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List of Publications by Year in descending order

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Version: 2024-02-01

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papers

929
citations

1040018

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22
all docs

22
docs citations

22
times ranked

1842
citing authors

#	ARTICLE	IF	CITATIONS
1	TEsorter: An accurate and fast method to classify LTR-retrotransposons in plant genomes. Horticulture Research, 2022, 9, .	6.3	70
2	Methods to Identify and Study the Evolution of Pseudogenes Using a Phylogenetic Approach. Methods in Molecular Biology, 2021, 2324, 21-34.	0.9	1
3	Genome assemblies of three closely related leaf beetle species (<i>Galerucella</i> spp.). G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	2
4	Genome assembly of the basket willow, <i>Salix viminalis</i> , reveals earliest stages of sex chromosome expansion. BMC Biology, 2020, 18, 78.	3.8	39
5	Assembly and Analysis of the Genome Sequence of the Yeast <i>Brettanomyces naardenensis</i> CBS 7540. Microorganisms, 2019, 7, 489.	3.6	8
6	Pervasive hybridizations in the history of wheat relatives. Science Advances, 2019, 5, eaav9188.	10.3	79
7	Chromosomal genome assembly of the ethanol production strain CBS 11270 indicates a highly dynamic genome structure in the yeast species <i>Brettanomyces bruxellensis</i> . PLoS ONE, 2019, 14, e0215077.	2.5	8
8	The genomic footprint of sexual conflict. Nature Ecology and Evolution, 2019, 3, 1725-1730.	7.8	57
9	GUESSmyLT: Software to guess the RNA-Seq library type of paired and single end read files. Journal of Open Source Software, 2019, 4, 1344.	4.6	0
10	EMBLmyGFF3: a converter facilitating genome annotation submission to European Nucleotide Archive. BMC Research Notes, 2018, 11, 584.	1.4	19
11	Complete Genome Sequences of the Xylose-Fermenting <i>Candida intermedia</i> Strains CBS 141442 and PYCC 4715. Genome Announcements, 2017, 5, .	0.8	8
12	Global analysis of biosynthetic gene clusters reveals vast potential of secondary metabolite production in <i>Penicillium</i> species. Nature Microbiology, 2017, 2, 17044.	13.3	198
13	The genetic basis for ecological adaptation of the Atlantic herring revealed by genome sequencing. ELife, 2016, 5, .	6.0	143
14	The Bee Microbiome: Impact on Bee Health and Model for Evolution and Ecology of Host-Microbe Interactions. MBio, 2016, 7, e02164-15.	4.1	215
15	A universal genomic coordinate translator for comparative genomics. BMC Bioinformatics, 2014, 15, 227.	2.6	7
16	Impact of recurrent gene duplication on adaptation of plant genomes. BMC Plant Biology, 2014, 14, 151.	3.6	32
17	Methods to Study the Occurrence and the Evolution of Pseudogenes Through a Phylogenetic Approach. Methods in Molecular Biology, 2014, 1167, 87-99.	0.9	0
18	The Chordate Proteome History Database. Evolutionary Bioinformatics, 2012, 8, EBO.S9186.	1.2	5

#	ARTICLE	IF	CITATIONS
19	GLADX: An Automated Approach to Analyze the Lineage-Specific Loss and Pseudogenization of Genes. PLoS ONE, 2012, 7, e38792.	2.5	9
20	Integration of Evolutionary Biology Concepts for Functional Annotation and Automation of Complex Research in Evolution: The Multi-Agent Software System DAGOBAN. , 2011, , 71-87.		26