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List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

1,947
citations

236925

25
h-index

276875

41
g-index

60
all docs

60
docs citations

60
times ranked

3007
citing authors

#	ARTICLE	IF	CITATIONS
1	A molecularâ€based identification resource for the arthropods of Finland. <i>Molecular Ecology Resources</i> , 2022, 22, 803-822.	4.8	26
2	Alternative developmental and transcriptomic responses to host plant water limitation in a butterfly metapopulation. <i>Molecular Ecology</i> , 2022, 31, 5666-5683.	3.9	5
3	Mathematical and simulation methods for deriving extinction thresholds in spatial and stochastic models of interacting agents. <i>Methods in Ecology and Evolution</i> , 2021, 12, 162-169.	5.2	1
4	High resolution DNA barcode library for European butterflies reveals continental patterns of mitochondrial genetic diversity. <i>Communications Biology</i> , 2021, 4, 315.	4.4	57
5	Fungal communities decline with urbanizationâ€more in air than in soil. <i>ISME Journal</i> , 2020, 14, 2806-2815.	9.8	53
6	Higher host plant specialization of rootâ€associated endophytes than mycorrhizal fungi along an arctic elevational gradient. <i>Ecology and Evolution</i> , 2020, 10, 8989-9002.	1.9	11
7	Data collected by fruit bodyâ€and DNAâ€based survey methods yield consistent speciesâ€toâ€species association networks in woodâ€inhabiting fungal communities. <i>Oikos</i> , 2020, 129, 1833-1843.	2.7	8
8	Accounting for environmental variation in coâ€occurrence modelling reveals the importance of positive interactions in rootâ€associated fungal communities. <i>Molecular Ecology</i> , 2020, 29, 2736-2746.	3.9	29
9	Monitoring Fungal Communities With the Global Spore Sampling Project. <i>Frontiers in Ecology and Evolution</i> , 2020, 7, .	2.2	25
10	A general mathematical method for predicting spatio-temporal correlations emerging from agent-based models. <i>Journal of the Royal Society Interface</i> , 2020, 17, 20200655.	3.4	4
11	A unified framework for analysis of individual-based models in ecology and beyond. <i>Nature Communications</i> , 2019, 10, 4716.	12.8	21
12	Scaling up the effects of inbreeding depression from individuals to metapopulations. <i>Journal of Animal Ecology</i> , 2019, 88, 1202-1214.	2.8	21
13	Timeâ€frequency warping of spectrograms applied to bird sound analyses. <i>Bioacoustics</i> , 2019, 28, 257-268.	1.7	7
14	Phytotoxin produced by the netted scab pathogen, <i>Streptomyces turgidiscabies</i> strain 65, isolated in Sweden. <i>Journal of General Plant Pathology</i> , 2018, 84, 108-117.	1.0	11
15	Give me a sample of air and I will tell which species are found from your region: Molecular identification of fungi from airborne spore samples. <i>Molecular Ecology Resources</i> , 2018, 18, 511-524.	4.8	54
16	Animal Sound Identifier (<sc>ASI</sc>): software for automated identification of vocal animals. <i>Ecology Letters</i> , 2018, 21, 1244-1254.	6.4	35
17	<sc>Protax</sc>â€fungi: a webâ€based tool for probabilistic taxonomic placement of fungal internal transcribed spacer sequences. <i>New Phytologist</i> , 2018, 220, 517-525.	7.3	69
18	BARCOSEL: a tool for selecting an optimal barcode set for high-throughput sequencing. <i>BMC Bioinformatics</i> , 2018, 19, 257.	2.6	35

