# Luisa Statello

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1562434/publications.pdf

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| 18 | 3,314 | 567281 15 | 839539 18 |
|---|---|---|---|
| papers | citations | h-index | g-index |

| 19 | 19 | 19 | 4147 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Gene regulation by long non-coding RNAs and its biological functions. Nature Reviews Molecular Cell Biology, 2021, 22, 96-118. | 37.0 | 2,319 |
| 2 | 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 |
| 3 | 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 |
| 4 | 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 |
| 5 | PAN-cancer analysis of S-phase enriched lncRNAs identifies oncogenic drivers and biomarkers. Nature Communications, 2018, 9, 883. | 12.8 | 93 |
| 6 | 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 |
| 7 | Non-coding landscapes of colorectal cancer. World Journal of Gastroenterology, 2015, 21, 11709. | 3.3 | 73 |
| 8 | miR-296-3p, miR-298-5p and their downstream networks are causally involved in the higher resistance of mammalian pancreatic Î± cells to cytokine-induced apoptosis as compared to Î² cells. BMC Genomics, 2013, 14, 62. | 2.8 | 48 |
| 9 | 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 |
| 10 | STAT3 induces breast cancer growth via ANGPTL4, MMP13 and STC1 secretion by cancer associated fibroblasts. Oncogene, 2022, 41, 1456-1467. | 5.9 | 38 |
| 11 | 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 |
| 12 | Delivery of Small Interfering RNAs to Cells via Exosomes. Methods in Molecular Biology, 2016, 1364, 105-125. | 0.9 | 30 |
| 13 | 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 |
| 14 | 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 |
| 15 | LY6K-AS lncRNA is a lung adenocarcinoma prognostic biomarker and regulator of mitotic progression. Oncogene, 2021, 40, 2463-2478. | 5.9 | 17 |
| 16 | The DNA damage inducible lncRNA SCAT7 regulates genomic integrity and topoisomerase 1 turnover in lung adenocarcinoma. NAR Cancer, 2021, 3, zcab002. | 3.1 | 6 |
| 17 | In Vivo Administration of Therapeutic Antisense Oligonucleotides. Methods in Molecular Biology, 2021, 2254, 273-282. | 0.9 | 2 |
| 18 | MicroRNA expression profile and network in colorectal carcinoma after chemotherapy. New Biotechnology, 2010, 27, S67. | 4.4 | 0 |