Andrea Ventura

List of Publications by Year
in descending order

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55
papers

9,984
citations

136740
32
h-index

155451
55
g-index

64
all docs

64
docs citations

64
times ranked

17787
citing authors

#	ARTICLE	IF	CITATIONS
1	Interplay between K-RAS and miRNAs. Trends in Cancer, 2022, 8, 384-396.	3.8	9
2	TRK xDFG Mutations Trigger a Sensitivity Switch from Type I to II Kinase Inhibitors. Cancer Discovery, 2021, 11, 126-141.	7.7	34
3	The origins and consequences of UPF1 variants in pancreatic adenosquamous carcinoma. ELife, 2021, 10, .	2.8	8
4	<i>Rlfâ€"Mycl</i> Gene Fusion Drives Tumorigenesis and Metastasis in a Mouse Model of Small Cell Lung Cancer. Cancer Discovery, 2021, 11, 3214-3229.	7.7	24
5	Inducible and reversible inhibition of miRNA-mediated gene repression in vivo. ELife, 2021, 10, .	2.8	23
6	High-Resolution InÂVivo Identification of miRNA Targets by Halo-Enhanced Ago2 Pull-Down. Molecular Cell, 2020, 79, 167-179.e11.	4.5	36
7	Altered RNA Splicing by Mutant p53 Activates Oncogenic RAS Signaling in Pancreatic Cancer. Cancer Cell, 2020, 38, 198-211.e8.	7.7	99
8	Dual role for miR-34a in the control of early progenitor proliferation and commitment in the mammary gland and in breast cancer. Oncogene, 2019, 38, 360-374.	2.6	39
9	The Fusion Oncogene FUS-CHOP Drives Sarcomagenesis of High-Grade Spindle Cell Sarcomas in Mice. Sarcoma, 2019, 2019, 1-14.	0.7	9
10	ALK7 Erects a Suppressive Barrier to Tumor Progression and Metastasis. Developmental Cell, 2019, 49, 304-305.	3.1	4
11	Cancer diagnosis and immunotherapy in the age of CRISPR. Genes Chromosomes and Cancer, 2019, 58, 233-243.	1.5	4
12	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.	2.9	284
13	Modeling Cancer in the CRISPR Era. Annual Review of Cancer Biology, 2018, 2, 111-131.	2.3	15
14	Characterization of hepatocellular adenoma and carcinoma using microRNA profiling and targeted gene sequencing. PLoS ONE, 2018, 13, e0200776.	1.1	30
15	GuideScan software for improved single and paired CRISPR guide RNA design. Nature Biotechnology, 2017, 35, 347-349.	9.4	205
16	Somatic chromosomal engineering identifies BCAN-NTRK1 as a potent glioma driver and therapeutic target. Nature Communications, 2017, 8, 15987.	5.8	53
17	Effects of lack of microRNA-34 on the neural circuitry underlying the stress response and anxiety. Neuropharmacology, 2016, 107, 305-316.	2.0	56
18	NORAD: Defender of the Genome. Trends in Genetics, 2016, 32, 390-392.	2.9	23

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19	Somatic Engineering of Oncogenic Chromosomal Rearrangements: A Perspective. Cancer Research, 2016, 76, 4918-4923.	0.4	7
20	The present and future of genome editing in cancer research. Human Genetics, 2016, 135, 1083-1092.	1.8	13
21	Circulating Plasma Levels of MicroRNA-21 and MicroRNA-221 Are Potential Diagnostic Markers for Primary Intrahepatic Cholangiocarcinoma. PLoS ONE, 2016, 11, e0163699.	1.1	52
22	The CRISPR revolution and its impact on cancer research. Swiss Medical Weekly, 2015, 145, w14230.	0.8	13
23	An allelic series of miR-17â^¼92â€"mutant mice uncovers functional specialization and cooperation among members of a microRNA polycistron. Nature Genetics, 2015, 47, 766-775.	9.4	101
24	In vivo, Argonaute-bound microRNAs exist predominantly in a reservoir of low molecular weight complexes not associated with mRNA. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 767-772.	3.3	108
25	Rapid and efficient one-step generation of paired gRNA CRISPR-Cas9 libraries. Nature Communications, 2015, 6, 8083.	5.8	109
26	The biological functions of miRNAs: lessons from in vivo studies. Trends in Cell Biology, 2015, 25, 137-147.	3.6	455
27	Involvement of <i>MBD4</i> inactivation in mismatch repair-deficient tumorigenesis. Oncotarget, 2015, 6, 42892-42904.	0.8	43
28	Role of the <i>miR-17â^¼92</i> cluster family in cerebellar and medulloblastoma development. Biology Open, 2014, 3, 597-605.	0.6	29
29	In vivo engineering of oncogenic chromosomal rearrangements with the CRISPR/Cas9 system. Nature, 2014, 516, 423-427.	13.7	538
30	Control of TFH differentiation by a microRNA cluster. Nature Immunology, 2013, 14, 770-771.	7.0	0
31	Intact p53-Dependent Responses in miR-34â€"Deficient Mice. PLoS Genetics, 2012, 8, e1002797.	1.5	178
32	The MicroRNA-17-92 Family of MicroRNA Clusters in Development and Disease. Cancer Journal (Sudbury,) Tj ETQq0 0 0 rgBT /Overlock 1	1.0	242
33	Embryonic stem cell miRNAs and their roles in development and disease. Seminars in Cancer Biology, 2012, 22, 428-436.	4.3	26
34	A New Role for miR-182 in DNA Repair. Molecular Cell, 2011, 41, 135-137.	4.5	15
35	microRNA-34a regulates neurite outgrowth, spinal morphology, and function. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 21099-21104.	3.3	175
36	miR than meets the eye: Figure 1.. Genes and Development, 2011, 25, 1663-1667.	2.7	16