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19	Quantifying uncertainty of taxonomic placement in <sc>DNA</sc> barcoding and metabarcoding. <i>Methods in Ecology and Evolution</i> , 2017, 8, 398-407.	5.2	77
20	Carrion fly-derived <sc>DNA</sc> metabarcoding is an effective tool for mammal surveys: Evidence from a known tropical mammal community. <i>Molecular Ecology Resources</i> , 2017, 17, e133-e145.	4.8	60
21	Heat shock and prolonged heat stress attenuate neurotoxin and sporulation gene expression in group I <i>Clostridium botulinum</i> strain ATCC 3502. <i>PLoS ONE</i> , 2017, 12, e0176944.	2.5	11
22	PROTAX-Sound: A probabilistic framework for automated animal sound identification. <i>PLoS ONE</i> , 2017, 12, e0184048.	2.5	8
23	Reintroduction of threatened fungal species via inoculation. <i>Biological Conservation</i> , 2016, 203, 120-124.	4.1	15
24	Minimum information required for a DMET experiment reporting. <i>Pharmacogenomics</i> , 2016, 17, 1533-1545.	1.3	6
25	SANSparallel: interactive homology search against Uniprot. <i>Nucleic Acids Research</i> , 2015, 43, W24-W29.	14.5	38
26	Flight-induced changes in gene expression in the Glanville fritillary butterfly. <i>Molecular Ecology</i> , 2015, 24, 4886-4900.	3.9	28
27	Differential Isoform Expression and Selective Muscle Involvement in Muscular Dystrophies. <i>American Journal of Pathology</i> , 2015, 185, 2833-2842.	3.8	12
28	Transcriptomic Analysis of (Group I) <i>Clostridium botulinum</i> ATCC 3502 Cold Shock Response. <i>PLoS ONE</i> , 2014, 9, e89958.	2.5	24
29	Transcriptome Analysis Reveals Signature of Adaptation to Landscape Fragmentation. <i>PLoS ONE</i> , 2014, 9, e101467.	2.5	24
30	The Cold-Induced Two-Component System CBO0366/CBO0365 Regulates Metabolic Pathways with Novel Roles in Group I <i>Clostridium botulinum</i> ATCC 3502 Cold Tolerance. <i>Applied and Environmental Microbiology</i> , 2014, 80, 306-319.	3.1	11
31	Protein Secretome of Moss Plants (<i>Physcomitrella patens</i>) with Emphasis on Changes Induced by a Fungal Elicitor. <i>Journal of Proteome Research</i> , 2014, 13, 447-459.	3.7	37
32	<i>Arabidopsis</i> NAC45/86 direct sieve element morphogenesis culminating in enucleation. <i>Science</i> , 2014, 345, 933-937.	12.6	173
33	Comparison of <i>Clostridium botulinum</i> genomes shows the absence of cold shock protein coding genes in type E neurotoxin producing strains. <i>Botulinum Journal</i> , 2013, 2, 189.	0.2	8
34	Sequencing of Virulence Genes Shows Limited Genetic Variability in <i>Yersinia pseudotuberculosis</i> . <i>Foodborne Pathogens and Disease</i> , 2013, 10, 21-27.	1.8	2
35	Alternative Sigma Factor σ^E Has an Important Role in Stress Tolerance of <i>Yersinia pseudotuberculosis</i> IP32953. <i>Applied and Environmental Microbiology</i> , 2013, 79, 5970-5977.	3.1	14
36	Significance of Heme-Based Respiration in Meat Spoilage Caused by <i>Leuconostoc gasicomitatum</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 1078-1085.	3.1	59

