Huub Jm Op Den Camp

List of Publications by Year
in descending order

Version: 2024-02-01

282 papers	24,143 citations	10351 72 h-index	9311 143 g-index
293 all docs	293 docs citations	293 times ranked	15782 citing authors

#	Article	IF	Citations
1	Nitrite-driven anaerobic methane oxidation by oxygenic bacteria. Nature, 2010, 464, 543-548.	13.7	1,521
2	Complete nitrification by a single microorganism. Nature, 2015, 528, 555-559.	13.7	1,336
3	A microbial consortium couples anaerobic methane oxidation to denitrification. Nature, 2006, 440, 918-921.	13.7	1,115
4	Deciphering the evolution and metabolism of an anammox bacterium from a community genome. Nature, 2006, 440, 790-794.	13.7	1,075
5	Molecular mechanism of anaerobic ammonium oxidation. Nature, 2011, 479, 127-130.	13.7	707
6	Anammox bacteria disguised as denitrifiers: nitrate reduction to dinitrogen gas via nitrite and ammonium. Environmental Microbiology, 2007, 9, 635-642.	1.8	462
7	Biochemistry and molecular biology of anammox bacteria. Critical Reviews in Biochemistry and Molecular Biology, 2009, 44, 65-84.	2.3	441
8	How to make a living from anaerobic ammonium oxidation. FEMS Microbiology Reviews, 2013, 37, 428-461.	3.9	433
9	Rare earth metals are essential for methanotrophic life in volcanic mudpots. Environmental Microbiology, 2014, 16, 255-264.	1.8	433
10	Environmental, genomic and taxonomic perspectives on methanotrophic Verrucomicrobia. Environmental Microbiology Reports, 2009, 1, 293-306.	1.0	431
11	Evidence for complete denitrification in a benthic foraminifer. Nature, 2006, 443, 93-96.	13.7	407
12	Denitrifying bacteria anaerobically oxidize methane in the absence of Archaea. Environmental Microbiology, 2008, 10, 3164-3173.	1.8	404
13	Methanotrophy below pHâ€‰1 by a new Verrucomicrobia species. Nature, 2007, 450, 874-878.	13.7	388
14	Methanotrophic symbionts provide carbon for photosynthesis in peat bogs. Nature, 2005, 436, 1153-1156.	13.7	379
15	Propionate Oxidation by and Methanol Inhibition of Anaerobic Ammonium-Oxidizing Bacteria. Applied and Environmental Microbiology, 2005, 71, 1066-1071.	1.4	353
16	PQQ-dependent methanol dehydrogenases: rare-earth elements make a difference. Applied Microbiology and Biotechnology, 2014, 98, 6163-6183.	1.7	323
17	Anaerobic ammonium-oxidizing bacteria in marine environments: widespread occurrence but low diversity. Environmental Microbiology, 2007, 9, 1476-1484.	1.8	307
18	High-level functional expression of a fungal xylose isomerase: the key to efficient ethanolic fermentation of xylose by ?. FEMS Yeast Research, 2003, 4, 69-78.	1.1	300

#	Article	IF	Citations
19	Hotspots of anaerobic ammonium oxidation at landâ€“freshwater interfaces. Nature Geoscience, 2013, 6, 103-107.	5.4	260
20	The metagenome of the marine anammox bacterium â€˜Candidatus Scalindua profundaâ€™ illustrates the versatility of this globally important nitrogen cycle bacterium. Environmental Microbiology, 2013, 15, 1275-1289.	1.8	246
21	Microbial cycling of volatile organic sulfur compounds. Cellular and Molecular Life Sciences, 2002, 59, 575-588.	2.4	228
22	Hydrazine Synthase, a Unique Phylomarker with Which To Study the Presence and Biodiversity of Anammox Bacteria. Applied and Environmental Microbiology, 2012, 78, 752-758.	1.4	228
23	Global prevalence of methane oxidation by symbiotic bacteria in peat-moss ecosystems. Nature Geoscience, 2010, 3, 617-621.	5.4	227
24	Co-occurrence and distribution of nitrite-dependent anaerobic ammonium and methane-oxidizing bacteria in a paddy soil. FEMS Microbiology Letters, 2012, 336, 79-88.	0.7	201
25	Pyrosequencing of 16S rRNA gene amplicons to study the microbiota in the gastrointestinal tract of carp (Cyprinus carpio L.). AMB Express, 2011, 1, 41.	1.4	186
26	Isolation and Characterization of Methanomethylovorans hollandica gen. nov., sp. nov., Isolated from Freshwater Sediment, a Methylotrophic Methanogen Able To Grow on Dimethyl Sulfide and Methanethiol. Applied and Environmental Microbiology, 1999, 65, 3641-3650.	1.4	176
27	Environmental detection of octahaem cytochrome c hydroxylamine/hydrazine oxidoreductase genes of aerobic and anaerobic ammoniumâ€oxidizing bacteria. Environmental Microbiology, 2008, 10, 3140-3149.	1.8	175
28	Anammoxâ€”Growth Physiology, Cell Biology, and Metabolism. Advances in Microbial Physiology, 2012, 60, 211-262.	1.0	175
29	A Metagenomics-Based Metabolic Model of Nitrate-Dependent Anaerobic Oxidation of Methane by Methanoperedens-Like Archaea. Frontiers in Microbiology, 2015, 6, 1423.	1.5	170
30	Cultivation and functional characterization of 79 planctomycetes uncovers their unique biology. Nature Microbiology, 2020, 5, 126-140.	5.9	164
31	1994â€“2004: 10Âyears of research on the anaerobic oxidation of ammonium. Biochemical Society Transactions, 2005, 33, 119-123.	1.6	163
32	Expanding the Verrucomicrobial Methanotrophic World: Description of Three Novel Species of Methylacidimicrobium gen. nov. Applied and Environmental Microbiology, 2014, 80, 6782-6791.	1.4	161
33	Diversity and enrichment of nitrite-dependent anaerobic methane oxidizing bacteria from wastewater sludge. Applied Microbiology and Biotechnology, 2011, 92, 845-854.	1.7	157
34	Autotrophic Methanotrophy in Verrucomicrobia: Methylacidiphilum fumariolicumSolV Uses the Calvin-Benson-Bassham Cycle for Carbon Dioxide Fixation. Journal of Bacteriology, 2011, 193, 4438-4446.	1.0	157
35	Anaerobic ammonium oxidation by marine and freshwater planctomycete-like bacteria. Applied Microbiology and Biotechnology, 2003, 63, 107-114.	1.7	156
36	Wholeâ€genome analysis of the ammoniaâ€oxidizing bacterium, Nitrosomonas eutropha C91: implications for niche adaptation. Environmental Microbiology, 2007, 9, 2993-3007.	1.8	150

