

# Antonis Chatzinotas

## List of Publications by Year in descending order

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Version: 2024-02-01

98  
papers

5,704  
citations

87888

38  
h-index

85541

71  
g-index

103  
all docs

103  
docs citations

103  
times ranked

7882  
citing authors

#	ARTICLE	IF	CITATIONS
1	Transport of marine tracer phage particles in soil. <i>Science of the Total Environment</i> , 2022, 814, 152704.	8.0	2
2	Mycelia-Assisted Isolation of Non-Host Bacteria Able to Co-Transport Phages. <i>Viruses</i> , 2022, 14, 195.	3.3	3
3	Phage co-transport with hyphal-riding bacteria fuels bacterial invasion in a water-unsaturated microbial model system. <i>ISME Journal</i> , 2022, 16, 1275-1283.	9.8	24
4	Nutritional interdependencies and a carbazole dioxygenase are key elements of a bacterial consortium relying on a <i>Sphingomonas</i> for the degradation of the fungicide thiabendazole. <i>Environmental Microbiology</i> , 2022, 24, 5105-5122.	3.8	9
5	Tracking, targeting, and conserving soil biodiversity. <i>Science</i> , 2021, 371, 239-241.	12.6	151
6	Beyond nitrogen: phosphorus – estimating the minimum niche dimensionality for resource competition between phytoplankton. <i>Ecology Letters</i> , 2021, 24, 761-771.	6.4	16
7	Mining Synergistic Microbial Interactions: A Roadmap on How to Integrate Multi-Omics Data. <i>Microorganisms</i> , 2021, 9, 840.	3.6	8
8	Disentangling multiple chemical and non-chemical stressors in a lotic ecosystem using a longitudinal approach. <i>Science of the Total Environment</i> , 2021, 769, 144324.	8.0	24
9	OrtSuite: from genomes to prediction of microbial interactions within targeted ecosystem processes. <i>Life Science Alliance</i> , 2021, 4, e202101167.	2.8	4
10	Community and single cell analyses reveal complex predatory interactions between bacteria in high diversity systems. <i>Nature Communications</i> , 2021, 12, 5481.	12.8	14
11	Phage strategies facilitate bacterial coexistence under environmental variability. <i>PeerJ</i> , 2021, 9, e12194.	2.0	14
12	Near streambed flow shapes microbial guilds within and across trophic levels in fluvial biofilms. <i>Limnology and Oceanography</i> , 2020, 65, 2261-2277.	3.1	16
13	Blind spots in global soil biodiversity and ecosystem function research. <i>Nature Communications</i> , 2020, 11, 3870.	12.8	192
14	Environmental Factors and Host Microbiomes Shape Host Pathogen Dynamics. <i>Trends in Parasitology</i> , 2020, 36, 616-633.	3.3	74
15	Resilience trinity: safeguarding ecosystem functioning and services across three different time horizons and decision contexts. <i>Oikos</i> , 2020, 129, 445-456.	2.7	33
16	Prospects for Integrating Disturbances, Biodiversity and Ecosystem Functioning Using Microbial Systems. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	2.2	2
17	Diversity and coexistence are influenced by time-dependent species interactions in a predator-prey system. <i>Ecology Letters</i> , 2020, 23, 983-993.	6.4	39
18	Intraguild Predation: Predatory Networks at the Microbial Scale. , 2020, , 65-87.		3

