Cristian Del Fabbro

List of Publications by Year in descending order

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932766 1372195 6,301 13 10 10 citations g-index h-index papers 14 14 14 9430 docs citations times ranked citing authors all docs

#	Article	lF	CITATIONS
1	The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. Nature, 2007, 449, 463-467.	13.7	3,384
2	The high-quality draft genome of peach (Prunus persica) identifies unique patterns of genetic diversity, domestication and genome evolution. Nature Genetics, 2013, 45, 487-494.	9.4	1,031
3	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. GigaScience, 2013, 2, 10.	3. 3	582
4	Sequencing of diverse mandarin, pummelo and orange genomes reveals complex history of admixture during citrus domestication. Nature Biotechnology, 2014, 32, 656-662.	9.4	572
5	An Extensive Evaluation of Read Trimming Effects on Illumina NGS Data Analysis. PLoS ONE, 2013, 8, e85024.	1.1	358
6	Comparative study of RNA-seq- and Microarray-derived coexpression networks in <i>Arabidopsis thaliana</i> . Bioinformatics, 2013, 29, 717-724.	1.8	128
7	Grapevine field experiments reveal the contribution of genotype, the influence of environment and the effect of their interaction (G×E) on the berry transcriptome. Plant Journal, 2018, 93, 1143-1159.	2.8	75
8	High throughput approaches reveal splicing of primary microRNA transcripts and tissue specific expression of mature microRNAs in Vitis vinifera. BMC Genomics, 2009, 10, 558.	1.2	62
9	rNA: a fast and accurate short reads numerical aligner. Bioinformatics, 2012, 28, 123-124.	1.8	37
10	ERNE-BS5., 2012,,.		14
11	GAM: Genomic Assemblies Merger: A Graph Based Method to Integrate Different Assemblies. , 2009, , .		9
12	mrNA: The MPI Randomized Numerical Aligner. , 2011, , .		1
13	A Parallel Algorithm for the Best k-Mismatches Alignment Problem. , 2014, , .		0