Mitchell S Stark

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4554783/publications.pdf

Version: 2024-02-01

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	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
2	InÂVivo Melanoma Cell Morphology and TumorÂAggressiveness: The Promise of ReflectanceÂConfocal Microscopy in ReducingÂUnnecessary Excisions. Journal of Investigative Dermatology, 2022, , .	0.3	0
3	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
4	Current Trends in Circulating Biomarkers for Melanoma Detection. Frontiers in Medicine, 2022, 9, 873728.	1.2	11
5	The Distinctive Genomic Landscape of Giant Congenital Melanocytic Nevi. Journal of Investigative Dermatology, 2021, 141, 692-695.e2.	0.3	8
6	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
7	On Naevi and Melanomas: Two Sides of the Same Coin?. Frontiers in Medicine, 2021, 8, 635316.	1.2	6
8	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
9	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
10	The deacylase SIRT5 supports melanoma viability by influencing chromatin dynamics. Journal of Clinical Investigation, 2021, 131, .	3.9	23
11	The Future of Precision Prevention for Advanced Melanoma. Frontiers in Medicine, 2021, 8, 818096.	1.2	7
12	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
13	Prognostic Gene Expression Profiling in Cutaneous Melanoma. JAMA Dermatology, 2020, 156, 1004.	2.0	59
14	Regional Variation in Epidermal Susceptibility to UV-Induced Carcinogenesis Reflects Proliferative Activity of Epidermal Progenitors. Cell Reports, 2020, 31, 107702.	2.9	9
15	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
16	Mutation Signatures in Melanocytic Nevi Reveal Characteristics of Defective DNA Repair. Journal of Investigative Dermatology, 2020, 140, 2093-2096.e2.	0.3	7
17	Germline and somatic albinism variants in amelanotic/hypomelanotic melanoma: Increased carriage of TYR and OCA2 variants. PLoS ONE, 2020, 15, e0238529.	1.1	12
18	Title is missing!. , 2020, 15, e0238529.		0

#	Article	IF	Citations
19	Title is missing!. , 2020, 15, e0238529.		0
20	Title is missing!. , 2020, 15, e0238529.		0
21	Title is missing!. , 2020, 15, e0238529.		0
22	Title is missing!. , 2020, 15, e0238529.		0
23	Title is missing!. , 2020, 15, e0238529.		0
24	Title is missing!. , 2020, 15, e0238529.		0
25	Naevus count and MC1R R alleles contribute to melanoma risk. British Journal of Dermatology, 2019, 181, e119.	1.4	0
26	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
27	Large-Giant Congenital Melanocytic Nevi: Moving Beyond NRAS Mutations. Journal of Investigative Dermatology, 2019, 139, 756-759.	0.3	6
28	A Panel of Circulating MicroRNAs Detects Uveal Melanoma With High Precision. Translational Vision Science and Technology, 2019, 8, 12.	1.1	33
29	Defining the Molecular Genetics of Dermoscopic Naevus Patterns. Dermatology, 2019, 235, 19-34.	0.9	10
30	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
31	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
32	Assessment of precision melanoma diagnostics. Impact, 2018, 2018, 18-20.	0.0	0
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	Distinct histone modifications denote early stress-induced drug tolerance in cancer. Oncotarget, 2018, 9, 8206-8222.	0.8	54
35	Gene Expression Array Analysis to Identify Candidate Tumor Suppressor Genes in Melanoma. Methods in Molecular Biology, 2017, , 1.	0.4	0
36	Melanoma treatment guided by a panel of microRNA biomarkers. Melanoma Management, 2017, 4, 75-77.	0.1	1

