

# Matthias Wolf

## List of Publications by Year in descending order

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papers

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3191  
citing authors

#	ARTICLE	IF	CITATIONS
1	18S and ITS2 rDNA sequence-structure phylogeny of Prototheca (Chlorophyta, Trebouxiophyceae). <i>Biologia (Poland)</i> , 2022, 77, 569-582.	1.5	4
2	How to Teach about What Is a Species. <i>Biology</i> , 2021, 10, 523.	2.8	0
3	18S rRNA gene sequence-structure phylogeny of the Trypanosomatida (Kinetoplastea, Euglenozoa) with special reference to Trypanosoma. <i>European Journal of Protistology</i> , 2021, 81, 125824.	1.5	9
4	Cryptic species in the parasitic Amoebophrya species complex revealed by a polyphasic approach. <i>Scientific Reports</i> , 2020, 10, 2531.	3.3	28
5	RNA consensus structures for inferring green algal phylogeny: A three-taxon analysis for Golenkinia/Jenufa, Sphaeropleales and Volvocales (Chlorophyta, Chlorophyceae). <i>Fottea</i> , 2020, 20, 68-74.	0.9	5
6	Phylogeny and species delineation in the marine diatom <i>Pseudo-nitzschia</i> (Bacillariophyta) using <i>cox1</i> , <i>LSU</i> , and <i>ITS2</i> <i>rRNA</i> genes: A perspective in character evolution. <i>Journal of Phycology</i> , 2018, 54, 234-248.	2.3	37
7	Species distinctions among closely related strains of Eustigmatophyceae (Stramenopiles) emphasizing ITS2 sequence-structure data: <i>Eustigmatos</i> and <i>Vischeria</i> . <i>European Journal of Phycology</i> , 2018, 53, 471-491.	2.0	26
8	The internal transcribed spacer 2 of Jenufa (Chlorophyta, Chlorophyceae) is extraordinarily long: A hypothesis. <i>Gene</i> , 2018, 678, 100-104.	2.2	2
9	THESES db: the algae 18S rDNA sequence-structure database for inferring phylogenies. <i>Phycologia</i> , 2017, 56, 186-192.	1.4	5
10	18S rDNA sequence-structure phylogeny of the Chlorophyceae with special emphasis on the Sphaeropleales. <i>Plant Gene</i> , 2017, 10, 45-50.	2.3	8
11	Taxonomic assignment of the benthic toxigenic dinoflagellate Gambierdiscus sp. type 6 as Gambierdiscus balechii (Dinophyceae), including its distribution and ciguatoxicity. <i>Harmful Algae</i> , 2017, 67, 107-118.	4.8	31
12	New scenario for speciation in the benthic dinoflagellate genus Coolia (Dinophyceae). <i>Harmful Algae</i> , 2016, 55, 137-149.	4.8	50
13	18S rDNA phylogeny of <i>Pseudo-nitzschia</i> (Bacillariophyceae) inferred from sequence-structure information. <i>Phycologia</i> , 2016, 55, 134-146.	1.4	17
14	A non-toxicogenic but morphologically and phylogenetically distinct new species of <i>Pseudo-nitzschia</i> , <i>P. Asabit</i> sp. nov. (Bacillariophyceae). <i>Journal of Phycology</i> , 2015, 51, 706-725.	2.3	44
15	ITS2 and 18S rDNA sequence-structure phylogeny of Chlorella and allies (Chlorophyta.) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50</i>	2.3	46
16	ITS2 Database V: Twice as Much: Table 1.. <i>Molecular Biology and Evolution</i> , 2015, 32, 3030-3032.	8.9	231
17	Morphological diversity masks phylogenetic similarity of Ettlia and Haematococcus (Chlorophyceae). <i>Phycologia</i> , 2015, 54, 385-397.	1.4	19
18	ITS so much more. <i>Trends in Genetics</i> , 2015, 31, 175-176.	6.7	16

