A Non-Synonymous Mutation in the Canine Pkd1 Gene Is Associated with Autosomal Dominant Polycystic Kidney Disease in Bull Terriers. PLoS ONE, 2011, 6, e22455.	2.5	14
110	Genome-Scale DNA Methylation Analysis Identifies Repeat Element Alterations that Modulate the Genomic Stability of Melanocytic Nevi. Journal of Investigative Dermatology, 2022, 142, 1893-1902.e7.	0.7	14
111	MC1R Expression in Skin: Is it Confined to Melanocytes?. Journal of Investigative Dermatology, 2007, 127, 2472-2473.	0.7	13
112	Inheritance of a novel mutated allele of the OCA2 gene associated with high incidence of oculocutaneous albinism in a Polynesian community. Journal of Human Genetics, 2010, 55, 103-111.	2.3	13
113	BRAFWild-Type Melanoma in Situ Arising In aBRAFV600E Mutant Dysplastic Nevus. JAMA Dermatology, 2015, 151, 417.	4.1	13
114	Genes Determining Nevus Count and Dermoscopic Appearance in Australian Melanoma Cases and Controls. Journal of Investigative Dermatology, 2020, 140, 498-501.e17.	0.7	13
115	Assignment of the Tyrosinase-Related Protein-2 Gene (TYRP2) to Human Chromosome 13q31-q32 by Fluorescence in Situ Hybridization: Extended Synteny with Mouse Chromosome 14. Genomics, 1994, 21, 293-296.	2.9	12
116	The Microphthalmia-Associated Transcription Factor p.E318K Mutation Does Not Play a Major Role in Sporadic Renal Cell Tumors from Caucasian Patients. Pathobiology, 2016, 83, 165-169.	3.8	12
117	<scp>GSTP</scp>1 does not modify <scp>MC</scp>1R effects on melanoma risk. Experimental Dermatology, 2017, 26, 730-733.	2.9	12
118	Germline and somatic albinism variants in amelanotic/hypomelanotic melanoma: Increased carriage of TYR and OCA2 variants. PLoS ONE, 2020, 15, e0238529.	2.5	12
119	Frontiers in pigment cell and melanoma research. Pigment Cell and Melanoma Research, 2018, 31, 728-735.	3.3	10
120	Multiple Primary Melanomas in a CDKN2A Mutation Carrier Exposed to Ionizing Radiation. Archives of Dermatology, 2007, 143, 1409-12.	1.4	8
121	Multiple Genes and Locus Interactions in Susceptibility to Vitiligo. Journal of Investigative Dermatology, 2010, 130, 643-645.	0.7	8
122	NR4A2 Promotes DNA Double-strand Break Repair Upon Exposure to UVR. Molecular Cancer Research, 2017, 15, 1184-1196.	3.4	8
123	The Distinctive Genomic Landscape of Giant Congenital Melanocytic Nevi. Journal of Investigative Dermatology, 2021, 141, 692-695.e2.	0.7	8
124	Classifying dermoscopic patterns of naevi in a case-control study of melanoma. PLoS ONE, 2017, 12, e0186647.	2.5	8
125	Mutation Signatures in Melanocytic Nevi Reveal Characteristics of Defective DNA Repair. Journal of Investigative Dermatology, 2020, 140, 2093-2096.e2.	0.7	7
126	Dinucleotide repeat polymorphism at the human TYRP1 locus. Human Molecular Genetics, 1994, 3, 2270-2270.	2.9	6