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19	Ecological Functions of Agricultural Soil Bacteria and Microeukaryotes in Chitin Degradation: A Case Study. <i>Frontiers in Microbiology</i> , 2019, 10, 1293.	3.5	52
20	Drought modulates interactions between arbuscular mycorrhizal fungal diversity and barley genotype diversity. <i>Scientific Reports</i> , 2019, 9, 9650.	3.3	42
21	Temperature and stoichiometric dependence of phytoplankton traits. <i>Ecology</i> , 2019, 100, e02875.	3.2	12
22	Mycelial Effects on Phage Retention during Transport in a Microfluidic Platform. <i>Environmental Science &amp; Technology</i> , 2019, 53, 11755-11763.	10.0	19
23	Bacteria and microeukaryotes are differentially segregated in sympatric wastewater microhabitats. <i>Environmental Microbiology</i> , 2019, 21, 1757-1770.	3.8	13
24	Capacity of Ecosystems to Degrade Anthropogenic Chemicals. , 2019, , 179-182.		0
25	Evaluation of Sequencing Library Preparation Protocols for Viral Metagenomic Analysis from Pristine Aquifer Groundwaters. <i>Viruses</i> , 2019, 11, 484.	3.3	27
26	Complete genome sequence of Pseudoalteromonas virus vB_PspP-H6/1 that infects Pseudoalteromonas sp. strain H6. <i>Marine Genomics</i> , 2019, 47, 100667.	1.1	2
27	Have an Ion on It: The Life Cycle of <i>Bdellovibrio bacteriovorus</i> Viewed by Helium Ion Microscopy. <i>Advanced Biology</i> , 2019, 3, e1800250.	3.0	17
28	Changes of the Specific Infectivity of Tracer Phages during Transport in Porous Media. <i>Environmental Science &amp; Technology</i> , 2018, 52, 3486-3492.	10.0	5
29	Different Recovery Processes of Soil Ammonia Oxidizers from Flooding Disturbance. <i>Microbial Ecology</i> , 2018, 76, 1041-1052.	2.8	18
30	Interactions between predation and disturbances shape prey communities. <i>Scientific Reports</i> , 2018, 8, 2968.	3.3	21
31	People, pollution and pathogens – Global change impacts in mountain freshwater ecosystems. <i>Science of the Total Environment</i> , 2018, 622-623, 756-763.	8.0	99
32	Rhizosphere Protists Change Metabolite Profiles in <i>Zea mays</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 857.	3.5	20
33	Molecular quantification and differentiation of <i>Candida</i> species in biological specimens of patients with liver cirrhosis. <i>PLoS ONE</i> , 2018, 13, e0197319.	2.5	33
34	Where less may be more: how the rare biosphere pulls ecosystems strings. <i>ISME Journal</i> , 2017, 11, 853-862.	9.8	857
35	Isolation of a bacterial consortium able to degrade the fungicide thiabendazole: the key role of a <i>Sphingomonas</i> phylotype. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 3881-3893.	3.6	23
36	Soil protistology rebooted: 30 fundamental questions to start with. <i>Soil Biology and Biochemistry</i> , 2017, 111, 94-103.	8.8	130