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37	Germline deletion of the miR-17âˆ¼92 cluster causes skeletal and growth defects in humans. Nature Genetics, 2011, 43, 1026-1030.	9.4	275
38	Widespread regulatory activity of vertebrate microRNA* species. Rna, 2011, 17, 312-326.	1.6	293
39	Capture of MicroRNAâ€“Bound mRNAs Identifies the Tumor Suppressor miR-34a as a Regulator of Growth Factor Signaling. PLoS Genetics, 2011, 7, e1002363.	1.5	222
40	MicroRNAs in Mammalian Development. Modecular Medicine and Medicinal, 2010, , 95-123.	0.4	0
41	Genetic dissection of the <i>miR-17âˆ¼92</i> cluster of microRNAs in Myc-induced B-cell lymphomas. Genes and Development, 2009, 23, 2806-2811.	2.7	425
42	MicroRNAs and Cancer: Short RNAs Go a Long Way. Cell, 2009, 136, 586-591.	13.5	824
43	Targeted Deletion Reveals Essential and Overlapping Functions of the miR-17âˆ¼92 Family of miRNA Clusters. Cell, 2008, 132, 875-886.	13.5	1,504
44	Restoration of p53 function leads to tumour regression in vivo. Nature, 2007, 445, 661-665.	13.7	1,662
45	Expression in T-cells of the proapoptotic protein p66SHC is controlled by promoter demethylation. Biochemical and Biophysical Research Communications, 2006, 349, 322-328.	1.0	14
46	Mammalian RNAi: a practical guide. BioTechniques, 2005, 39, 215-224.	0.8	121
47	Factor V Leiden and G20210A prothrombin mutation and the risk of subclavian vein thrombosis in patients with breast cancer and a central venous catheter. Annals of Oncology, 2004, 15, 590-593.	0.6	52
48	Cre-lox-regulated conditional RNA interference from transgenes. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 10380-10385.	3.3	575
49	A Cryptic Targeting Signal Induces Isoform-specific Localization of p46Shc to Mitochondria. Journal of Biological Chemistry, 2004, 279, 2299-2306.	1.6	55
50	p66SHC Promotes Apoptosis and Antagonizes Mitogenic Signaling in T Cells. Molecular and Cellular Biology, 2004, 24, 1747-1757.	1.1	124
51	Semaphorins: Green Light for Redox Signaling?. Science Signaling, 2002, 2002, pe44-pe44.	1.6	32
52	The p66Shc Longevity Gene Is Silenced through Epigenetic Modifications of an Alternative Promoter. Journal of Biological Chemistry, 2002, 277, 22370-22376.	1.6	148
53	A p53-p66Shc signalling pathway controls intracellular redox status, levels of oxidation-damaged DNA and oxidative stress-induced apoptosis. Oncogene, 2002, 21, 3872-3878.	2.6	410
54	Direct Transactivation of the Anti-apoptotic Gene Apolipoprotein J (Clusterin) by B-MYB. Journal of Biological Chemistry, 2000, 275, 21055-21060.	1.6	106

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55	Characterization of MLH1 and MSH2 alternative splicing and its relevance to molecular testing of colorectal cancer susceptibility. Human Genetics, 1998, 102, 15-20.	1.8	56