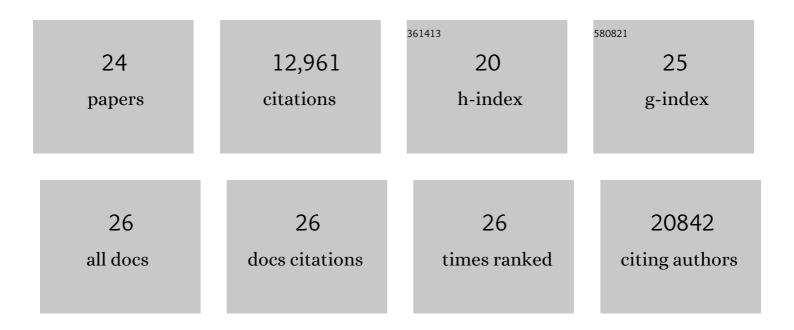
## Mario Caccamo

List of Publications by Year in descending order

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ΜΑΡΙΟ CACCAMO

#	Article	IF	CITATIONS
1	Yerba mate (llex paraguariensis, A. StHil.) de novo transcriptome assembly based on tissue specific genomic expression profiles. BMC Genomics, 2018, 19, 891.	2.8	9
2	Primula vulgaris (primrose) genome assembly, annotation and gene expression, with comparative genomics on the heterostyly supergene. Scientific Reports, 2018, 8, 17942.	3.3	40
3	A chromosome conformation capture ordered sequence of the barley genome. Nature, 2017, 544, 427-433.	27.8	1,365
4	Construction of a map-based reference genome sequence for barley, Hordeum vulgare L Scientific Data, 2017, 4, 170044.	5.3	130
5	Whole-Genome Characteristics and Polymorphic Analysis of Vietnamese Rice Landraces as a Comprehensive Information Resource for Marker-Assisted Selection. International Journal of Genomics, 2017, 2017, 1-11.	1.6	6
6	gEVAL — a web-based browser for evaluating genome assemblies. Bioinformatics, 2016, 32, 2508-251	0.4.1	319
7	CerealsDB 3.0: expansion of resources and data integration. BMC Bioinformatics, 2016, 17, 256.	2.6	42
8	Red clover (Trifolium pratense L.) draft genome provides a platform for trait improvement. Scientific Reports, 2015, 5, 17394.	3.3	136
9	A syntenyâ€based draft genome sequence of the forage grass <i>Lolium perenne</i> . Plant Journal, 2015, 84, 816-826.	5.7	166
10	Host Subtraction, Filtering and Assembly Validations for Novel Viral Discovery Using Next Generation Sequencing Data. PLoS ONE, 2015, 10, e0129059.	2.5	44
11	<scp>RNA</scp> â€ <scp>S</scp> eq bulked segregant analysis enables the identification of highâ€resolution genetic markers for breeding in hexaploid wheat. Plant Biotechnology Journal, 2015, 13, 613-624.	8.3	202
12	The zebrafish reference genome sequence and its relationship to the human genome. Nature, 2013, 496, 498-503.	27.8	3,708
13	Metagenomic study of the viruses of African straw-coloured fruit bats: Detection of a chiropteran poxvirus and isolation of a novel adenovirus. Virology, 2013, 441, 95-106.	2.4	121
14	StatsDB: platform-agnostic storage and understanding of next generation sequencing run metrics. F1000Research, 2013, 2, 248.	1.6	14
15	Identifying and Classifying Trait Linked Polymorphisms in Non-Reference Species by Walking Coloured de Bruijn Graphs. PLoS ONE, 2013, 8, e60058.	2.5	26
16	Analyses of pig genomes provide insight into porcine demography and evolution. Nature, 2012, 491, 393-398.	27.8	1,190
17	De novo assembly and genotyping of variants using colored de Bruijn graphs. Nature Genetics, 2012, 44, 226-232.	21.4	564
18	Assemblathon 1: A competitive assessment of de novo short read assembly methods. Genome Research, 2011, 21, 2224-2241.	5.5	443

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#	Article	IF	CITATIONS
19	Adaptive Autoimmunity and Foxp3-Based Immunoregulation in Zebrafish. PLoS ONE, 2010, 5, e9478.	2.5	83
20	Control of Treg and TH17 cell differentiation by the aryl hydrocarbon receptor. Nature, 2008, 453, 65-71.	27.8	1,544
21	Conservation and divergence of gene families encoding components of innate immune response systems in zebrafish. Genome Biology, 2007, 8, R251.	9.6	384
22	ESTGenes: Alternative Splicing From ESTs in Ensembl. Genome Research, 2004, 14, 976-987.	5.5	76
23	An Overview of Ensembl. Genome Research, 2004, 14, 925-928.	5.5	391
24	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	27.8	1,943