A Hunter Shain

List of Publications by Year
in descending order

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

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24	4,811	394421 19	580821 25
papers	citations	h-index	g-index

31	31	31	10800
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	CNVkit: Genome-Wide Copy Number Detection and Visualization from Targeted DNA Sequencing. PLoS Computational Biology, 2016, 12, e1004873.	3.2	1,260
2	The Genetic Evolution of Melanoma from Precursor Lesions. New England Journal of Medicine, 2015, 373, 1926-1936.	27.0	824
3	From melanocytes to melanomas. Nature Reviews Cancer, 2016, 16, 345-358.	28.4	596
4	The Spectrum of SWI/SNF Mutations, Ubiquitous in Human Cancers. PLoS ONE, 2013, 8, e55119.	2.5	458
5	Mutations in the promoter of the telomerase gene TERT contribute to tumorigenesis by a two-step mechanism. Science, 2017, 357, 1416-1420.	12.6	224
6	Exome sequencing of desmoplastic melanoma identifies recurrent NFKBIE promoter mutations and diverse activating mutations in the MAPK pathway. Nature Genetics, 2015, 47, 1194-1199.	21.4	221
7	Genomic and Transcriptomic Analysis Reveals Incremental Disruption of Key Signaling Pathways during Melanoma Evolution. Cancer Cell, 2018, 34, 45-55.e4.	16.8	157
8	The genetic evolution of metastatic uveal melanoma. Nature Genetics, 2019, 51, 1123-1130.	21.4	148
9	Activating MET kinase rearrangements in melanoma and Spitz tumours. Nature Communications, 2015, 6, 7174.	12.8	139
10	<scp>NTRK3</scp> kinase fusions in Spitz tumours. Journal of Pathology, 2016, 240, 282-290.	4.5	128
11	Bi-allelic Loss of CDKN2A Initiates Melanoma Invasion via BRN2 Activation. Cancer Cell, 2018, 34, 56-68.e9.	16.8	113
12	Combined activation of MAP kinase pathway and Î²-catenin signaling cause deep penetrating nevi. Nature Communications, 2017, 8, 644.	12.8	107
13	Genomic profiling of combined hepatocellularâ€cholangiocarcinoma reveals similar genetics to hepatocellular carcinoma. Journal of Pathology, 2019, 248, 164-178.	4.5	82
14	The genomic landscapes of individual melanocytes from human skin. Nature, 2020, 586, 600-605.	27.8	79
15	Genetic Heterogeneity of BRAF Fusion Kinases in Melanoma Affects Drug Responses. Cell Reports, 2019, 29, 573-588.e7.	6.4	62
16	The landscape of driver mutations in cutaneous squamous cell carcinoma. Npj Genomic Medicine, 2021, 6, 61.	3.8	54
17	MicroRNA Ratios Distinguish Melanomas fromÂNevi. Journal of Investigative Dermatology, 2020, 140, 164-173.e7.	0.7	32
18	The Genetic Evolution of Melanoma. New England Journal of Medicine, 2016, 374, 993-996.	27.0	26

#	Article	IF	Citations
19	Integrative genomic and functional profiling of the pancreatic cancer genome. BMC Genomics, 2013, 14, 624.	2.8	22
20	BRAFV600E induces reversible mitotic arrest in human melanocytes via microRNA-mediated suppression of AURKB. ELife, 2021, 10, .	6.0	16
21	Integrated genomic analyses of acral and mucosal melanomas nominate novel driver genes. Genome Medicine, 2022, 14, .	8.2	13
22	The tumor suppressor <scp>BAP</scp>1 cooperates with <scp>BRAFV</scp>600E to promote tumor formation in cutaneous melanoma. Pigment Cell and Melanoma Research, 2019, 32, 269-279.	3.3	9
23	UVB mutagenesis differs in Nras- and Braf-mutant mouse models of melanoma. Life Science Alliance, 2021, 4, e202101135.	2.8	8
24	The Evolution of Melanoma â€“ Moving beyond Binary Models of Genetic Progression. Journal of Investigative Dermatology, 2020, 140, 291-297.	0.7	7