Luisa Statello

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1562434/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	STAT3 induces breast cancer growth via ANGPTL4, MMP13 and STC1 secretion by cancer associated fibroblasts. Oncogene, 2022, 41, 1456-1467.	5.9	38
2	Gene regulation by long non-coding RNAs and its biological functions. Nature Reviews Molecular Cell Biology, 2021, 22, 96-118.	37.0	2,319
3	The DNA damage inducible lncRNA SCAT7 regulates genomic integrity and topoisomerase 1 turnover in lung adenocarcinoma. NAR Cancer, 2021, 3, zcab002.	3.1	6
4	LY6K-AS lncRNA is a lung adenocarcinoma prognostic biomarker and regulator of mitotic progression. Oncogene, 2021, 40, 2463-2478.	5.9	17
5	In Vivo Administration of Therapeutic Antisense Oligonucleotides. Methods in Molecular Biology, 2021, 2254, 273-282.	0.9	2
6	PAN-cancer analysis of S-phase enriched IncRNAs identifies oncogenic drivers and biomarkers. Nature Communications, 2018, 9, 883.	12.8	93
7	Identification of RNA-binding proteins in exosomes capable of interacting with different types of RNA: RBP-facilitated transport of RNAs into exosomes. PLoS ONE, 2018, 13, e0195969.	2.5	185
8	Delivery of Small Interfering RNAs to Cells via Exosomes. Methods in Molecular Biology, 2016, 1364, 105-125.	0.9	30
9	miRNA profiling in vitreous humor, vitreal exosomes and serum from uveal melanoma patients: Pathological and diagnostic implications. Cancer Biology and Therapy, 2015, 16, 1387-1396.	3.4	140
10	Non-coding landscapes of colorectal cancer. World Journal of Gastroenterology, 2015, 21, 11709.	3.3	73
11	Highly skewed distribution of miRNAs and proteins between colorectal cancer cells and their exosomes following Cetuximab treatment: biomolecular, genetic and translational implications. Oncoscience, 2014, 1, 132-157.	2.2	42
12	miR-296-3p, miR-298-5p and their downstream networks are causally involved in the higher resistance of mammalian pancreatic α cells to cytokine-induced apoptosis as compared to β cells. BMC Genomics, 2013, 14, 62.	2.8	48
13	Specific alterations of the microRNA transcriptome and global network structure in colorectal cancer after treatment with MAPK/ERK inhibitors. Journal of Molecular Medicine, 2012, 90, 1421-1438.	3.9	82
14	MIR152, MIR200B, and MIR338, human positional and functional neuroblastoma candidates, are involved in neuroblast differentiation and apoptosis. Journal of Molecular Medicine, 2010, 88, 1041-1053.	3.9	37
15	MicroRNA expression profile and network in colorectal carcinoma after chemotherapy. New Biotechnology, 2010, 27, S67.	4.4	Ο
16	Expression profile and specific network features of the apoptotic machinery explain relapse of acute myeloid leukemia after chemotherapy. BMC Cancer, 2010, 10, 377.	2.6	26
17	Specific Alterations of MicroRNA Transcriptome and Global Network Structure in Colorectal Carcinoma after Cetuximab Treatment. Molecular Cancer Therapeutics, 2010, 9, 3396-3409.	4.1	95
18	The apoptotic machinery as a biological complex system: analysis of its omics and evolution, identification of candidate genes for fourteen major types of cancer, and experimental validation in CML and neuroblastoma. BMC Medical Genomics, 2009, 2, 20.	1.5	20