Mitchell S Stark

List of Publications by Year
in descending order

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88 papers	7,605 citations	81743 39 h-index	74018 75 g-index
90 all docs	90 docs citations	90 times ranked	10731 citing authors

#	Article	IF	Citations
1	High frequency of BRAF mutations in nevi. Nature Genetics, 2003, 33, 19-20.	9.4	1,547
2	A novel recurrent mutation in MITF predisposes to familial and sporadic melanoma. Nature, 2011, 480, 99-103.	13.7	413
3	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
4	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
5	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
6	POT1 loss-of-function variants predispose to familial melanoma. Nature Genetics, 2014, 46, 478-481.	9.4	319
7	MC1R Genotype Modifies Risk of Melanoma in Families Segregating CDKN2A Mutations. American Journal of Human Genetics, 2001, 69, 765-773.	2.6	292
8	Activation of the MAPK pathway is a common event in uveal melanomas although it rarely occurs through mutation of BRAF or RAS. British Journal of Cancer, 2005, 92, 2032-2038.	2.9	222
9	Transcriptional Pathway Signatures Predict MEK Addiction and Response to Selumetinib (AZD6244). Cancer Research, 2010, 70, 2264-2273.	0.4	222
10	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
11	Common sequence variants on 20q11.22 confer melanoma susceptibility. Nature Genetics, 2008, 40, 838-840.	9.4	209
12	Characterization of the Melanoma miRNAome by Deep Sequencing. PLoS ONE, 2010, 5, e9685.	1.1	181
13	Frequent somatic mutations in MAP3K5 and MAP3K9 in metastatic melanoma identified by exome sequencing. Nature Genetics, 2012, 44, 165-169.	9.4	170
14	Microarray expression profiling in melanoma reveals a BRAF mutation signature. Oncogene, 2004, 23, 4060-4067.	2.6	169
15	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
16	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. Nature Genetics, 2011, 43, 1114-1118.	9.4	140
17	Nonsense Mutations in the Shelterin Complex Genes ACD and TERF2IP in Familial Melanoma. Journal of the National Cancer Institute, 2015, 107, .	3.0	134
18	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

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19	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
20	Localization of a Novel Melanoma Susceptibility Locus to 1p22. American Journal of Human Genetics, 2003, 73, 301-313.	2.6	113
21	Association of MC1R Variants and Host Phenotypes With Melanoma Risk in CDKN2A Mutation Carriers: A GenoMEL Study. Journal of the National Cancer Institute, 2010, 102, 1568-1583.	3.0	108
22	Smchd1 regulates a subset of autosomal genes subject to monoallelic expression in addition to being critical for X inactivation. Epigenetics and Chromatin, 2013, 6, 19.	1.8	88
23	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
24	Most common â€˜sporadicâ€™ cancers have a significant germline genetic component. Human Molecular Genetics, 2014, 23, 6112-6118.	1.4	85
25	Broad tumor spectrum in a mouse model of multiple endocrine neoplasia type 1. International Journal of Cancer, 2007, 120, 259-267.	2.3	83
26	miR-514a regulates the tumour suppressor NF1 and modulates BRAFi sensitivity in melanoma. Oncotarget, 2015, 6, 17753-17763.	0.8	81
27	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
28	MicroRNA regulation of melanoma progression. Melanoma Research, 2012, 22, 101-113.	0.6	67
29	Polymorphisms in MGMT and DNA repair genes and the risk of esophageal adenocarcinoma. International Journal of Cancer, 2008, 123, 174-180.	2.3	65
30	PI3-Kinase Subunits Are Infrequent Somatic Targets in Melanoma. Journal of Investigative Dermatology, 2006, 126, 1660-1663.	0.3	59
31	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
32	Prognostic Gene Expression Profiling in Cutaneous Melanoma. JAMA Dermatology, 2020, 156, 1004.	2.0	59
33	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
34	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
35	Distinct histone modifications denote early stress-induced drug tolerance in cancer. Oncotarget, 2018, 9, 8206-8222.	0.8	54
36	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

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37	Whole-Exome Sequencing of Acquired Nevi Identifies Mechanisms for Development and Maintenance of Benign Neoplasms. Journal of Investigative Dermatology, 2018, 138, 1636-1644.	0.3	43
38	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
39	Meta-Analysis Combining New and Existing Data Sets Confirms that the TERTâ€“CLPTM1L Locus Influences Melanoma Risk. Journal of Investigative Dermatology, 2012, 132, 485-487.	0.3	39
40	SiDCoN: A Tool to Aid Scoring of DNA Copy Number Changes in SNP Chip Data. PLoS ONE, 2007, 2, e1093.	1.1	33
41	A Panel of Circulating MicroRNAs Detects Uveal Melanoma With High Precision. Translational Vision Science and Technology, 2019, 8, 12.	1.1	33
42	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.	1.4	30
43	An Integrated Microfluidicâ€SERS Platform Enables Sensitive Phenotyping of Serum Extracellular Vesicles in Early Stage Melanomas. Advanced Functional Materials, 2022, 32, 2010296.	7.8	30
44	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.	1.4	29
45	A comparison of CDKN2A mutation detection within the Melanoma Genetics Consortium (GenoMEL). European Journal of Cancer, 2008, 44, 1269-1274.	1.3	26
46	Identification of TFG (TRKâ€fused gene) as a putative metastatic melanoma tumor suppressor gene. Genes Chromosomes and Cancer, 2012, 51, 452-461.	1.5	25
47	BRAF Polymorphisms and Risk of Melanocytic Neoplasia. Journal of Investigative Dermatology, 2005, 125, 1252-1258.	0.3	23
48	Defective Decatenation Checkpoint Function Is a Common Feature of Melanoma. Journal of Investigative Dermatology, 2014, 134, 150-158.	0.3	23
49	The deacylase SIRT5 supports melanoma viability by influencing chromatin dynamics. Journal of Clinical Investigation, 2021, 131, .	3.9	23
50	Identification of ARHGEF17, DENND2D, FGFR3, and RB1 mutations in melanoma by inhibition of nonsenseâ€mediated mRNA decay. Genes Chromosomes and Cancer, 2008, 47, 1076-1085.	1.5	22
51	The â€˜melanoma-enrichedâ€™ microRNA miR-4731-5p acts as a tumour suppressor. Oncotarget, 2016, 7, 49677-49687.	0.8	21
52	Mutation analysis of theCDKN2A promoter in Australian melanoma families. Genes Chromosomes and Cancer, 2001, 32, 89-94.	1.5	20
53	Gene expression profiling in melanoma identifies novel downstream effectors ofp14ARF. International Journal of Cancer, 2007, 121, 784-790.	2.3	19
54	Lack of Genetic and Epigenetic Changes in CDKN2A in Melanocytic Nevi. Journal of Investigative Dermatology, 2001, 117, 383-384.	0.3	17

