

A Hunter Shain

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3832174/publications.pdf>

Version: 2024-02-01

24
papers

4,811
citations

448610

19
h-index

651938

25
g-index

31
all docs

31
docs citations

31
times ranked

11578
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrated genomic analyses of acral and mucosal melanomas nominate novel driver genes. <i>Genome Medicine</i> , 2022, 14, .	3.6	13
2	The landscape of driver mutations in cutaneous squamous cell carcinoma. <i>Npj Genomic Medicine</i> , 2021, 6, 61.	1.7	54
3	UVB mutagenesis differs in <i>Nras</i> - and <i>Braf</i> -mutant mouse models of melanoma. <i>Life Science Alliance</i> , 2021, 4, e202101135.	1.3	8
4	BRAFV600E induces reversible mitotic arrest in human melanocytes via microRNA-mediated suppression of AURKB. <i>ELife</i> , 2021, 10, .	2.8	16
5	MicroRNA Ratios Distinguish Melanomas from \hat{A} Nevi. <i>Journal of Investigative Dermatology</i> , 2020, 140, 164-173.e7.	0.3	32
6	The Evolution of Melanoma – Moving beyond Binary Models of Genetic Progression. <i>Journal of Investigative Dermatology</i> , 2020, 140, 291-297.	0.3	7
7	The genomic landscapes of individual melanocytes from human skin. <i>Nature</i> , 2020, 586, 600-605.	13.7	79
8	The genetic evolution of metastatic uveal melanoma. <i>Nature Genetics</i> , 2019, 51, 1123-1130.	9.4	148
9	Genetic Heterogeneity of BRAF Fusion Kinases in Melanoma Affects Drug Responses. <i>Cell Reports</i> , 2019, 29, 573-588.e7.	2.9	62
10	Genomic profiling of combined hepatocellular–cholangiocarcinoma reveals similar genetics to hepatocellular carcinoma. <i>Journal of Pathology</i> , 2019, 248, 164-178.	2.1	82
11	The tumor suppressor <i>BAP1</i> cooperates with <i>BRAFV600E</i> to promote tumor formation in cutaneous melanoma. <i>Pigment Cell and Melanoma Research</i> , 2019, 32, 269-279.	1.5	9
12	Bi-allelic Loss of CDKN2A Initiates Melanoma Invasion via BRN2 Activation. <i>Cancer Cell</i> , 2018, 34, 56-68.e9.	7.7	113
13	Genomic and Transcriptomic Analysis Reveals Incremental Disruption of Key Signaling Pathways during Melanoma Evolution. <i>Cancer Cell</i> , 2018, 34, 45-55.e4.	7.7	157
14	Combined activation of MAP kinase pathway and β -catenin signaling cause deep penetrating nevi. <i>Nature Communications</i> , 2017, 8, 644.	5.8	107
15	Mutations in the promoter of the telomerase gene <i>TERT</i> contribute to tumorigenesis by a two-step mechanism. <i>Science</i> , 2017, 357, 1416-1420.	6.0	224
16	CNVkit: Genome-Wide Copy Number Detection and Visualization from Targeted DNA Sequencing. <i>PLoS Computational Biology</i> , 2016, 12, e1004873.	1.5	1,260
17	From melanocytes to melanomas. <i>Nature Reviews Cancer</i> , 2016, 16, 345-358.	12.8	596
18	<i>NTRK3</i> kinase fusions in Spitz tumours. <i>Journal of Pathology</i> , 2016, 240, 282-290.	2.1	128

#	ARTICLE	IF	CITATIONS
19	The Genetic Evolution of Melanoma. <i>New England Journal of Medicine</i> , 2016, 374, 993-996.	13.9	26
20	Activating MET kinase rearrangements in melanoma and Spitz tumours. <i>Nature Communications</i> , 2015, 6, 7174.	5.8	139
21	Exome sequencing of desmoplastic melanoma identifies recurrent NFKBIE promoter mutations and diverse activating mutations in the MAPK pathway. <i>Nature Genetics</i> , 2015, 47, 1194-1199.	9.4	221
22	The Genetic Evolution of Melanoma from Precursor Lesions. <i>New England Journal of Medicine</i> , 2015, 373, 1926-1936.	13.9	824
23	Integrative genomic and functional profiling of the pancreatic cancer genome. <i>BMC Genomics</i> , 2013, 14, 624.	1.2	22
24	The Spectrum of SWI/SNF Mutations, Ubiquitous in Human Cancers. <i>PLoS ONE</i> , 2013, 8, e55119.	1.1	458