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19	Support for the coevolution of Neoparamoeba and their endosymbionts, Perkinsela amoebae-like organisms. <i>European Journal of Protistology</i> , 2014, 50, 509-523.	1.5	28
20	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.	2.2	63
21	Internal Transcribed Spacer 1 Secondary Structure Analysis Reveals a Common Core throughout the Anaerobic Fungi (Neocallimastigomycota). <i>PLoS ONE</i> , 2014, 9, e91928.	2.5	88
22	Congruence of chloroplast- and nuclear-encoded DNA sequence variations used to assess species boundaries in the soil microalga <i>Heterococcus</i> (Stramenopiles, Xanthophyceae). <i>BMC Evolutionary Biology</i> , 2013, 13, 39.	3.2	26
23	The blood alga: phylogeny of <i>Haematococcus</i> (Chlorophyceae) inferred from ribosomal RNA gene sequence data. <i>European Journal of Phycology</i> , 2013, 48, 318-329.	2.0	49
24	Phylogenetic analysis of ITS2 sequences suggests the taxonomic restructing of <i>Dunaliella viridis</i> (Chlorophyceae), <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 537.7d</i> ( <i>Dunaliella</i> )	2.5	115
25	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.	2.5	115
26	Phylogeny of Oedogoniales, Chaetophorales and Chaetopeltidales (Chlorophyceae): inferences from sequence-structure analysis of ITS2. <i>Annals of Botany</i> , 2012, 109, 109-116.	2.9	38
27	The ITS2 Database. <i>Journal of Visualized Experiments</i> , 2012, , .	0.3	30
28	ITS2 Database IV: Interactive taxon sampling for internal transcribed spacer 2 based phylogenies. <i>Molecular Phylogenetics and Evolution</i> , 2012, 63, 585-588.	2.7	130
29	Internal Transcribed Spacer 2 (nu ITS2 rRNA) Sequence-Structure Phylogenetics: Towards an Automated Reconstruction of the Green Algal Tree of Life. <i>PLoS ONE</i> , 2011, 6, e16931.	2.5	80
30	SSU rRNA GENE PHYLOGENY OF MORPHOSPECIES AFFILIATED TO THE BIOASSAY ALGA "SELENASTRUM CAPRICORNUTUM" RECOVERED THE POLYPHYLETIC ORIGIN OF CRESCENT-SHAPED CHLOROPHYTA1. <i>Journal of Phycology</i> , 2011, 47, 880-893.	2.3	52
31	Ribosomal RNA phylogenetics: the third dimension. <i>Biologia (Poland)</i> , 2010, 65, 388-391.	1.5	6
32	Using compensatory base change analysis of internal transcribed spacer 2 secondary structures to identify three new species in <i>Paramacrobiotus</i> (Tardigrada). <i>Organisms Diversity and Evolution</i> , 2010, 10, 287-296.	1.6	58
33	Microevolution and Speciation in <i>Thalassiosira weissflogii</i> (Bacillariophyta). <i>Protist</i> , 2010, 161, 237-249.	1.5	33
34	A molecular phylogeny of Hypnales (Bryophyta) inferred from ITS2 sequence-structure data. <i>BMC Research Notes</i> , 2010, 3, 320.	1.4	22
35	Compensatory base changes illuminate morphologically difficult taxonomy. <i>Molecular Phylogenetics and Evolution</i> , 2010, 54, 664-669.	2.7	61
36	Including RNA secondary structures improves accuracy and robustness in reconstruction of phylogenetic trees. <i>Biology Direct</i> , 2010, 5, 4.	4.6	154