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37	Killing the killer: predation between protists and predatory bacteria. <i>FEMS Microbiology Letters</i> , 2017, 364, .	1.8	29
38	Transient recovery dynamics of a predator-prey system under press and pulse disturbances. <i>BMC Ecology</i> , 2017, 17, 13.	3.0	13
39	Complete genome sequence of Pseudoalteromonas phage vB_PspS-H40/1 (formerly H40/1) that infects Pseudoalteromonas sp. strain H40 and is used as biological tracer in hydrological transport studies. <i>Standards in Genomic Sciences</i> , 2017, 12, 20.	1.5	8
40	Complete Genome Sequence of Alteromonas Virus vB_AspP-H4/4. <i>Genome Announcements</i> , 2017, 5, .	0.8	10
41	A Generalist Protist Predator Enables Coexistence in Multitrophic Predator-Prey Systems Containing a Phage and the Bacterial Predator Bdellovibrio. <i>Frontiers in Ecology and Evolution</i> , 2017, 5, .	2.2	28
42	Soil Viral Communities Vary Temporally and along a Land Use Transect as Revealed by Virus-Like Particle Counting and a Modified Community Fingerprinting Approach (fRAPD). <i>Frontiers in Microbiology</i> , 2017, 8, 1975.	3.5	47
43	Genetic diversity in chrysophytes: Comparison of different gene markers. <i>Fottea</i> , 2017, 17, 209-221.	0.9	15
44	Root exudate cocktails: the link between plant diversity and soil microorganisms?. <i>Ecology and Evolution</i> , 2016, 6, 7387-7396.	1.9	183
45	Marine Phages As Tracers: Effects of Size, Morphology, and Physico-Chemical Surface Properties on Transport in a Porous Medium. <i>Environmental Science &amp; Technology</i> , 2016, 50, 12816-12824.	10.0	22
46	Trade-off between taxon diversity and functional diversity in European lake ecosystems. <i>Molecular Ecology</i> , 2016, 25, 5876-5888.	3.9	24
47	Trophic complexity in aqueous systems: bacterial species richness and protistan predation regulate dissolved organic carbon and dissolved total nitrogen removal. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20152724.	2.6	47
48	Kombucha tea fermentation: Microbial and biochemical dynamics. <i>International Journal of Food Microbiology</i> , 2016, 220, 63-72.	4.7	272
49	Studying Protistan Communities in Hydrocarbon-Contaminated Environments. <i>Springer Protocols</i> , 2015, , 225-252.	0.3	1
50	The extent of functional redundancy changes as species' roles shift in different environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14888-14893.	7.1	126
51	The influence of environmental factors on protistan microorganisms in grassland soils along a land-use gradient. <i>Science of the Total Environment</i> , 2015, 537, 33-42.	8.0	20
52	Interannual variation in land-use intensity enhances grassland multidiversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 308-313.	7.1	243
53	Multiple micro-predators controlling bacterial communities in the environment. <i>Current Opinion in Biotechnology</i> , 2014, 27, 185-190.	6.6	81
54	Phylogenetic and Functional Diversity Within Toluene-Degrading, Sulphate-Reducing Consortia Enriched from a Contaminated Aquifer. <i>Microbial Ecology</i> , 2014, 68, 222-234.	2.8	30

