Xi Zhang

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/9919689/publications.pdf

Version: 2024-02-01

12

papers

138

citations

1478505

6

h-index

1372567

10

g-index

13

all docs

13

docs citations

13

times ranked

228

citing authors

#	ARTICLE	IF	CITATIONS
1	Complete Sequence of pABTJ2, A Plasmid from Acinetobacter baumannii MDR-TJ, Carrying Many Phage-like Elements. Genomics, Proteomics and Bioinformatics, 2014, 12, 172-177.	6.9	28
2	Draft genome sequence of the Antarctic green alga Chlamydomonas sp. UWO241. IScience, 2021, 24, 102084.	4.1	26
3	Recent advances in the genome-wide study of DNA replication origins in yeast. Frontiers in Microbiology, 2015, 6, 117.	3.5	19
4	Photosynthetic adaptation to polar life: Energy balance, photoprotection and genetic redundancy. Journal of Plant Physiology, 2022, 268, 153557.	3.5	17
5	The mitochondrial and chloroplast genomes of the green alga Haematococcus are made up of nearly identical repetitive sequences. Current Biology, 2019, 29, R736-R737.	3.9	14
6	Comparative analysis of essential genes in prokaryotic genomic islands. Scientific Reports, 2015, 5, 12561.	3.3	11
7	Protocol for HSDFinder: Identifying, annotating, categorizing, and visualizing duplicated genes in eukaryotic genomes. STAR Protocols, 2021, 2, 100619.	1.2	8
8	A constitutive stress response is a result of low temperature growth in the Antarctic green alga<i>Chlamydomonas</i>sp.<scp>UWO241</scp>. Plant, Cell and Environment, 2022, 45, 156-177.	5.7	8
9	HSDFinder: A BLAST-Based Strategy for Identifying Highly Similar Duplicated Genes in Eukaryotic Genomes. Frontiers in Bioinformatics, 2021, 1, .	2.1	5
10	Protocol for using NoBadWordsCombiner to merge and minimize â€œbad wordsâ€• from BLAST hits against multiple eukaryotic gene annotation databases. STAR Protocols, 2021, 2, 100888.	1.2	1
11	Is Gene Duplication Driving Cold Adaptation in the Antarctic Green Alga <i>Chlamydomonas</i> Sp. UWO241?. SSRN Electronic Journal, 0, , .	0.4	1
12	TreeTuner: A pipeline for minimizing redundancy and complexity in large phylogenetic datasets. STAR Protocols, 2022, 3, 101175.	1.2	0