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37	The ITS2 Database III—sequences and structures for phylogeny. <i>Nucleic Acids Research</i> , 2010, 38, D275-D279.	14.5	223
38	ITS2 sequence-structure phylogeny in the Scenedesmaceae with special reference to <i>Coelastrum</i> (Chlorophyta, Chlorophyceae), including the new genera <i>Comasiella</i> and <i>Pectinodesmus</i> . <i>Phycologia</i> , 2010, 49, 325-335.	1.4	77
39	Evolutionary Distances in the Twilight Zone—A Rational Kernel Approach. <i>PLoS ONE</i> , 2010, 5, e15788.	2.5	13
40	ITS2 secondary structure improves phylogeny estimation in a radiation of blue butterflies of the subgenus <i>Agrodiaetus</i> (Lepidoptera: Lycaenidae: Polyommatus). <i>BMC Evolutionary Biology</i> , 2009, 9, 300.	3.2	69
41	Evolutionary Diversification Indicated by Compensatory Base Changes in ITS2 Secondary Structures in a Complex Fungal Species, <i>Rhizoctonia solani</i> . <i>Journal of Molecular Evolution</i> , 2009, 69, 150-163.	1.8	52
42	ITS2 sequence—structure analysis in phylogenetics: A how-to manual for molecular systematics. <i>Molecular Phylogenetics and Evolution</i> , 2009, 52, 520-523.	2.7	164
43	5.8S-28S rRNA interaction and HMM-based ITS2 annotation. <i>Gene</i> , 2009, 430, 50-57.	2.2	394
44	Modelling cross-hybridization on phylogenetic DNA microarrays increases the detection power of closely related species. <i>Molecular Ecology Resources</i> , 2009, 9, 83-93.	4.8	24
45	ITS2 data corroborate a monophyletic chlorophycean DO-group (Sphaeropleales). <i>BMC Evolutionary Biology</i> , 2008, 8, 218.	3.2	56
46	Synchronous visual analysis and editing of RNA sequence and secondary structure alignments using 4SALE. <i>BMC Research Notes</i> , 2008, 1, 91.	1.4	253
47	ProfDistS: (profile-) distance based phylogeny on sequence—structure alignments. <i>Bioinformatics</i> , 2008, 24, 2401-2402.	4.1	116
48	The ITS2 Database II: homology modelling RNA structure for molecular systematics. <i>Nucleic Acids Research</i> , 2007, 36, D377-D380.	14.5	135
49	Placozoa: at least two. <i>Biologia (Poland)</i> , 2007, 62, 641-645.	1.5	11
50	Distinguishing species. <i>Rna</i> , 2007, 13, 1469-1472.	3.5	284
51	Deep metazoan phylogeny. <i>In Silico Biology</i> , 2007, 7, 151-4.	0.9	5
52	4SALE—a tool for synchronous RNA sequence and secondary structure alignment and editing. <i>BMC Bioinformatics</i> , 2006, 7, 498.	2.6	327
53	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.	14.5	161
54	Efficient and Robust Analysis of Large Phylogenetic Datasets. , 2006, , 104-117.		11

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55	Homology modeling revealed more than 20,000 rRNA internal transcribed spacer 2 (ITS2) secondary structures. <i>Rna</i> , 2005, 11, 1616-1623.	3.5	169
56	PHYLOGENY OF THE HYDRODICTYACEAE (CHLOROPHYCEAE): INFERENCES FROM rDNA DATA1. <i>Journal of Phycology</i> , 2005, 41, 1039-1054.	2.3	72
57	ITS-2 and 18S rRNA Gene Phylogeny of Aplysiniidae (Verongida, Demospongiae). <i>Journal of Molecular Evolution</i> , 2005, 60, 327-336.	1.8	36
58	ProfDist: a tool for the construction of large phylogenetic trees based on profile distances. <i>Bioinformatics</i> , 2005, 21, 2108-2109.	4.1	58
59	A common core of secondary structure of the internal transcribed spacer 2 (ITS2) throughout the Eukaryota. <i>Rna</i> , 2005, 11, 361-364.	3.5	320
60	CBCAnalyzer: inferring phylogenies based on compensatory base changes in RNA secondary structures. <i>In Silico Biology</i> , 2005, 5, 291-4.	0.9	65
61	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
62	THE SECONDARY STRUCTURE OF THE ITS2 TRANSCRIPT INCYCLOTELLA AND STEPHANODISCUS (THALASSIOSIRACEAE, BACILLARIOPHYTA). <i>Diatom Research</i> , 2004, 19, 135-142.	1.2	4
63	Phylogenetic relationship of <i>Chlorella</i> and <i>Parachlorella</i> gen. nov. (Chlorophyta, Trebouxiophyceae). <i>Phycologia</i> , 2004, 43, 529-542.	1.4	214
64	<i>STEPHANODISCUS NEOASTRAEA</i> AND <i>STEPHANODISCUS HETEROSTYLUS</i> (BACILLARIOPHYTA) ARE ONE AND THE SAME SPECIES. <i>Diatom Research</i> , 2002, 17, 445-451.	1.2	5
65	Phylogenetic placement of <i>Chlorotetraedron incus</i> , <i>C. polymorphum</i> and <i>Polyedriopsis spinulosa</i> (Neochloridaceae, Chlorophyta). <i>Phycologia</i> , 2001, 40, 399-402.	1.4	14