

# Teresa Colombo

## List of Publications by Year in descending order

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Version: 2024-02-01

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	A Genome-Wide Map of Conserved MicroRNA Targets in <i>C. elegans</i> . <i>Current Biology</i> , 2006, 16, 460-471.	1.8	380
2	miR-223 is overexpressed in T-lymphocytes of patients affected by rheumatoid arthritis. <i>Human Immunology</i> , 2010, 71, 206-211.	1.2	329
3	Computational analysis identifies a sponge interaction network between long non-coding RNAs and messenger RNAs in human breast cancer. <i>BMC Systems Biology</i> , 2014, 8, 83.	3.0	233
4	PVT1: A Rising Star among Oncogenic Long Noncoding RNAs. <i>BioMed Research International</i> , 2015, 2015, 1-10.	0.9	191
5	The oncogenic role of circPVT1 in head and neck squamous cell carcinoma is mediated through the mutant p53/YAP/TEAD transcription-competent complex. <i>Genome Biology</i> , 2017, 18, 237.	3.8	179
6	MicroRNAs Cooperatively Inhibit a Network of Tumor Suppressor Genes to Promote Pancreatic Tumor Growth and Progression. <i>Gastroenterology</i> , 2014, 146, 268-277.e18.	0.6	141
7	Role of the long non-coding RNA PVT1 in the dysregulation of the ceRNA-ceRNA network in human breast cancer. <i>PLoS ONE</i> , 2017, 12, e0171661.	1.1	92
8	Large-scale sorting of <i>C. elegans</i> embryos reveals the dynamics of small RNA expression. <i>Nature Methods</i> , 2009, 6, 745-751.	9.0	91
9	Characterization of B $\alpha$ and T $\alpha$ lineage acute lymphoblastic leukemia by integrated analysis of MicroRNA and mRNA expression profiles. <i>Genes Chromosomes and Cancer</i> , 2009, 48, 1069-1082.	1.5	87
10	Altered microRNA Expression Patterns in Hepatoblastoma Patients. <i>Translational Oncology</i> , 2009, 2, 157-163.	1.7	68
11	Growth Arrest-Specific Transcript 5 Associated snoRNA Levels Are Related to p53 Expression and DNA Damage in Colorectal Cancer. <i>PLoS ONE</i> , 2014, 9, e98561.	1.1	66
12	Integrated molecular analysis to investigate the role of microRNAs in pancreatic tumour growth and progression. <i>Lancet, The</i> , 2015, 385, S37.	6.3	54
13	TP53 regulates miRNA association with AGO2 to remodel the miRNA-mRNA interaction network. <i>Genome Research</i> , 2016, 26, 331-341.	2.4	51
14	miR-21 is a negative modulator of T-cell activation. <i>Biochimie</i> , 2014, 107, 319-326.	1.3	50
15	SWIM: a computational tool to unveiling crucial nodes in complex biological networks. <i>Scientific Reports</i> , 2017, 7, 44797.	1.6	50
16	Characterization of epithelial-mesenchymal transition intermediate/hybrid phenotypes associated to resistance to EGFR inhibitors in non-small cell lung cancer cell lines. <i>Oncotarget</i> , 2017, 8, 103340-103363.	0.8	44
17	Mutant p53 inhibits miRNA biogenesis by interfering with the microprocessor complex. <i>Oncogene</i> , 2016, 35, 3760-3770.	2.6	43
18	Arsenic exposure triggers a shift in microRNA expression. <i>Science of the Total Environment</i> , 2014, 472, 672-680.	3.9	41

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19	AI applications in functional genomics. Computational and Structural Biotechnology Journal, 2021, 19, 5762-5790.	1.9	34
20	A Census and Categorization Method of Epitranscriptomic Marks. International Journal of Molecular Sciences, 2020, 21, 4684.	1.8	29
21	The p53 miRNA interactome and its potential role in the cancer clinic. Epigenomics, 2013, 5, 417-428.	1.0	27
22	Increased chronic lymphocytic leukemia proliferation upon IgM stimulation is sustained by the upregulation of miR-132 and miR-212. Genes Chromosomes and Cancer, 2015, 54, 222-234.	1.5	26
23	The role of TP53 in miRNA loading onto AGO2 and in remodelling the miRNA-mRNA interaction network. Lancet, The, 2015, 385, S15.	6.3	23
24	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
25	Specific molecular interactions between <i>Vitis vinifera</i> and <i>Botrytis cinerea</i> are required for noble rot development in grape berries. Postharvest Biology and Technology, 2019, 156, 110924.	2.9	22
26	Inverse Problems in Systems Biology: A Critical Review. Methods in Molecular Biology, 2018, 1702, 69-94.	0.4	19
27	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
28	The Onset of Type 2 Diabetes: Proposal for a Multi-Scale Model. JMIR Research Protocols, 2013, 2, e44.	0.5	13
29	Multi-scale Simulation of T Helper Lymphocyte Differentiation. Lecture Notes in Computer Science, 2014, , 123-134.	1.0	10
30	3dLOGO: a web server for the identification, analysis and use of conserved protein substructures. Nucleic Acids Research, 2007, 35, W416-W419.	6.5	6
31	Plant and fungus transcriptomic data from grapevine berries undergoing artificially-induced noble rot caused by <i>Botrytis cinerea</i> . Data in Brief, 2019, 25, 104150.	0.5	3
32	A New Procedure to Analyze RNA Non-Branching Structures. Current Bioinformatics, 2015, 10, 242-258.	0.7	3
33	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
34	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
35	A three-microRNA signature for predicting survival in pancreatic cancer. Pancreatology, 2012, 12, 588.	0.5	0
36	Mining sponge phenomena in RNA expression data. Journal of Bioinformatics and Computational Biology, 2021, , 2150022.	0.3	0