

Martin Taubert

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

1,326
citations

430442

18
h-index

377514

34
g-index

38
all docs

38
docs citations

38
times ranked

1563
citing authors

#	ARTICLE	IF	CITATIONS
1	Dark CO ₂ fixation in temperate beech and pine forest soils. <i>Soil Biology and Biochemistry</i> , 2022, 165, 108526.	4.2	11
2	Nematode grazing increases the allocation of plant-derived carbon to soil bacteria and saprophytic fungi, and activates bacterial species of the rhizosphere. <i>Pedobiologia</i> , 2022, 90, 150787.	0.5	10
3	Bolstering fitness via CO ₂ fixation and organic carbon uptake: mixotrophs in modern groundwater. <i>ISME Journal</i> , 2022, 16, 1153-1162.	4.4	21
4	Microbial community functioning during plant litter decomposition. <i>Scientific Reports</i> , 2022, 12, 7451.	1.6	12
5	Biogeochemical Cycling of Carbon and Nitrogen in Groundwater—Key Processes and Microbial Drivers. , 2022, , 412-427.		0
6	Phenotypic Differentiation of Autotrophic and Heterotrophic Bacterial Cells Using Raman-D ₂ O Labeling. <i>Analytical Chemistry</i> , 2022, 94, 7759-7766.	3.2	4
7	Bacterial Necromass Is Rapidly Metabolized by Heterotrophic Bacteria and Supports Multiple Trophic Levels of the Groundwater Microbiome. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5
8	Carbon fixation rates in groundwater similar to those in oligotrophic marine systems. <i>Nature Geoscience</i> , 2022, 15, 561-567.	5.4	28
9	Phylogenetic and metabolic diversity have contrasting effects on the ecological functioning of bacterial communities. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	3
10	Monitoring Deuterium Uptake in Single Bacterial Cells via Two-Dimensional Raman Correlation Spectroscopy. <i>Analytical Chemistry</i> , 2021, 93, 7714-7723.	3.2	18
11	The economical lifestyle of CPR bacteria in groundwater allows little preference for environmental drivers. <i>Environmental Microbiomes</i> , 2021, 16, 24.	2.2	36
12	Rates of dark CO ₂ fixation are driven by microbial biomass in a temperate forest soil. <i>Soil Biology and Biochemistry</i> , 2020, 150, 107950.	4.2	33
13	Influence of Carbon Sources on Quantification of Deuterium Incorporation in Heterotrophic Bacteria: A Raman-Stable Isotope Labeling Approach. <i>Analytical Chemistry</i> , 2020, 92, 11429-11437.	3.2	17
14	SIP-Metaproteomics: Linking Microbial Taxonomy, Function, and Activity. <i>Methods in Molecular Biology</i> , 2019, 2046, 57-69.	0.4	2
15	Predominance of <i>Cand. Patescibacteria</i> in Groundwater Is Caused by Their Preferential Mobilization From Soils and Flourishing Under Oligotrophic Conditions. <i>Frontiers in Microbiology</i> , 2019, 10, 1407.	1.5	160
16	Communal metabolism by <i>Methylococcaceae</i> and <i>Methylophilaceae</i> is driving rapid aerobic methane oxidation in sediments of a shallow seep near Elba, Italy. <i>Environmental Microbiology</i> , 2019, 21, 3780-3795.	1.8	28
17	Divergent microbial communities in groundwater and overlying soils exhibit functional redundancy for plant-polysaccharide degradation. <i>PLoS ONE</i> , 2019, 14, e0212937.	1.1	30
18	Tracking active groundwater microbes with D ₂ O labelling to understand their ecosystem function. <i>Environmental Microbiology</i> , 2018, 20, 369-384.	1.8	57

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19	Comparative Genomics and Mutational Analysis Reveals a Novel XoxF-Utilizing Methylophile in the Roseobacter Group Isolated From the Marine Environment. <i>Frontiers in Microbiology</i> , 2018, 9, 766.	1.5	13
20	Growth promotion and inhibition induced by interactions of groundwater bacteria. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	16
21	Methylamine as a nitrogen source for microorganisms from a coastal marine environment. <i>Environmental Microbiology</i> , 2017, 19, 2246-2257.	1.8	50
22	DNA-, RNA-, and Protein-Based Stable-Isotope Probing for High-Throughput Biomarker Analysis of Active Microorganisms. <i>Methods in Molecular Biology</i> , 2017, 1539, 57-74.	0.4	21
23	Analysis of Active Methylophile Communities: When DNA-SIP Meets High-Throughput Technologies. <i>Methods in Molecular Biology</i> , 2016, 1399, 235-255.	0.4	5
24	<i>xoxF</i> encoding an alternative methanol dehydrogenase is widespread in coastal marine environments. <i>Environmental Microbiology</i> , 2015, 17, 3937-3948.	1.8	108
25	Combining metagenomics with metaproteomics and stable isotope probing reveals metabolic pathways used by a naturally occurring marine methylophile. <i>Environmental Microbiology</i> , 2015, 17, 4007-4018.	1.8	51
26	MetaProSIP: Automated Inference of Stable Isotope Incorporation Rates in Proteins for Functional Metaproteomics. <i>Journal of Proteome Research</i> , 2015, 14, 619-627.	1.8	64
27	Limitations in detection of ¹⁵ N incorporation by mass spectrometry in protein-based stable isotope probing (protein-SIP). <i>Analytical and Bioanalytical Chemistry</i> , 2013, 405, 3989-3996.	1.9	13
28	Insights from quantitative metaproteomics and protein-stable isotope probing into microbial ecology. <i>ISME Journal</i> , 2013, 7, 1877-1885.	4.4	107
29	Sulfur-34S Stable Isotope Labeling of Amino Acids for Quantification (SULAQ34) of Proteomic Changes in <i>Pseudomonas fluorescens</i> during Naphthalene Degradation. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2060-2069.	2.5	17
30	Protein-SIP enables time-resolved analysis of the carbon flux in a sulfate-reducing, benzene-degrading microbial consortium. <i>ISME Journal</i> , 2012, 6, 2291-2301.	4.4	109
31	Protein-based stable isotope probing (protein-SIP) in functional metaproteomics. <i>Mass Spectrometry Reviews</i> , 2012, 31, 683-697.	2.8	61
32	Exploring the limits of robust detection of incorporation of ¹³ C by mass spectrometry in protein-based stable isotope probing (protein-SIP). <i>Analytical and Bioanalytical Chemistry</i> , 2011, 401, 1975-1982.	1.9	31
33	Time resolved protein-based stable isotope probing (Protein-SIP) analysis allows quantification of induced proteins in substrate shift experiments. <i>Proteomics</i> , 2011, 11, 2265-2274.	1.3	40
34	Protein-based stable isotope probing. <i>Nature Protocols</i> , 2010, 5, 1957-1966.	5.5	97
35	Decarboxylating and Nondecarboxylating Glutaryl-Coenzyme A Dehydrogenases in the Aromatic Metabolism of Obligately Anaerobic Bacteria. <i>Journal of Bacteriology</i> , 2009, 191, 4401-4409.	1.0	40