## Antonio Marco

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

30 908 15 30 g-index

36 1,041 6.2 4.49 ext. papers ext. citations avg, IF L-index

#	Paper	IF	Citations
30	Pervasive Selection against MicroRNA Target Sites in Human Populations. <i>Molecular Biology and Evolution</i> , <b>2020</b> , 37, 3399-3408	8.3	O
29	Comment on "microRNAs in the Same Clusters Evolve to Coordinately Regulate Functionally Related Genes". <i>Molecular Biology and Evolution</i> , <b>2019</b> , 36, 1843	8.3	3
28	The Impact of Population Variation in the Analysis of microRNA Target Sites. <i>Non-coding RNA</i> , <b>2019</b> , 5,	7.1	3
27	PopTargs: a database for studying population evolutionary genetics of human microRNA target sites. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2019</b> , 2019,	5	3
26	SeedVicious: Analysis of microRNA target and near-target sites. <i>PLoS ONE</i> , <b>2018</b> , 13, e0195532	3.7	12
25	Clearance of Maternal RNAs: Not a Mummyes Embryo Anymore. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1605, 1-10	1.4	5
24	The Origin and Evolution of Maternal Genes. <i>Results and Problems in Cell Differentiation</i> , <b>2017</b> , 63, 483-4	1944	1
23	Rapid Functional and Sequence Differentiation of a Tandemly Repeated Species-Specific Multigene Family in Drosophila. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 51-65	8.3	9
22	Selection Against Maternal microRNA Target Sites in Maternal Transcripts. <i>G3: Genes, Genomes, Genetics</i> , <b>2015</b> , 5, 2199-207	3.2	18
21	Sex-biased expression of microRNAs in Drosophila melanogaster. <i>Open Biology</i> , <b>2014</b> , 4, 140024	7	29
20	Multiple products from microRNA transcripts. <i>Biochemical Society Transactions</i> , <b>2013</b> , 41, 850-4	5.1	17
19	Sex-biased expression of microRNAs in Schistosoma mansoni. <i>PLoS Neglected Tropical Diseases</i> , <b>2013</b> , 7, e2402	4.8	47
18	Clusters of microRNAs emerge by new hairpins in existing transcripts. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, 7745-52	20.1	65
17	Structure, evolution and function of the bi-directionally transcribed iab-4/iab-8 microRNA locus in arthropods. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, 3352-61	20.1	26
16	Regulatory RNAs in the light of Drosophila genomics. <i>Briefings in Functional Genomics</i> , <b>2012</b> , 11, 356-65	4.9	8
15	MicroRNAs from the same precursor have different targeting properties. <i>Silence: A Journal of RNA Regulation</i> , <b>2012</b> , 3, 8		50
14	Evolution and function of the extended miR-2 microRNA family. RNA Biology, 2012, 9, 242-8	4.8	66

## LIST OF PUBLICATIONS

	13	Detection of microRNAs in color space. <i>Bioinformatics</i> , <b>2012</b> , 28, 318-23	7.2	57	
	12	MicroRNA evolution by arm switching. <i>EMBO Reports</i> , <b>2011</b> , 12, 172-7	6.5	166	
	11	Functional shifts in insect microRNA evolution. <i>Genome Biology and Evolution</i> , <b>2010</b> , 2, 686-96	3.9	109	
	10	Positional conservation and amino acids shape the correct diagnosis and population frequencies of benign and damaging personal amino acid mutations. <i>Genome Research</i> , <b>2009</b> , 19, 1562-9	9.7	50	
	9	Relationship between gene co-expression and sharing of transcription factor binding sites in Drosophila melanogaster. <i>Bioinformatics</i> , <b>2009</b> , 25, 2473-7	7.2	35	
	8	CGIN1: a retroviral contribution to mammalian genomes. <i>Molecular Biology and Evolution</i> , <b>2009</b> , 26, 216	578750	26	
	7	Interactome and Gene Ontology provide congruent yet subtly different views of a eukaryotic cell. <i>BMC Systems Biology</i> , <b>2009</b> , 3, 69	3.5	5	
	6	How Athila retrotransposons survive in the Arabidopsis genome. <i>BMC Genomics</i> , <b>2008</b> , 9, 219	4.5	14	
	5	A general strategy to determine the congruence between a hierarchical and a non-hierarchical classification. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 442	3.6	6	
	4	Evolutionary and structural analyses of GDAP1, involved in Charcot-Marie-Tooth disease, characterize a novel class of glutathione transferase-related genes. <i>Molecular Biology and Evolution</i> , <b>2004</b> , 21, 176-87	8.3	73	
,	3	No evidence of functional co-adaptation between clustered microRNAs		2	
	2	Pervasive selection against microRNA target sites in human populations		1	
	1	SeedVicious: analysis of microRNA target and near-target sites		1	