

Panu Somervuo

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	Self-organizing maps of symbol strings. <i>Neurocomputing</i> , 1998, 21, 19-30.	5.9	214
2	<i>Arabidopsis</i> NAC45/86 direct sieve element morphogenesis culminating in enucleation. <i>Science</i> , 2014, 345, 933-937.	12.6	173
3	Self-Organizing Maps and Learning Vector Quantization for Feature Sequences. <i>Neural Processing Letters</i> , 1999, 10, 151-159.	3.2	105
4	Quantifying uncertainty of taxonomic placement in DNA barcoding and metabarcoding. <i>Methods in Ecology and Evolution</i> , 2017, 8, 398-407.	5.2	77
5	Protax-fungi: a web-based tool for probabilistic taxonomic placement of fungal internal transcribed spacer sequences. <i>New Phytologist</i> , 2018, 220, 517-525.	7.3	69
6	Quickly released peroxidase of moss in defense against fungal invaders. <i>New Phytologist</i> , 2009, 183, 432-443.	7.3	61
7	Carrion fly-derived DNA 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
8	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
9	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
10	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
11	Fungal communities decline with urbanization—more in air than in soil. <i>ISME Journal</i> , 2020, 14, 2806-2815.	9.8	53
12	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
13	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
14	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
15	SANSparallel: interactive homology search against Uniprot. <i>Nucleic Acids Research</i> , 2015, 43, W24-W29.	14.5	38
16	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
17	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
18	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

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19	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 Clostridium botulinum Strain ATCC 3502. Applied and Environmental Microbiology, 2011, 77, 2823-2830.	3.1	35
20	Animal Sound Identifier (<scp>ASI</scp>): software for automated identification of vocal animals. Ecology Letters, 2018, 21, 1244-1254.	6.4	35
21	BARCOSEL: a tool for selecting an optimal barcode set for high-throughput sequencing. BMC Bioinformatics, 2018, 19, 257.	2.6	35
22	Role of flhA and motA in growth of Listeria monocytogenes at low temperatures. International Journal of Food Microbiology, 2011, 148, 177-83.	4.7	33
23	Comparative Genomic Hybridization Analysis of Two Predominant Nordic Group I (Proteolytic) Clostridium botulinum Type B Clusters. Applied and Environmental Microbiology, 2009, 75, 2643-2651.	3.1	29
24	Accounting for environmental variation in co-occurrence modelling reveals the importance of positive interactions in root-associated fungal communities. Molecular Ecology, 2020, 29, 2736-2746.	3.9	29
25	Evolutionary Conservation of Orthoretroviral Long Terminal Repeats (LTRs) and ab initio Detection of Single LTRs in Genomic Data. PLoS ONE, 2009, 4, e5179.	2.5	28
26	Flight-induced changes in gene expression in the Glanville fritillary butterfly. Molecular Ecology, 2015, 24, 4886-4900.	3.9	28
27	A molecular-based identification resource for the arthropods of Finland. Molecular Ecology Resources, 2022, 22, 803-822.	4.8	26
28	Monitoring Fungal Communities With the Global Spore Sampling Project. Frontiers in Ecology and Evolution, 2020, 7, .	2.2	25
29	Transcriptomic Analysis of (Group I) Clostridium botulinum ATCC 3502 Cold Shock Response. PLoS ONE, 2014, 9, e89958.	2.5	24
30	Transcriptome Analysis Reveals Signature of Adaptation to Landscape Fragmentation. PLoS ONE, 2014, 9, e101467.	2.5	24
31	PCR assay for differentiating between Group I (proteolytic) and Group II (nonproteolytic) strains of Clostridium botulinum. International Journal of Food Microbiology, 2008, 124, 108-111.	4.7	23
32	Physiology, Pathology and Relatedness of Human Tissues from Gene Expression Meta-Analysis. PLoS ONE, 2008, 3, e1880.	2.5	23
33	Expression of multiple nebulin isoforms in human skeletal muscle and brain. Muscle and Nerve, 2012, 46, 730-737.	2.2	21
34	A unified framework for analysis of individual-based models in ecology and beyond. Nature Communications, 2019, 10, 4716.	12.8	21
35	Scaling up the effects of inbreeding depression from individuals to metapopulations. Journal of Animal Ecology, 2019, 88, 1202-1214.	2.8	21
36	Involvement of Two-Component System CBO0366/CBO0365 in the Cold Shock Response and Growth of Group I (Proteolytic) Clostridium botulinum ATCC 3502 at Low Temperatures. Applied and Environmental Microbiology, 2012, 78, 5466-5470.	3.1	19

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37	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
38	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
39	Reintroduction of threatened fungal species via inoculation. <i>Biological Conservation</i> , 2016, 203, 120-124.	4.1	15
40	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
41	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
42	Differential Isoform Expression and Selective Muscle Involvement in Muscular Dystrophies. <i>American Journal of Pathology</i> , 2015, 185, 2833-2842.	3.8	12
43	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
44	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
45	Higher host plant specialization of root-associated endophytes than mycorrhizal fungi along an arctic elevational gradient. <i>Ecology and Evolution</i> , 2020, 10, 8989-9002.	1.9	11
46	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
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	Speech Dimensionality Analysis on Hypercubical Self-Organizing Maps. <i>Neural Processing Letters</i> , 2003, 17, 125-136.	3.2	8
49	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
50	Data collected by fruit body- and DNA-based survey methods yield consistent species-species association networks in wood-inhabiting fungal communities. <i>Oikos</i> , 2020, 129, 1833-1843.	2.7	8
51	PROTAX-Sound: A probabilistic framework for automated animal sound identification. <i>PLoS ONE</i> , 2017, 12, e0184048.	2.5	8
52	Time-frequency warping of spectrograms applied to bird sound analyses. <i>Bioacoustics</i> , 2019, 28, 257-268.	1.7	7
53	Minimum information required for a DMET experiment reporting. <i>Pharmacogenomics</i> , 2016, 17, 1533-1545.	1.3	6
54	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

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55	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
56	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
57	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
58	Redundant Hash Addressing of Feature Sequences Using the Self-Organizing Map. <i>Neural Processing Letters</i> , 1999, 10, 25-34.	3.2	0