

# 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  | 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         |
| 2  | 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        |
| 3  | Nutrient-driven genome evolution revealed by comparative genomics of chryomonad flagellates. <i>Communications Biology</i> , 2021, 4, 328.   | 4.4  | 7         |
| 4  | A multi-omics study on quantifying antimicrobial resistance in European freshwater lakes. <i>Environment International</i> , 2021, 157, 106821.  | 10.0 | 9         |
| 5  | Molecular Data Reveal a Cryptic Diversity in the Genus <i>Urotricha</i> (Alveolata, Ciliophora,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 505 Distribution. <i>Frontiers in Microbiology</i> , 2021, 12, 787290. | 3.5  | 12        |
| 6  | Matrix: a Snakemake-based workflow for processing, clustering, and taxonomically assigning amplicon sequencing reads. <i>BMC Bioinformatics</i> , 2020, 21, 526.   | 2.6  | 13        |
| 7  | 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        |
| 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  | Ecological Differentiation in Two Major Freshwater Bacterial Taxa Along Environmental Gradients. <i>Frontiers in Microbiology</i> , 2020, 11, 154.   | 3.5  | 17        |
| 10 | 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         |
| 11 | Intraspecific Variation in Protists: Clues for Microevolution from <i>Poteroispumella lacustris</i> (Chrysophyceae). <i>Genome Biology and Evolution</i> , 2019, 11, 2492-2504.                                  | 2.5  | 7         |
| 12 | Silver stress differentially affects growth of phototrophic and heterotrophic chryomonad flagellate populations. <i>Environmental Pollution</i> , 2019, 244, 314-322.  | 7.5  | 6         |
| 13 | Putatively asexual chrysophytes have meiotic genes: evidence from transcriptomic data. <i>PeerJ</i> , 2019, 6, e5894.  | 2.0  | 7         |
| 14 | Evolution of heterotrophy in chrysophytes as reflected by comparative transcriptomics. <i>FEMS Microbiology Ecology</i> , 2018, 94, .  | 2.7  | 40        |
| 15 | Bioconda: sustainable and comprehensive software distribution for the life sciences. <i>Nature Methods</i> , 2018, 15, 475-476.  | 19.0 | 714       |
| 16 | TaxMapper: an analysis tool, reference database and workflow for metatranscriptome analysis of eukaryotic microorganisms. <i>BMC Genomics</i> , 2017, 18, 787.   | 2.8  | 8         |
| 17 | Quantitative Proteomics Reveals Ecophysiological Effects of Light and Silver Stress on the Mixotrophic Protist <i>Poteroiochromonas malhamensis</i> . <i>PLoS ONE</i> , 2017, 12, e0168183.                      | 2.5  | 8         |
| 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 | Comprehensive transcriptome analysis provides new insights into nutritional strategies and phylogenetic relationships of chrysophytes. <i>PeerJ</i> , 2017, 5, e2832.  | 2.0  | 38        |
| 20 | Trade-off between taxon diversity and functional diversity in European lake ecosystems. <i>Molecular Ecology</i> , 2016, 25, 5876-5888.  | 3.9  | 24        |
| 21 | Characterization of pancreatic glucagon-producing tumors and pituitary gland tumors in transgenic mice overexpressing MYCN in hGFAP-positive cells. <i>Oncotarget</i> , 2016, 7, 74415-74426.                            | 1.8  | 21        |
| 22 | Human TLR 8 senses UR / URR motifs in bacterial and mitochondrial RNA. <i>EMBO Reports</i> , 2015, 16, 1656-1663.  | 4.5  | 110       |
| 23 | xHeinz: an algorithm for mining cross-species network modules under a flexible conservation model. <i>Bioinformatics</i> , 2015, 31, 3147-3155.  | 4.1  | 4         |
| 24 | Mutational dynamics between primary and relapse neuroblastomas. <i>Nature Genetics</i> , 2015, 47, 872-877.  | 21.4 | 253       |
| 25 | 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        |
| 26 | Robustness and accuracy of functional modules in integrated network analysis. <i>Bioinformatics</i> , 2012, 28, 1887-1894.   | 4.1  | 29        |
| 27 | 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        |
| 28 | 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        |
| 29 | 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         |
| 30 | BioNet: an R-Package for the functional analysis of biological networks. <i>Bioinformatics</i> , 2010, 26, 1129-1130.  | 4.1  | 215       |
| 31 | 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        |
| 32 | Functional and phylogenetic analysis of the core transcriptome of Ochromonadales. <i>Metabarcoding and Metagenomics</i> , 0, 1, e19862.  | 0.0  | 1         |
| 33 | Geographic distance and mountain ranges structure freshwater protist communities on a European scale. <i>Metabarcoding and Metagenomics</i> , 0, 2, e21519.  | 0.0  | 87        |