

Daniela Beisser

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

1,909
citations

623734

14
h-index

434195

31
g-index

35
all docs

35
docs citations

35
times ranked

4413
citing authors

#	ARTICLE	IF	CITATIONS
1	Bioconda: sustainable and comprehensive software distribution for the life sciences. <i>Nature Methods</i> , 2018, 15, 475-476.	19.0	714
2	Mutational dynamics between primary and relapse neuroblastomas. <i>Nature Genetics</i> , 2015, 47, 872-877.	21.4	253
3	BioNet: an R-Package for the functional analysis of biological networks. <i>Bioinformatics</i> , 2010, 26, 1129-1130.	4.1	215
4	Human <sc>TLR</sc> 8 senses <sc>UR</sc> / <sc>URR</sc> motifs in bacterial and mitochondrial <sc>RNA</sc>. <i>EMBO Reports</i> , 2015, 16, 1656-1663.	4.5	110
5	Geographic distance and mountain ranges structure freshwater protist communities on a European scale. <i>Metabarcoding and Metagenomics</i> , 0, 2, e21519.	0.0	87
6	Effects of Silver Nitrate and Silver Nanoparticles on a Planktonic Community: General Trends after Short-Term Exposure. <i>PLoS ONE</i> , 2014, 9, e95340.	2.5	65
7	Tardigrade workbench: comparing stress-related proteins, sequence-similar and functional protein clusters as well as RNA elements in tardigrades. <i>BMC Genomics</i> , 2009, 10, 469.	2.8	59
8	Factors shaping community patterns of protists and bacteria on a European scale. <i>Environmental Microbiology</i> , 2020, 22, 2243-2260.	3.8	49
9	Evolution of heterotrophy in chrysophytes as reflected by comparative transcriptomics. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	40
10	Transcriptome Analysis in Tardigrade Species Reveals Specific Molecular Pathways for Stress Adaptations. <i>Bioinformatics and Biology Insights</i> , 2012, 6, BBI.S9150.	2.0	39
11	Comprehensive transcriptome analysis provides new insights into nutritional strategies and phylogenetic relationships of chrysophytes. <i>PeerJ</i> , 2017, 5, e2832.	2.0	38
12	Robustness and accuracy of functional modules in integrated network analysis. <i>Bioinformatics</i> , 2012, 28, 1887-1894.	4.1	29
13	Trade-off between taxon diversity and functional diversity in European lake ecosystems. <i>Molecular Ecology</i> , 2016, 25, 5876-5888.	3.9	24
14	Characterization of pancreatic glucagon-producing tumors and pituitary gland tumors in transgenic mice overexpressing <i>MYCN</i> in <i>hGFAP</i>-positive cells. <i>Oncotarget</i> , 2016, 7, 74415-74426.	1.8	21
15	Ecological Differentiation in Two Major Freshwater Bacterial Taxa Along Environmental Gradients. <i>Frontiers in Microbiology</i> , 2020, 11, 154.	3.5	17
16	Propionate supplementation promotes the expansion of peripheral regulatory T-Cells in patients with end-stage renal disease. <i>Journal of Nephrology</i> , 2020, 33, 817-827.	2.0	14
17	Natrix: a Snakemake-based workflow for processing, clustering, and taxonomically assigning amplicon sequencing reads. <i>BMC Bioinformatics</i> , 2020, 21, 526.	2.6	13
18	Effects of short-term flooding on aquatic and terrestrial microeukaryotic communities: a mesocosm approach. <i>Aquatic Microbial Ecology</i> , 2017, 80, 257-272.	1.8	13

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19	Molecular Data Reveal a Cryptic Diversity in the Genus <i>Urotricha</i> (Alveolata, Ciliophora,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 507 Distribution. <i>Frontiers in Microbiology</i> , 2021, 12, 787290.	3.5	12
20	Integrated pathway modules using time-course metabolic profiles and EST data from <i>Milnesium tardigradum</i> . <i>BMC Systems Biology</i> , 2012, 6, 72.	3.0	11
21	Quantification of the covariation of lake microbiomes and environmental variables using a machine learning-based framework. <i>Molecular Ecology</i> , 2021, 30, 2131-2144.	3.9	11
22	A multi-omics study on quantifying antimicrobial resistance in European freshwater lakes. <i>Environment International</i> , 2021, 157, 106821.	10.0	9
23	TaxMapper: an analysis tool, reference database and workflow for metatranscriptome analysis of eukaryotic microorganisms. <i>BMC Genomics</i> , 2017, 18, 787.	2.8	8
24	Quantitative Proteomics Reveals Ecophysiological Effects of Light and Silver Stress on the Mixotrophic Protist <i>Poterioochromonas malhamensis</i> . <i>PLoS ONE</i> , 2017, 12, e0168183.	2.5	8
25	Intraspecific Variation in Protists: Clues for Microevolution from <i>Poteriospumella lacustris</i> (Chrysophyceae). <i>Genome Biology and Evolution</i> , 2019, 11, 2492-2504.	2.5	7
26	Nutrient-driven genome evolution revealed by comparative genomics of chryomonad flagellates. <i>Communications Biology</i> , 2021, 4, 328.	4.4	7
27	Putatively asexual chrysophytes have meiotic genes: evidence from transcriptomic data. <i>PeerJ</i> , 2019, 6, e5894.	2.0	7
28	Bioinformatics identifies tardigrade molecular adaptations including the DNA- family and first steps towards dynamical modelling. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2011, 49, 120-126.	1.4	6
29	Silver stress differentially affects growth of phototrophic and heterotrophic chryomonad flagellate populations. <i>Environmental Pollution</i> , 2019, 244, 314-322.	7.5	6
30	Interaction-Specific Changes in the Transcriptome of <i>Polynucleobacter asymbioticus</i> Caused by Varying Protistan Communities. <i>Frontiers in Microbiology</i> , 2019, 10, 1498.	3.5	5
31	The relationship between land cover and microbial community composition in European lakes. <i>Science of the Total Environment</i> , 2022, 825, 153732.	8.0	5
32	xHeinz: an algorithm for mining cross-species network modules under a flexible conservation model. <i>Bioinformatics</i> , 2015, 31, 3147-3155.	4.1	4
33	Functional and phylogenetic analysis of the core transcriptome of Ochromonadales. <i>Metabarcoding and Metagenomics</i> , 0, 1, e19862.	0.0	1