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55	Primer pairs for the specific environmental detection and T-RFLP analysis of the ubiquitous flagellate taxa Chrysophyceae and Kinetoplastea. <i>Journal of Microbiological Methods</i> , 2014, 100, 8-16.	1.6	10
56	Evaluating T-RFLP protocols to sensitively analyze the genetic diversity and community changes of soil alkane degrading bacteria. <i>European Journal of Soil Biology</i> , 2014, 65, 107-113.	3.2	9
57	Application of Qualitative and Quantitative Real-Time PCR, Direct Sequencing, and Terminal Restriction Fragment Length Polymorphism Analysis for Detection and Identification of Polymicrobial 16S rRNA Genes in Ascites. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1754-1757.	3.9	14
58	Effects of long-term differential fertilization on eukaryotic microbial communities in an arable soil: a multiple barcoding approach. <i>Molecular Ecology</i> , 2014, 23, 3341-3355.	3.9	163
59	Evaluating the Assignment of <i>alkB</i> Terminal Restriction Fragments and Sequence Types to Distinct Bacterial Taxa. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3129-3132.	3.1	10
60	Alkane-degrading bacteria at the soil-litter interface: comparing isolates with T-RFLP-based community profiles. <i>FEMS Microbiology Ecology</i> , 2013, 86, 45-58.	2.7	28
61	Diversity of protists and bacteria determines predation performance and stability. <i>ISME Journal</i> , 2013, 7, 1912-1921.	9.8	93
62	Assimilation of Cellulose-Derived Carbon by Microeukaryotes in Oxidic and Anoxic Slurries of an Aerated Soil. <i>Applied and Environmental Microbiology</i> , 2013, 79, 5777-5781.	3.1	16
63	Predator richness increases the effect of prey diversity on prey yield. <i>Nature Communications</i> , 2012, 3, 1305.	12.8	116
64	Field Testing of Arsenic in Groundwater Samples of Bangladesh Using a Test Kit Based on Lyophilized Bioreporter Bacteria. <i>Environmental Science &amp; Technology</i> , 2012, 46, 3281-3287.	10.0	70
65	Plant litter and soil type drive abundance, activity and community structure of <i>alkB</i> harbouring microbes in different soil compartments. <i>ISME Journal</i> , 2012, 6, 1763-1774.	9.8	45
66	Use of mycelia as paths for the isolation of contaminant-degrading bacteria from soil. <i>Microbial Biotechnology</i> , 2012, 5, 142-148.	4.2	35
67	Evaluation of FT-IR spectroscopy as a tool to quantify bacteria in binary mixed cultures. <i>Journal of Microbiological Methods</i> , 2011, 86, 182-187.	1.6	12
68	Visualisation of gradients in arsenic concentrations around individual roots of <i>Zea mays</i> L. using agar-immobilized bioreporter bacteria. <i>Plant and Soil</i> , 2010, 329, 295-306.	3.7	13
69	Application of the denaturing gradient gel electrophoresis (DGGE) technique as an efficient diagnostic tool for ciliate communities in soil. <i>Science of the Total Environment</i> , 2010, 408, 1221-1225.	8.0	42
70	TAXONOMIC AND ECOLOGICAL CHARACTERIZATION OF STOMATOCYSTS OF SPUMELLA-LIKE FLAGELLATES (CHRYSOPHYCEAE)1. <i>Journal of Phycology</i> , 2010, 46, 868-881.	2.3	46
71	Enrichment and characterization of a sulfate-reducing toluene-degrading microbial consortium by combining <i>in situ</i> microcosms and stable isotope probing techniques. <i>FEMS Microbiology Ecology</i> , 2010, 71, 237-246.	2.7	63
72	Functional characterization of an anaerobic benzene-degrading enrichment culture by DNA stable isotope probing. <i>Environmental Microbiology</i> , 2010, 12, 401-411.	3.8	103

