Tobias MÃ¼ller

List of Publications by Year
in descending order

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28 papers	3,879 citations	304602 22 h-index	526166 27 g-index
29 all docs	29 docs citations	29 times ranked	3747 citing authors

#	Article	IF	Citations
1	Identifying functional modules in proteinâ€“protein interaction networks: an integrated exact approach. Bioinformatics, 2008, 24, i223-i231.	1.8	485
2	5.8S-28S rRNA interaction and HMM-based ITS2 annotation. Gene, 2009, 430, 50-57.	1.0	394
3	4SALE--a tool for synchronous RNA sequence and secondary structure alignment and editing. BMC Bioinformatics, 2006, 7, 498.	1.2	327
4	A common core of secondary structure of the internal transcribed spacer 2 (ITS2) throughout the Eukaryota. Rna, 2005, 11, 361-364.	1.6	320
5	Modeling Amino Acid Replacement. Journal of Computational Biology, 2000, 7, 761-776.	0.8	312
6	Distinguishing species. Rna, 2007, 13, 1469-1472.	1.6	284
7	The ITS2 Database IIIâ€”sequences and structures for phylogeny. Nucleic Acids Research, 2010, 38, D275-D279.	6.5	223
8	BioNet: an R-Package for the functional analysis of biological networks. Bioinformatics, 2010, 26, 1129-1130.	1.8	215
9	Homology modeling revealed more than 20,000 rRNA internal transcribed spacer 2 (ITS2) secondary structures. Rna, 2005, 11, 1616-1623.	1.6	169
10	The internal transcribed spacer 2 database--a web server for (not only) low level phylogenetic analyses. Nucleic Acids Research, 2006, 34, W704-W707.	6.5	161
11	The ITS2 Database II: homology modelling RNA structure for molecular systematics. Nucleic Acids Research, 2007, 36, D377-D380.	6.5	135
12	ProfDistS: (profile-) distance based phylogeny on sequenceâ€”structure alignments. Bioinformatics, 2008, 24, 2401-2402.	1.8	116
13	The role of Arabidopsis ABA receptors from the PYR/PYL/RCAR family in stomatal acclimation and closure signal integration. Nature Plants, 2019, 5, 1002-1011.	4.7	115
14	Compensatory Base Changes in ITS2 Secondary Structures Correlate with the Biological Species Concept Despite Intragenomic Variability in ITS2 Sequences â€“ A Proof of Concept. PLoS ONE, 2013, 8, e66726.	1.1	115
15	Internal Transcribed Spacer 1 Secondary Structure Analysis Reveals a Common Core throughout the Anaerobic Fungi (Neocallimastigomycota). PLoS ONE, 2014, 9, e91928.	1.1	88
16	CBCAnalyzer: inferring phylogenies based on compensatory base changes in RNA secondary structures. In Silico Biology, 2005, 5, 291-4.	0.4	65
17	ITS2, 18S, 16S or any other RNA â€” simply aligning sequences and their individual secondary structures simultaneously by an automatic approach. Gene, 2014, 546, 145-149.	1.0	63
18	ProfDist: a tool for the construction of large phylogenetic trees based on profile distances. Bioinformatics, 2005, 21, 2108-2109.	1.8	58

#	Article	IF	Citations
19	ITS2 data corroborate a monophyletic chlorophycean DO-group (Sphaeropleales). BMC Evolutionary Biology, 2008, 8, 218.	3.2	56
20	Accurate and robust phylogeny estimation based on profile distances: a study of the Chlorophyceae (Chlorophyta). BMC Evolutionary Biology, 2004, 4, 20.	3.2	43
21	The ITS2 Database. Journal of Visualized Experiments, 2012, , .	0.2	30
22	Modelling crossâ€hybridization on phylogenetic DNA microarrays increases the detection power of closely related species. Molecular Ecology Resources, 2009, 9, 83-93.	2.2	24
23	The influence of tree species, stratum and forest management on beetle assemblages responding to deadwood enrichment. Forest Ecology and Management, 2014, 323, 57-64.	1.4	23
24	Under salt stress guard cells rewire ion transport and abscisic acid signaling. New Phytologist, 2021, 231, 1040-1055.	3.5	23
25	Diversity and Interactions of Wood-Inhabiting Fungi and Beetles after Deadwood Enrichment. PLoS ONE, 2015, 10, e0143566.	1.1	18
26	Placozoa: at least two. Biologia (Poland), 2007, 62, 641-645.	0.8	11
27	A probabilistic model of cell size reduction in Pseudo-nitzschia delicatissima (Bacillariophyta). Journal of Theoretical Biology, 2009, 258, 316-322.	0.8	6
28	covRNA: discovering covariate associations in large-scale gene expression data. BMC Research Notes, 2020, 13, 92.	0.6	0