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37	Lack of RsmA-Mediated Control Results in Constant Hypervirulence, Cell Elongation, and Hyperflagellation in <i>Pectobacterium wasabiae</i> . <i>PLoS ONE</i> , 2013, 8, e54248.	2.5	19
38	Role and Regulation of the Flp/Tad Pilus in the Virulence of <i>Pectobacterium atrosepticum</i> SCRI1043 and <i>Pectobacterium wasabiae</i> SCC3193. <i>PLoS ONE</i> , 2013, 8, e73718.	2.5	53
39	Involvement of Two-Component System CBO0366/CBO0365 in the Cold Shock Response and Growth of Group I (Proteolytic) <i>Clostridium botulinum</i> ATCC 3502 at Low Temperatures. <i>Applied and Environmental Microbiology</i> , 2012, 78, 5466-5470.	3.1	19
40	Requirement for RNA Helicase CsdA for Growth of <i>Yersinia pseudotuberculosis</i> IP32953 at Low Temperatures. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1298-1301.	3.1	19
41	Phenotypic and transcriptomic analyses of Sigma L-dependent characteristics in <i>Listeria monocytogenes</i> EGD-e. <i>Food Microbiology</i> , 2012, 32, 152-164.	4.2	43
42	Expression of multiple nebulin isoforms in human skeletal muscle and brain. <i>Muscle and Nerve</i> , 2012, 46, 730-737.	2.2	21
43	Species' identification and microarray-based comparative genome analysis of <i>Streptomyces</i> species isolated from potato scab lesions in Norway. <i>Molecular Plant Pathology</i> , 2012, 13, 174-186.	4.2	12
44	Expression of Signal Transduction System Encoding Genes of <i>Yersinia pseudotuberculosis</i> IP32953 at 28°C and 3°C. <i>PLoS ONE</i> , 2011, 6, e25063.	2.5	35
45	Role of flhA and motA in growth of <i>Listeria monocytogenes</i> at low temperatures. <i>International Journal of Food Microbiology</i> , 2011, 148, 177-83.	4.7	33
46	Important Role of Class I Heat Shock Genes <i>hrcA</i> and <i>dnaK</i> in the Heat Shock Response and the Response to pH and NaCl Stress of Group I <i>Clostridium botulinum</i> Strain ATCC 3502. <i>Applied and Environmental Microbiology</i> , 2011, 77, 2823-2830.	3.1	35
47	Microarray-based comparison of genetic differences between strains of <i>Streptomyces turgidiscabies</i> with focus on the pathogenicity island. <i>Molecular Plant Pathology</i> , 2010, 11, 733-746.	4.2	10
48	Differential gene expression in senescing leaves of two silver birch genotypes in response to elevated CO ₂ and tropospheric ozone. <i>Plant, Cell and Environment</i> , 2010, 33, 1016-1028.	5.7	37
49	Evolutionary Conservation of Orthoretroviral Long Terminal Repeats (LTRs) and ab initio Detection of Single LTRs in Genomic Data. <i>PLoS ONE</i> , 2009, 4, e5179.	2.5	28
50	Comparative Genomic Hybridization Analysis of Two Predominant Nordic Group I (Proteolytic) <i>Clostridium botulinum</i> Type B Clusters. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2643-2651.	3.1	29
51	Quickly released peroxidase of moss in defense against fungal invaders. <i>New Phytologist</i> , 2009, 183, 432-443.	7.3	61
52	Preliminary study of ion mobility based electronic nose MGD-1 for discrimination of hard cheeses. <i>Journal of Food Engineering</i> , 2009, 92, 202-207.	5.2	40
53	PCR assay for differentiating between Group I (proteolytic) and Group II (nonproteolytic) strains of <i>Clostridium botulinum</i> . <i>International Journal of Food Microbiology</i> , 2008, 124, 108-111.	4.7	23
54	Physiology, Pathology and Relatedness of Human Tissues from Gene Expression Meta-Analysis. <i>PLoS ONE</i> , 2008, 3, e1880.	2.5	23

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55	Speech Dimensionality Analysis on Hypercubical Self-Organizing Maps. Neural Processing Letters, 2003, 17, 125-136.	3.2	8
56	Redundant Hash Addressing of Feature Sequences Using the Self-Organizing Map. Neural Processing Letters, 1999, 10, 25-34.	3.2	0
57	Self-Organizing Maps and Learning Vector Quantization for Feature Sequences. Neural Processing Letters, 1999, 10, 151-159.	3.2	105
58	Self-organizing maps of symbol strings. Neurocomputing, 1998, 21, 19-30.	5.9	214