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127	Osteopontin in Melanocytic Lesionsâ€"A First Step Towards Invasion?. Journal of Investigative Dermatology, 2005, 124, xiv-xv.	0.7	6
128	GSTP1 and MC1R in melanoma susceptibility. British Journal of Dermatology, 2012, 166, 1155-1156.	1.5	6
129	The evolving universe of BRAF mutations in melanoma. British Journal of Dermatology, 2017, 177, 893-893.	1.5	6
130	On Naevi and Melanomas: Two Sides of the Same Coin?. Frontiers in Medicine, 2021, 8, 635316.	2.6	6
131	Analysis of human leukocyte antigen associations in human papillomavirusâ€"positive and â€"negative head and neck cancer: Comparison with cervical cancer. Cancer, 2022, 128, 1937-1947.	4.1	6
132	The human OTF1 locus which overlaps the CD3Z gene is located at 1q22→q23. Cytogenetic and Genome Research, 1995, 68, 231-232.	1.1	5
133	UVB-specific regulation of gene expression in human melanocytic cells: cell cycle effects and implication in the generation of melanoma. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 1998, 422, 31-41.	1.0	5
134	Human â€˜coat colourâ€™ genetics. Pigment Cell and Melanoma Research, 2008, 21, 115-116.	3.3	5
135	Src and <scp>SCC</scp>: getting to the <scp>FAK</scp>s. Experimental Dermatology, 2015, 24, 487-488.	2.9	5
136	Melanoma mutations modify melanocyte dynamics in coculture with keratinocytes or fibroblasts. Journal of Cell Science, 2019, 132, .	2.0	5
137	DNA cleavage by restriction endonucleasePflMI is inhibited in recognition sites modified bydcmmethylation. Nucleic Acids Research, 1989, 17, 3615-3615.	14.5	4
138	Effect of MC1R variant allele status on MSH-ligand induction of dopachrome tautomerase in melanocytes co-cultured with keratinocytes. Experimental Dermatology, 2011, 20, 681-684.	2.9	4
139	Lack of protection from development of multiple melanomas by an injected melanocortin analogue in a combined highâ€risk MC1R/CDKN2A genotype patient. Journal of the European Academy of Dermatology and Venereology, 2016, 30, e65-e67.	2.4	4
140	The Experience of 3D Total-Body Photography to Monitor Nevi: Results From an Australian General Population-Based Cohort Study. JMIR Dermatology, 2022, 5, e37034.	0.7	4
141	Human pigmentation: painting by numbers or ancestry?. Pigment Cell and Melanoma Research, 2013, 26, 605-606.	3.3	3
142	IRF4 rs12203592*T/T genotype is associated with nodular melanoma. Melanoma Research, 2019, 29, 445-446.	1.2	3
143	Genetic analysis of multiple primary melanomas arising within the boundaries of congenital nevi depigmentosa. Pigment Cell and Melanoma Research, 2021, 34, 1123-1130.	3.3	3
144	BRN2 in Melanocytic Cell Development, Differentiation, and Transformation. , 2006, , 149-167.		3

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145	Improved Î²-galactosidase reporter assays: optimization for low activity in mammalian cells. Technical Tips Online, 1998, 3, 29-31.	0.2	2
146	High incidence of primary melanomas in an MC1R RHC homozygote/CDKN2A mutant genotype patient. Archives of Dermatological Research, 2015, 307, 741-745.	1.9	2
147	Dermoscopy, reflectance confocal microscopy and histopathology of a melanoma in situ from an individual homozygous for <scp>GSTP</scp>1*105<scp>V</scp>al/<scp>MC</scp>1<scp>R</scp>*92<scp>M</scp>et. Australasian Journal of Dermatology, 2016, 57, 64-67.	0.7	2
148	Testing of viable human skin cell dilution cultures as an approach to validating microsampling. Archives of Dermatological Research, 2017, 309, 305-310.	1.9	2
149	Towards the full spectrum of genes for human skin colour. Pigment Cell and Melanoma Research, 2018, 31, 457-458.	3.3	2
150	Point mutation in p14ARF-specific exon 1Î² of CDKN2A causing familial melanoma and astrocytoma. British Journal of Dermatology, 2018, 178, e263-e264.	1.5	2
151	CDKN2A testing threshold in a highâ€risk Australian melanoma cohort: number of primaries, family history and young age of onset impact risk. Journal of the European Academy of Dermatology and Venereology, 2020, 34, e797-e798.	2.4	2
152	Slim-YOLO: A Simplified Object Detection Model for the Detection of Pigmented Iris Freckles as a Potential Biomarker for Cutaneous Melanoma. , 2021, , .		2
153	Genome-Wide Association Study Suggests the Variant rs7551288*A within the DHCR24 Gene Is Associated with Poor Overall Survival in Melanoma Patients. Cancers, 2022, 14, 2410.	3.7	2
154	Identification of a marsupial OTF1 gene: Cross-species STS analysis and in situ cross-hybridization to Macropus eugenii chromosomes 3/4 and 5. Cytogenetic and Genome Research, 1994, 65, 272-275.	1.1	1
155	Iris pigmented lesions as a marker of cutaneous melanoma risk: an Australian case-control study. British Journal of Dermatology, 2018, 178, e372-e372.	1.5	1
156	Reciprocal Regulation of BRN2 and NOTCH1/2 Signaling Synergistically Drives Melanoma Cell Migration and Invasion. Journal of Investigative Dermatology, 2022, 142, 1845-1857.	0.7	1
157	An STS in the humanoct-1 gene located on chromosome 1. Nucleic Acids Research, 1991, 19, 6963-6963.	14.5	0
158	Dot Bennett. Pigment Cell and Melanoma Research, 2011, 24, 986-986.	3.3	0
159	Four! Drivers of melanoma differentiationâ€"When to use iron. Pigment Cell and Melanoma Research, 2018, 31, 658-660.	3.3	0
160	Title is missing!. , 2020, 15, e0238529.		0
161	Title is missing!. , 2020, 15, e0238529.		0
162	Title is missing!. , 2020, 15, e0238529.		0

#	Article	IF	Citations
163	Title is missing!. , 2020, 15, e0238529.		0
164	Title is missing!. , 2020, 15, e0238529.		0
165	Title is missing!. , 2020, 15, e0238529.		0
166	Title is missing!. , 2020, 15, e0238529.		0