

Stefan Zoller

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

2,561
citations

361296

20
h-index

454834

30
g-index

31
all docs

31
docs citations

31
times ranked

3559
citing authors

#	ARTICLE	IF	CITATIONS
1	Bayes or Bootstrap? A Simulation Study Comparing the Performance of Bayesian Markov Chain Monte Carlo Sampling and Bootstrapping in Assessing Phylogenetic Confidence. <i>Molecular Biology and Evolution</i> , 2003, 20, 255-266.	3.5	971
2	Integrating Ambiguously Aligned Regions of DNA Sequences in Phylogenetic Analyses Without Violating Positional Homology. <i>Systematic Biology</i> , 2000, 49, 628-651.	2.7	334
3	Signatures of local adaptation in candidate genes of oaks (<i>Quercus</i> spp.) with respect to present and future climatic conditions. <i>Molecular Ecology</i> , 2016, 25, 5907-5924.	2.0	141
4	Population genomic footprints of selection and associations with climate in natural populations of <i>Arabidopsis halleri</i> from the Alps. <i>Molecular Ecology</i> , 2013, 22, 5594-5607.	2.0	113
5	Slow algae, fast fungi: exceptionally high nucleotide substitution rate differences between lichenized fungi <i>Omphalina</i> and their symbiotic green algae <i>Coccomyxa</i> . <i>Molecular Phylogenetics and Evolution</i> , 2003, 29, 629-640.	1.2	91
6	Accumulation of Mutational Load at the Edges of a Species Range. <i>Molecular Biology and Evolution</i> , 2018, 35, 781-791.	3.5	86
7	Validation of SNP Allele Frequencies Determined by Pooled Next-Generation Sequencing in Natural Populations of a Non-Model Plant Species. <i>PLoS ONE</i> , 2013, 8, e80422.	1.1	81
8	Walking the thin line – ten years later: the dilemma of above- versus below-ground features to support phylogenies in the Russulaceae (Basidiomycota). <i>Fungal Diversity</i> , 2018, 89, 267-292.	4.7	73
9	Rust fungi on Annonaceae II: the genus <i>Dasyscyra</i> Berk. & M.A. Curtis. <i>Mycologia</i> , 2012, 104, 659-681.	0.8	71
10	New approach to an old problem: Incorporating signal from gap-rich regions of ITS and rDNA large subunit into phylogenetic analyses to resolve the <i>Peltigera canina</i> species complex. <i>Mycologia</i> , 2003, 95, 1181-1203.	0.8	62
11	Cysteine-rich angiogenic inducer 61 (Cyr61): a novel soluble biomarker of acute myocardial injury improves risk stratification after acute coronary syndromes. <i>European Heart Journal</i> , 2017, 38, 3493-3502.	1.0	46
12	Genomic vulnerability to rapid climate warming in a tree species with a long generation time. <i>Global Change Biology</i> , 2021, 27, 1181-1195.	4.2	46
13	Distinct evolutionary strategies in the GGPPS family from plants. <i>Frontiers in Plant Science</i> , 2014, 5, 230.	1.7	45
14	Phylogenetic study of <i>Fulgensia</i> and allied <i>Caloplaca</i> and <i>Xanthoria</i> species (Teloschistaceae, lichen-forming ascomycota). <i>American Journal of Botany</i> , 2003, 90, 1095-1103.	0.8	42
15	Systematics of the genus <i>Chaetosphaeria</i> and its allied genera: morphological and phylogenetic diversity in north temperate and neotropical taxa. <i>Mycologia</i> , 2006, 98, 121-130.	0.8	36
16	Circulating FABP4 Is a Prognostic Biomarker in Patients With Acute Coronary Syndrome but Not in Asymptomatic Individuals. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015, 35, 1872-1879.	1.1	36
17	Transmembrane transport and stress response genes play an important role in adaptation of <i>Arabidopsis halleri</i> to metalliferous soils. <i>Scientific Reports</i> , 2018, 8, 16085.	1.6	32
18	Empirical Analysis of the Most Relevant Parameters of Codon Substitution Models. <i>Journal of Molecular Evolution</i> , 2010, 70, 605-612.	0.8	29

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19	A de novo chromosome-level genome assembly of <i>Coregonus</i> sp. "Balchen" One representative of the Swiss Alpine whitefish radiation. <i>Molecular Ecology Resources</i> , 2020, 20, 1093-1109.	2.2	29
20	Genomewide signatures of selection in <i>Epichloa</i> reveal candidate genes for host specialization. <i>Molecular Ecology</i> , 2018, 27, 3070-3086.	2.0	28
21	Improving Phylogenetic Inference with a Semiempirical Amino Acid Substitution Model. <i>Molecular Biology and Evolution</i> , 2013, 30, 469-479.	3.5	27
22	Using transcriptome sequencing and pooled exome capture to study local adaptation in the genome of <i>Pinus cembra</i> . <i>Molecular Ecology Resources</i> , 2019, 19, 536-551.	2.2	23
23	Disentangling the effects of geographic peripherality and habitat suitability on neutral and adaptive genetic variation in Swiss stone pine. <i>Molecular Ecology</i> , 2020, 29, 1972-1989.	2.0	20
24	New Approach to an Old Problem: Incorporating Signal from Gap-Rich Regions of ITS and rDNA Large Subunit into Phylogenetic Analyses to Resolve the <i>Peltigera canina</i> Species Complex. <i>Mycologia</i> , 2003, 95, 1181.	0.8	19
25	TRAL: tandem repeat annotation library. <i>Bioinformatics</i> , 2015, 31, 3051-3053.	1.8	17
26	Genomic signatures of convergent adaptation to Alpine environments in three Brassicaceae species. <i>Molecular Ecology</i> , 2020, 29, 4350-4365.	2.0	17
27	Genetic Evidence for Reproductive Isolation Among Sympatric <i>Epichloa</i> Endophytes as Inferred from Newly Developed Microsatellite Markers. <i>Microbial Ecology</i> , 2015, 70, 51-60.	1.4	15
28	Maximum-Likelihood Tree Estimation Using Codon Substitution Models with Multiple Partitions. <i>Molecular Biology and Evolution</i> , 2015, 32, 2208-2216.	3.5	14
29	A New Semiempirical Codon Substitution Model Based on Principal Component Analysis of Mammalian Sequences. <i>Molecular Biology and Evolution</i> , 2012, 29, 271-277.	3.5	10
30	Gene Duplication and Gain in the Trematode <i>Atriophallophorus winterbourni</i> Contributes to Adaptation to Parasitism. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7