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55	The M53I mutation inCDKN2A is a founder mutation that predominates in melanoma patients with Scottish ancestry. Genes Chromosomes and Cancer, 2007, 46, 277-287.	1.5	14
56	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.	0.3	14
57	Ocular melanoma is not associated with CDKN2A or MC1R variants â€" a population-based study. Melanoma Research, 2003, 13, 409-413.	0.6	13
58	Rapid Screening of 4000 Individuals for Germ-line Variations in the BRAF Gene. Clinical Chemistry, 2006, 52, 1675-1678.	1.5	13
59	Mutation of the tumour suppressor p33 ING1 b is rare in melanoma. British Journal of Dermatology, 2006, 155, 94-99.	1.4	12
60	Germline and somatic albinism variants in amelanotic/hypomelanotic melanoma: Increased carriage of TYR and OCA2 variants. PLoS ONE, 2020, 15, e0238529.	1.1	12
61	Current Trends in Circulating Biomarkers for Melanoma Detection. Frontiers in Medicine, 2022, 9, 873728.	1.2	11
62	Molecular characterization of a t(9;12)(p21;q13) balanced chromosome translocation in combination with integrative genomics analysis identifiesC9orf14as a candidate tumor-suppressor. Genes Chromosomes and Cancer, 2007, 46, 155-162.	1.5	10
63	Defining the Molecular Genetics of Dermoscopic Naevus Patterns. Dermatology, 2019, 235, 19-34.	0.9	10
64	Circulating Biomarkers for Early Stage Non-Small Cell Lung Carcinoma Detection: Supplementation to Lowâ€Dose Computed Tomography. Frontiers in Oncology, 2021, 11, 555331.	1.3	10
65	Regional Variation in Epidermal Susceptibility to UV-Induced Carcinogenesis Reflects Proliferative Activity of Epidermal Progenitors. Cell Reports, 2020, 31, 107702.	2.9	9
66	The Distinctive Genomic Landscape of Giant Congenital Melanocytic Nevi. Journal of Investigative Dermatology, 2021, 141, 692-695.e2.	0.3	8
67	MicroRNA expression is associated with human papillomavirus status and prognosis in mucosal head and neck squamous cell carcinomas. Oral Oncology, 2021, 113, 105136.	0.8	8
68	Mutation Signatures in Melanocytic Nevi Reveal Characteristics of Defective DNA Repair. Journal of Investigative Dermatology, 2020, 140, 2093-2096.e2.	0.3	7
69	The Future of Precision Prevention for Advanced Melanoma. Frontiers in Medicine, 2021, 8, 818096.	1.2	7
70	Large-Giant Congenital Melanocytic Nevi: Moving Beyond NRAS Mutations. Journal of Investigative Dermatology, 2019, 139, 756-759.	0.3	6
71	On Naevi and Melanomas: Two Sides of the Same Coin?. Frontiers in Medicine, 2021, 8, 635316.	1.2	6
72	Multiple interaction nodes define the postreplication repair response to UVâ€induced DNA damage that is defective in melanomas and correlated with UV signature mutation load. Molecular Oncology, 2020, 14, 22-41.	2.1	5

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73	Genetic analysis of multiple primary melanomas arising within the boundaries of congenital nevi depigmentosa. Pigment Cell and Melanoma Research, 2021, 34, 1123-1130.	1.5	3
74	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.	1.3	2
75	Melanoma treatment guided by a panel of microRNA biomarkers. Melanoma Management, 2017, 4, 75-77.	0.1	1
76	webFOG: A web tool to map genomic features onto genes. Biochemical and Biophysical Research Communications, 2010, 401, 447-450.	1.0	0
77	mi<scp>RNA</scp>s: back seat drivers no more. Pigment Cell and Melanoma Research, 2014, 27, 510-511.	1.5	0
78	Gene Expression Array Analysis to Identify Candidate Tumor Suppressor Genes in Melanoma. Methods in Molecular Biology, 2017, , 1.	0.4	0
79	Assessment of precision melanoma diagnostics. Impact, 2018, 2018, 18-20.	0.0	0
80	Naevus count and MC1R R alleles contribute to melanoma risk. British Journal of Dermatology, 2019, 181, e119.	1.4	0
81	InÂVivo Melanoma Cell Morphology and TumorÂAggressiveness: The Promise of ReflectanceÂConfocal Microscopy in ReducingÂUnnecessary Excisions. Journal of Investigative Dermatology, 2022, , .	0.3	0
82	Title is missing!. , 2020, 15, e0238529.		0
83	Title is missing!. , 2020, 15, e0238529.		0
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