

# Mariangela Santorsola

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1684151/publications.pdf>

Version: 2024-02-01

10  
papers

481  
citations

1163065

8  
h-index

1372553

10  
g-index

10  
all docs

10  
docs citations

10  
times ranked

1139  
citing authors

#	ARTICLE	IF	CITATIONS
1	Prediction of Metabolic Profiles from Transcriptomics Data in Human Cancer Cell Lines. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3867.	4.1	6
2	TGS1 mediates 2,2,7-trimethyl guanosine capping of the human telomerase RNA to direct telomerase dependent telomere maintenance. <i>Nature Communications</i> , 2022, 13, 2302.	12.8	11
3	The prolyl-isomerase PIN1 is essential for nuclear Lamin-B structure and function and protects heterochromatin under mechanical stress. <i>Cell Reports</i> , 2021, 36, 109694.	6.4	15
4	Breast Cancer Organoids Model Patient-Specific Response to Drug Treatment. <i>Cancers</i> , 2020, 12, 3869.	3.7	43
5	HmtDB 2016: data update, a better performing query system and human mitochondrial DNA haplogroup predictor. <i>Nucleic Acids Research</i> , 2017, 45, D698-D706.	14.5	52
6	A multi-parametric workflow for the prioritization of mitochondrial DNA variants of clinical interest. <i>Human Genetics</i> , 2016, 135, 121-136.	3.8	35
7	Mitochondrial Disease Sequence Data Resource (MSeqDR): A global grass-roots consortium to facilitate deposition, curation, annotation, and integrated analysis of genomic data for the mitochondrial disease clinical and research communities. <i>Molecular Genetics and Metabolism</i> , 2015, 114, 388-396.	1.1	76
8	A comprehensive characterization of mitochondrial DNA mutations in glioblastoma multiforme. <i>International Journal of Biochemistry and Cell Biology</i> , 2015, 63, 46-54.	2.8	22
9	MToolBox: a highly automated pipeline for heteroplasmy annotation and prioritization analysis of human mitochondrial variants in high-throughput sequencing. <i>Bioinformatics</i> , 2014, 30, 3115-3117.	4.1	166
10	Extraction and annotation of human mitochondrial genomes from 1000 Genomes Whole Exome Sequencing data. <i>BMC Genomics</i> , 2014, 15, S2.	2.8	55