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73	Development of a Fatty Acid and RNA Stable Isotope Probing-Based Method for Tracking Protist Grazing on Bacteria in Wastewater. <i>Applied and Environmental Microbiology</i> , 2010, 76, 8222-8230.	3.1	17
74	Short-term disturbance of a grazer has long-term effects on bacterial communities—Relevance of trophic interactions for recovery from pesticide effects. <i>Aquatic Toxicology</i> , 2010, 99, 205-211.	4.0	14
75	Evaluation of Single-Nucleotide Primer Extension for Detection and Typing of Phylogenetic Markers Used for Investigation of Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2850-2860.	3.1	13
76	Pilot-scale comparison of constructed wetlands operated under high hydraulic loading rates and attached biofilm reactors for domestic wastewater treatment. <i>Science of the Total Environment</i> , 2009, 407, 2996-3003.	8.0	60
77	Genetic Diversity of Eukaryotic Plankton Assemblages in Eastern Tibetan Lakes Differing by their Salinity and Altitude. <i>Microbial Ecology</i> , 2009, 58, 569-581.	2.8	51
78	Optimization of preservation conditions of As (III) bioreporter bacteria. <i>Applied Microbiology and Biotechnology</i> , 2009, 82, 785-792.	3.6	18
79	The single-nucleotide primer extension (SNUPE) method for the multiplex detection of various DNA sequences: from detection of point mutations to microbial ecology. <i>Biochemical Society Transactions</i> , 2009, 37, 454-459.	3.4	19
80	SSU rRNA gene variation resolves population heterogeneity and ecophysiological differentiation within a morphospecies ( <i>Stramenopiles</i> , <i>Chrysophyceae</i> ). <i>Limnology and Oceanography</i> , 2009, 54, 171-181.	3.1	30
81	Diversity and in situ quantification of <i>Acidobacteria</i> subdivision 1 in an acidic mining lake. <i>FEMS Microbiology Ecology</i> , 2008, 63, 107-117.	2.7	57
82	Internal arsenite bioassay calibration using multiple bioreporter cell lines. <i>Microbial Biotechnology</i> , 2008, 1, 149-157.	4.2	45
83	Improved coverage of fungal diversity in polluted groundwaters by semi-nested PCR. <i>Science of the Total Environment</i> , 2008, 406, 324-330.	8.0	11
84	Single-Nucleotide Primer Extension Assay for Detection and Sequence Typing of <i>Dehalococcoides</i> spp. <i>Applied and Environmental Microbiology</i> , 2008, 74, 300-304.	3.1	13
85	Cultivation-independent analysis reveals a shift in ciliate 18S rRNA gene diversity in a polycyclic aromatic hydrocarbon-polluted soil. <i>FEMS Microbiology Ecology</i> , 2007, 62, 365-373.	2.7	84
86	Molecular comparison of cultivable protozoa from a pristine and a polycyclic aromatic hydrocarbon polluted site. <i>Soil Biology and Biochemistry</i> , 2007, 39, 139-148.	8.8	49
87	Andalucia (n. gen.)-the Deepest Branch Within Jakobids ( <i>Jakobida</i> ; <i>Excavata</i> ), Based on Morphological and Molecular Study of a New Flagellate from Soil. <i>Journal of Eukaryotic Microbiology</i> , 2006, 53, 112-120.	1.7	53
88	Molecular Phylogeny of Litostome Ciliates ( <i>Ciliophora</i> , <i>Litostomatea</i> ) with Emphasis on Free-Living Haptorian Genera. <i>Protist</i> , 2006, 157, 261-278.	1.5	71
89	Evidence for Geographic Isolation and Signs of Endemism within a Protistan Morphospecies. <i>Applied and Environmental Microbiology</i> , 2006, 72, 5159-5164.	3.1	67
90	High diversity of the 'Spumella-like' flagellates: an investigation based on the SSU rRNA gene sequences of isolates from habitats located in six different geographic regions. <i>Environmental Microbiology</i> , 2005, 7, 685-697.	3.8	151

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91	Impacts of heavy metal contamination and phytoremediation on a microbial community during a twelve-month microcosm experiment. <i>FEMS Microbiology Ecology</i> , 2004, 48, 273-283.	2.7	135
92	Comparative 16S rDNA and 16S rRNA sequence analysis indicates that Actinobacteria might be a dominant part of the metabolically active bacteria in heavy metal-contaminated bulk and rhizosphere soil. <i>Environmental Microbiology</i> , 2003, 5, 896-907.	3.8	234
93	Use of isotopic and molecular techniques to link toluene degradation in denitrifying aquifer microcosms to specific microbial populations. <i>Archives of Microbiology</i> , 2001, 175, 270-281.	2.2	55
94	Tracing toluene-assimilating sulfate-reducing bacteria using <sup>13</sup> C-incorporation in fatty acids and whole-cell hybridization. <i>FEMS Microbiology Ecology</i> , 2001, 38, 123-131.	2.7	43
95	Tracing toluene-assimilating sulfate-reducing bacteria using <sup>13</sup> C-incorporation in fatty acids and whole-cell hybridization. <i>FEMS Microbiology Ecology</i> , 2001, 38, 123-131.	2.7	5
96	Analysis of Broad-scale Differences in Microbial Community Composition of Two Pristine Forest Soils. <i>Systematic and Applied Microbiology</i> , 1998, 21, 579-587.	2.8	75
97	Analysis of bacterial community structure in bulk soil by in situ hybridization. <i>Archives of Microbiology</i> , 1997, 168, 185-192.	2.2	219
98	Microbial diversity-ecosystem function relationships across environmental gradients. <i>Research Ideas and Outcomes</i> , 0, 6, .	1.0	8