

Tobias MÃ¼ller

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

3,879
citations

304602

22
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526166

27
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29
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29
docs citations

29
times ranked

3747
citing authors

#	ARTICLE	IF	CITATIONS
1	Under salt stress guard cells rewire ion transport and abscisic acid signaling. <i>New Phytologist</i> , 2021, 231, 1040-1055.	3.5	23
2	covRNA: discovering covariate associations in large-scale gene expression data. <i>BMC Research Notes</i> , 2020, 13, 92.	0.6	0
3	The role of Arabidopsis ABA receptors from the PYR/PYL/RCAR family in stomatal acclimation and closure signal integration. <i>Nature Plants</i> , 2019, 5, 1002-1011.	4.7	115
4	Diversity and Interactions of Wood-Inhabiting Fungi and Beetles after Deadwood Enrichment. <i>PLoS ONE</i> , 2015, 10, e0143566.	1.1	18
5	The influence of tree species, stratum and forest management on beetle assemblages responding to deadwood enrichment. <i>Forest Ecology and Management</i> , 2014, 323, 57-64.	1.4	23
6	ITS2, 18S, 16S or any other RNA " simply aligning sequences and their individual secondary structures simultaneously by an automatic approach. <i>Gene</i> , 2014, 546, 145-149.	1.0	63
7	Internal Transcribed Spacer 1 Secondary Structure Analysis Reveals a Common Core throughout the Anaerobic Fungi (Neocallimastigomycota). <i>PLoS ONE</i> , 2014, 9, e91928.	1.1	88
8	Compensatory Base Changes in ITS2 Secondary Structures Correlate with the Biological Species Concept Despite Intragenomic Variability in ITS2 Sequences " A Proof of Concept. <i>PLoS ONE</i> , 2013, 8, e66726.	1.1	115
9	The ITS2 Database. <i>Journal of Visualized Experiments</i> , 2012, , .	0.2	30
10	The ITS2 Database III "sequences and structures for phylogeny. <i>Nucleic Acids Research</i> , 2010, 38, D275-D279.	6.5	223
11	BioNet: an R-Package for the functional analysis of biological networks. <i>Bioinformatics</i> , 2010, 26, 1129-1130.	1.8	215
12	A probabilistic model of cell size reduction in <i>Pseudo-nitzschia delicatissima</i> (Bacillariophyta). <i>Journal of Theoretical Biology</i> , 2009, 258, 316-322.	0.8	6
13	5.8S-28S rRNA interaction and HMM-based ITS2 annotation. <i>Gene</i> , 2009, 430, 50-57.	1.0	394
14	Modelling cross-hybridization on phylogenetic DNA microarrays increases the detection power of closely related species. <i>Molecular Ecology Resources</i> , 2009, 9, 83-93.	2.2	24
15	ITS2 data corroborate a monophyletic chlorophycean DO-group (Sphaeropleales). <i>BMC Evolutionary Biology</i> , 2008, 8, 218.	3.2	56
16	Identifying functional modules in protein-protein interaction networks: an integrated exact approach. <i>Bioinformatics</i> , 2008, 24, i223-i231.	1.8	485
17	ProfDistS: (profile-) distance based phylogeny on sequence "structure alignments. <i>Bioinformatics</i> , 2008, 24, 2401-2402.	1.8	116
18	The ITS2 Database II: homology modelling RNA structure for molecular systematics. <i>Nucleic Acids Research</i> , 2007, 36, D377-D380.	6.5	135

#	ARTICLE	IF	CITATIONS
19	Placozoa: at least two. <i>Biologia (Poland)</i> , 2007, 62, 641-645.	0.8	11
20	Distinguishing species. <i>Rna</i> , 2007, 13, 1469-1472.	1.6	284
21	4SALE—a tool for synchronous RNA sequence and secondary structure alignment and editing. <i>BMC Bioinformatics</i> , 2006, 7, 498.	1.2	327
22	The internal transcribed spacer 2 database—a web server for (not only) low level phylogenetic analyses. <i>Nucleic Acids Research</i> , 2006, 34, W704-W707.	6.5	161
23	Homology modeling revealed more than 20,000 rRNA internal transcribed spacer 2 (ITS2) secondary structures. <i>Rna</i> , 2005, 11, 1616-1623.	1.6	169
24	ProfDist: a tool for the construction of large phylogenetic trees based on profile distances. <i>Bioinformatics</i> , 2005, 21, 2108-2109.	1.8	58
25	A common core of secondary structure of the internal transcribed spacer 2 (ITS2) throughout the Eukaryota. <i>Rna</i> , 2005, 11, 361-364.	1.6	320
26	CBCAnalyzer: inferring phylogenies based on compensatory base changes in RNA secondary structures. <i>In Silico Biology</i> , 2005, 5, 291-4.	0.4	65
27	Accurate and robust phylogeny estimation based on profile distances: a study of the Chlorophyceae (Chlorophyta). <i>BMC Evolutionary Biology</i> , 2004, 4, 20.	3.2	43
28	Modeling Amino Acid Replacement. <i>Journal of Computational Biology</i> , 2000, 7, 761-776.	0.8	312