Teresa Colombo

List of Publications by Year
in descending order

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36
papers

2,451
citations

279487
23
h-index

360668
35
g-index

38
all docs

38
docs citations

38
times ranked

4792
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptional Profiling of Three<i>Pseudomonas syringae</i>pv.<i>actinidiae</i>Biovars Reveals Different Responses to Apoplast-Like Conditions Related to Strain Virulence on the Host. Molecular Plant-Microbe Interactions, 2021, 34, 376-396.	1.4	15
2	AI applications in functional genomics. Computational and Structural Biotechnology Journal, 2021, 19, 5762-5790.	1.9	34
3	Mining sponge phenomena in RNA expression data. Journal of Bioinformatics and Computational Biology, 2021, , 2150022.	0.3	0
4	A Census and Categorization Method of Epitranscriptomic Marks. International Journal of Molecular Sciences, 2020, 21, 4684.	1.8	29
5	Specific molecular interactions between Vitis vinifera and Botrytis cinerea are required for noble rot development in grape berries. Postharvest Biology and Technology, 2019, 156, 110924.	2.9	22
6	Plant and fungus transcriptomic data from grapevine berries undergoing artificially-induced noble rot caused by Botrytis cinerea. Data in Brief, 2019, 25, 104150.	0.5	3
7	Inverse Problems in Systems Biology: A Critical Review. Methods in Molecular Biology, 2018, 1702, 69-94.	0.4	19
8	SWIM: a computational tool to unveiling crucial nodes in complex biological networks. Scientific Reports, 2017, 7, 44797.	1.6	50
9	Role of the long non-coding RNA PVT1 in the dysregulation of the ceRNA-ceRNA network in human breast cancer. PLoS ONE, 2017, 12, e0171661.	1.1	92
10	The oncogenic role of circPVT1 in head and neck squamous cell carcinoma is mediated through the mutant p53/YAP/TEAD transcription-competent complex. Genome Biology, 2017, 18, 237.	3.8	179
11	Characterization of epithelial-mesenchymal transition intermediate/hybrid phenotypes associated to resistance to EGFR inhibitors in non-small cell lung cancer cell lines. Oncotarget, 2017, 8, 103340-103363.	0.8	44
12	Comprehensive RNA dataset of AGO2 associated RNAs in Jurkat cells following miR-21 over-expression. Data in Brief, 2016, 7, 604-606.	0.5	1
13	Mutant p53 inhibits miRNA biogenesis by interfering with the microprocessor complex. Oncogene, 2016, 35, 3760-3770.	2.6	43
14	TP53 regulates miRNA association with AGO2 to remodel the miRNAâ€“mRNA interaction network. Genome Research, 2016, 26, 331-341.	2.4	51
15	PVT1: A Rising Star among Oncogenic Long Noncoding RNAs. BioMed Research International, 2015, 2015, 1-10.	0.9	191
16	Increased chronic lymphocytic leukemia proliferation upon IgM stimulation is sustained by the upregulation of miRâ€•132 and miRâ€•212. Genes Chromosomes and Cancer, 2015, 54, 222-234.	1.5	26
17	The role of TP53 in miRNA loading onto AGO2 and in remodelling the miRNAâ€“mRNA interaction network. Lancet, The, 2015, 385, S15.	6.3	23
18	Integrated molecular analysis to investigate the role of microRNAs in pancreatic tumour growth and progression. Lancet, The, 2015, 385, S37.	6.3	54

#	ARTICLE	IF	CITATIONS
19	Identification of linc-NeD125, a novel long non coding RNA that hosts miR-125b-1 and negatively controls proliferation of human neuroblastoma cells. RNA Biology, 2015, 12, 1323-1337.	1.5	23
20	A New Procedure to Analyze RNA Non-Branching Structures. Current Bioinformatics, 2015, 10, 242-258.	0.7	3
21	Growth Arrest-Specific Transcript 5 Associated snoRNA Levels Are Related to p53 Expression and DNA Damage in Colorectal Cancer. PLoS ONE, 2014, 9, e98561.	1.1	66
22	Computational analysis identifies a sponge interaction network between long non-coding RNAs and messenger RNAs in human breast cancer. BMC Systems Biology, 2014, 8, 83.	3.0	233
23	miR-21 is a negative modulator of T-cell activation. Biochimie, 2014, 107, 319-326.	1.3	50
24	A novel variant in the 3' untranslated region of the CDK4 gene: interference with microRNA target sites and role in increased risk of cutaneous melanoma. Cancer Genetics, 2014, 207, 168-169.	0.2	2
25	Arsenic exposure triggers a shift in microRNA expression. Science of the Total Environment, 2014, 472, 672-680.	3.9	41
26	MicroRNAs Cooperatively Inhibit a Network of Tumor Suppressor Genes to Promote Pancreatic Tumor Growth and Progression. Gastroenterology, 2014, 146, 268-277.e18.	0.6	141
27	Multi-scale Simulation of T Helper Lymphocyte Differentiation. Lecture Notes in Computer Science, 2014, , 123-134.	1.0	10
28	The p53 miRNA interactome and its potential role in the cancer clinic. Epigenomics, 2013, 5, 417-428.	1.0	27
29	The Onset of Type 2 Diabetes: Proposal for a Multi-Scale Model. JMIR Research Protocols, 2013, 2, e44.	0.5	13
30	A three-microRNA signature for predicting survival in pancreatic cancer. Pancreatology, 2012, 12, 588.	0.5	0
31	miR-223 is overexpressed in T-lymphocytes of patients affected by rheumatoid arthritis. Human Immunology, 2010, 71, 206-211.	1.2	329
32	Characterization of Bâ€•and Tâ€•lineage acute lymphoblastic leukemia by integrated analysis of MicroRNA and mRNA expression profiles. Genes Chromosomes and Cancer, 2009, 48, 1069-1082.	1.5	87
33	Large-scale sorting of C. elegans embryos reveals the dynamics of small RNA expression. Nature Methods, 2009, 6, 745-751.	9.0	91
34	Altered microRNA Expression Patterns in Hepatoblastoma Patients. Translational Oncology, 2009, 2, 157-163.	1.7	68
35	3dLOGO: a web server for the identification, analysis and use of conserved protein substructures. Nucleic Acids Research, 2007, 35, W416-W419.	6.5	6
36	A Genome-Wide Map of Conserved MicroRNA Targets in C. elegans. Current Biology, 2006, 16, 460-471.	1.8	380