#	Article	IF	Citations
37	The â€˜melanoma-enrichedâ€™ microRNA miR-4731-5p acts as a tumour suppressor. Oncotarget, 2016, 7, 49677-49687.	0.8	21
38	Nonsense Mutations in the Shelterin Complex Genes ACD and TERF2IP in Familial Melanoma. Journal of the National Cancer Institute, 2015, 107, .	3.0	134
39	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
40	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
41	miR-514a regulates the tumour suppressor NF1 and modulates BRAFi sensitivity in melanoma. Oncotarget, 2015, 6, 17753-17763.	0.8	81
42	Most common â€˜sporadicâ€™ cancers have a significant germline genetic component. Human Molecular Genetics, 2014, 23, 6112-6118.	1.4	85
43	Defective Decatenation Checkpoint Function Is a Common Feature of Melanoma. Journal of Investigative Dermatology, 2014, 134, 150-158.	0.3	23
44	mi<scp>RNA</scp>s: back seat drivers no more. Pigment Cell and Melanoma Research, 2014, 27, 510-511.	1.5	0
45	POT1 loss-of-function variants predispose to familial melanoma. Nature Genetics, 2014, 46, 478-481.	9.4	319
46	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
47	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
48	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
49	MicroRNA regulation of melanoma progression. Melanoma Research, 2012, 22, 101-113.	0.6	67
50	Frequent somatic mutations in MAP3K5 and MAP3K9 in metastatic melanoma identified by exome sequencing. Nature Genetics, 2012, 44, 165-169.	9.4	170
51	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
52	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
53	A novel recurrent mutation in MITF predisposes to familial and sporadic melanoma. Nature, 2011, 480, 99-103.	13.7	413
54	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. Nature Genetics, 2011, 43, 1114-1118.	9.4	140

#	Article	IF	Citations
55	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
56	Transcriptional Pathway Signatures Predict MEK Addiction and Response to Selumetinib (AZD6244). Cancer Research, 2010, 70, 2264-2273.	0.4	222
57	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
58	Characterization of the Melanoma miRNAome by Deep Sequencing. PLoS ONE, 2010, 5, e9685.	1.1	181
59	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
60	webFOG: A web tool to map genomic features onto genes. Biochemical and Biophysical Research Communications, 2010, 401, 447-450.	1.0	0
61	Polymorphisms in MGMT and DNA repair genes and the risk of esophageal adenocarcinoma. International Journal of Cancer, 2008, 123, 174-180.	2.3	65
62	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
63	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
64	Common sequence variants on 20q11.22 confer melanoma susceptibility. Nature Genetics, 2008, 40, 838-840.	9.4	209
65	A comparison of CDKN2A mutation detection within the Melanoma Genetics Consortium (GenoMEL). European Journal of Cancer, 2008, 44, 1269-1274.	1.3	26
66	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
67	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
68	SiDCoN: A Tool to Aid Scoring of DNA Copy Number Changes in SNP Chip Data. PLoS ONE, 2007, 2, e1093.	1.1	33
69	Broad tumor spectrum in a mouse model of multiple endocrine neoplasia type 1. International Journal of Cancer, 2007, 120, 259-267.	2.3	83
70	Gene expression profiling in melanoma identifies novel downstream effectors ofp14ARF. International Journal of Cancer, 2007, 121, 784-790.	2.3	19
71	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
72	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

#	Article	IF	Citations
73	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
74	Mutation of the tumour suppressor p33 ING1 b is rare in melanoma. British Journal of Dermatology, 2006, 155, 94-99.	1.4	12
75	PI3-Kinase Subunits Are Infrequent Somatic Targets in Melanoma. Journal of Investigative Dermatology, 2006, 126, 1660-1663.	0.3	59
76	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
77	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
78	Rapid Screening of 4000 Individuals for Germ-line Variations in the BRAF Gene. Clinical Chemistry, 2006, 52, 1675-1678.	1.5	13
79	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
80	BRAF Polymorphisms and Risk of Melanocytic Neoplasia. Journal of Investigative Dermatology, 2005, 125, 1252-1258.	0.3	23
81	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
82	Microarray expression profiling in melanoma reveals a BRAF mutation signature. Oncogene, 2004, 23, 4060-4067.	2.6	169
83	High frequency of BRAF mutations in nevi. Nature Genetics, 2003, 33, 19-20.	9.4	1,547
84	Localization of a Novel Melanoma Susceptibility Locus to 1p22. American Journal of Human Genetics, 2003, 73, 301-313.	2.6	113
85	Ocular melanoma is not associated with CDKN2A or MC1R variants â€" a population-based study. Melanoma Research, 2003, 13, 409-413.	0.6	13
86	MC1R Genotype Modifies Risk of Melanoma in Families Segregating CDKN2A Mutations. American Journal of Human Genetics, 2001, 69, 765-773.	2.6	292
87	Lack of Genetic and Epigenetic Changes in CDKN2A in Melanocytic Nevi. Journal of Investigative Dermatology, 2001, 117, 383-384.	0.3	17
88	Mutation analysis of theCDKN2A promoter in Australian melanoma families. Genes Chromosomes and Cancer, 2001, 32, 89-94.	1.5	20