# Martin Taubert

List of Publications by Year
in descending order



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|---|---|---|---|
| 35 papers | 1,326 citations | 430874 18 h-index | 377865 34 g-index |
| 38 all docs | 38 docs citations | 38 times ranked | 1563 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Predominance of Cand. Patescibacteria in Groundwater Is Caused by Their Preferential Mobilization From Soils and Flourishing Under Oligotrophic Conditions. Frontiers in Microbiology, 2019, 10, 1407. | 3.5 | 160 |
| 2 | Protein-SIP enables time-resolved analysis of the carbon flux in a sulfate-reducing, benzene-degrading microbial consortium. ISME Journal, 2012, 6, 2291-2301. | 9.8 | 109 |
| 3 | <scp>XoxF</scp> encoding an alternative methanol dehydrogenase is widespread in coastal marine environments. Environmental Microbiology, 2015, 17, 3937-3948. | 3.8 | 108 |
| 4 | Insights from quantitative metaproteomics and protein-stable isotope probing into microbial ecology. ISME Journal, 2013, 7, 1877-1885. | 9.8 | 107 |
| 5 | Protein-based stable isotope probing. Nature Protocols, 2010, 5, 1957-1966. | 12.0 | 97 |
| 6 | MetaProSIP: Automated Inference of Stable Isotope Incorporation Rates in Proteins for Functional Metaproteomics. Journal of Proteome Research, 2015, 14, 619-627. | 3.7 | 64 |
| 7 | Proteinâ€based stable isotope probing (proteinâ€SIP) in functional metaproteomics. Mass Spectrometry Reviews, 2012, 31, 683-697. | 5.4 | 61 |
| 8 | Tracking active groundwater microbes with D<sub>2</sub>O labelling to understand their ecosystem function. Environmental Microbiology, 2018, 20, 369-384. | 3.8 | 57 |
| 9 | Combining metagenomics with metaproteomics and stable isotope probing reveals metabolic pathways used by a naturally occurring marine methylotroph. Environmental Microbiology, 2015, 17, 4007-4018. | 3.8 | 51 |
| 10 | Methylamine as a nitrogen source for microorganisms from a coastal marine environment. Environmental Microbiology, 2017, 19, 2246-2257. | 3.8 | 50 |
| 11 | Decarboxylating and Nondecarboxylating Glutaryl-Coenzyme A Dehydrogenases in the Aromatic Metabolism of Obligately Anaerobic Bacteria. Journal of Bacteriology, 2009, 191, 4401-4409. | 2.2 | 40 |
| 12 | Time resolved proteinâ€based stable isotope probing (Proteinâ€SIP) analysis allows quantification of induced proteins in substrate shift experiments. Proteomics, 2011, 11, 2265-2274. | 2.2 | 40 |
| 13 | The economical lifestyle of CPR bacteria in groundwater allows little preference for environmental drivers. Environmental Microbiomes, 2021, 16, 24. | 5.0 | 36 |
| 14 | Rates of dark CO2 fixation are driven by microbial biomass in a temperate forest soil. Soil Biology and Biochemistry, 2020, 150, 107950. | 8.8 | 33 |
| 15 | Exploring the limits of robust detection of incorporation of 13C by mass spectrometry in protein-based stable isotope probing (protein-SIP). Analytical and Bioanalytical Chemistry, 2011, 401, 1975-1982. | 3.7 | 31 |
| 16 | Divergent microbial communities in groundwater and overlying soils exhibit functional redundancy for plant-polysaccharide degradation. PLoS ONE, 2019, 14, e0212937. | 2.5 | 30 |
| 17 | Communal metabolism by Methylococcaceae and Methylophilaceae is driving rapid aerobic methane oxidation in sediments of a shallow seep near Elba, Italy. Environmental Microbiology, 2019, 21, 3780-3795. | 3.8 | 28 |
| 18 | Carbon fixation rates in groundwater similar to those in oligotrophic marine systems. Nature Geoscience, 2022, 15, 561-567. | 12.9 | 28 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | DNA-, RNA-, and Protein-Based Stable-Isotope Probing for High-Throughput Biomarker Analysis of Active Microorganisms. Methods in Molecular Biology, 2017, 1539, 57-74. | 0.9 | 21 |
| 20 | Bolstering fitness via CO2 fixation and organic carbon uptake: mixotrophs in modern groundwater. ISME Journal, 2022, 16, 1153-1162. | 9.8 | 21 |
| 21 | Monitoring Deuterium Uptake in Single Bacterial Cells via Two-Dimensional Raman Correlation Spectroscopy. Analytical Chemistry, 2021, 93, 7714-7723. | 6.5 | 18 |
| 22 | Sulfur-34S Stable Isotope Labeling of Amino Acids for Quantification (SULAQ34) of Proteomic Changes in Pseudomonas fluorescens during Naphthalene Degradation. Molecular and Cellular Proteomics, 2013, 12, 2060-2069. | 3.8 | 17 |
| 23 | Influence of Carbon Sources on Quantification of Deuterium Incorporation in Heterotrophic Bacteria: A Raman-Stable Isotope Labeling Approach. Analytical Chemistry, 2020, 92, 11429-11437. | 6.5 | 17 |
| 24 | Growth promotion and inhibition induced by interactions of groundwater bacteria. FEMS Microbiology Ecology, 2018, 94, . | 2.7 | 16 |
| 25 | Limitations in detection of 15N incorporation by mass spectrometry in protein-based stable isotope probing (protein-SIP). Analytical and Bioanalytical Chemistry, 2013, 405, 3989-3996. | 3.7 | 13 |
| 26 | Comparative Genomics and Mutational Analysis Reveals a Novel XoxF-Utilizing Methylotroph in the Roseobacter Group Isolated From the Marine Environment. Frontiers in Microbiology, 2018, 9, 766. | 3.5 | 13 |
| 27 | Microbial community functioning during plant litter decomposition. Scientific Reports, 2022, 12, 7451. | 3.3 | 12 |
| 28 | Dark CO2 fixation in temperate beech and pine forest soils. Soil Biology and Biochemistry, 2022, 165, 108526. | 8.8 | 11 |
| 29 | Nematode grazing increases the allocation of plant-derived carbon to soil bacteria and saprophytic fungi, and activates bacterial species of the rhizosphere. Pedobiologia, 2022, 90, 150787. | 1.2 | 10 |
| 30 | Analysis of Active Methylotrophic Communities: When DNA-SIP Meets High-Throughput Technologies. Methods in Molecular Biology, 2016, 1399, 235-255. | 0.9 | 5 |
| 31 | Bacterial Necromass Is Rapidly Metabolized by Heterotrophic Bacteria and Supports Multiple Trophic Levels of the Groundwater Microbiome. Microbiology Spectrum, 2022, 10, . | 3.0 | 5 |
| 32 | Phenotypic Differentiation of Autotrophic and Heterotrophic Bacterial Cells Using Raman-D<sub>2</sub>O Labeling. Analytical Chemistry, 2022, 94, 7759-7766. | 6.5 | 4 |
| 33 | Phylogenetic and metabolic diversity have contrasting effects on the ecological functioning of bacterial communities. FEMS Microbiology Ecology, 2021, 97, . | 2.7 | 3 |
| 34 | SIP-Metaproteomics: Linking Microbial Taxonomy, Function, and Activity. Methods in Molecular Biology, 2019, 2046, 57-69. | 0.9 | 2 |
| 35 | Biogeochemical Cycling of Carbon and Nitrogen in Groundwaterâ€"Key Processes and Microbial Drivers. , 2022, , 412-427. | | 0 |