#	Article	IF	Citations
37	Nitrateâ€•and nitriteâ€dependent anaerobic oxidation of methane. Environmental Microbiology Reports, 2016, 8, 941-955.	1.0	150
38	Evolution of an octahaem cytochrome c protein family that is key to aerobic and anaerobic ammonia oxidation by bacteria. Environmental Microbiology, 2008, 10, 3150-3163.	1.8	147
39	Simultaneous Nitrite-Dependent Anaerobic Methane and Ammonium Oxidation Processes. Applied and Environmental Microbiology, 2011, 77, 6802-6807.	1.4	147
40	Rhizobium Lipo-chitooligosaccharide Signaling Triggers Accumulation of Cytokinins in Medicago truncatula Roots. Molecular Plant, 2015, 8, 1213-1226.	3.9	146
41	pmoA Primers for Detection of Anaerobic Methanotrophs. Applied and Environmental Microbiology, 2011, 77, 3877-3880.	1.4	145
42	Effect of oxygen on the anaerobic methanotroph â€˜Candidatus Methylomirabilis oxyferaâ€™: kinetic and transcriptional analysis. Environmental Microbiology, 2012, 14, 1024-1034.	1.8	142
43	Xylose metabolism in the anaerobic fungus Piromyces sp. strain E2 follows the bacterial pathway. Archives of Microbiology, 2003, 180, 134-141.	1.0	117
44	Physiologic and Proteomic Evidence for a Role of Nitric Oxide in Biofilm Formation by Nitrosomonas europaea and Other Ammonia Oxidizers. Journal of Bacteriology, 2004, 186, 2781-2788.	1.0	116
45	Diversity and abundance of aerobic and anaerobic ammoniumâ€oxidizing bacteria in freshwater sediments of the Xinyi River (China). Environmental Microbiology, 2007, 9, 2375-2382.	1.8	116
46	Serpins in Prokaryotes. Molecular Biology and Evolution, 2002, 19, 1881-1890.	3.5	112
47	Bifidobacterium lipoteichoic acid and false ELISA reactivity in aspergillus antigen detection. Lancet, The, 2004, 363, 325-327.	6.3	111
48	Bacteria in the Intestinal Tract of Different Species of Arthropods. Microbial Ecology, 1997, 33, 189-197.	1.4	110
49	Enrichment of denitrifying methanotrophic bacteria for application after direct low-temperature anaerobic sewage treatment. Journal of Hazardous Materials, 2012, 227-228, 164-171.	6.5	110
50	Nitrogen fixation by the verrucomicrobial methanotroph â€˜Methylacidiphilum fumariolicumâ€™ SolV. Microbiology (United Kingdom), 2010, 156, 1052-1059.	0.7	109
51	Ecology of Thermophilic Fungi in Mushroom Compost, with Emphasis on Scytalidium thermophilum and Growth Stimulation of Agaricus bisporus Mycelium. Applied and Environmental Microbiology, 1994, 60, 454-458.	1.4	103
52	Comparison of growth characteristics of anaerobic fungi isolated from ruminant and non-ruminant herbivores during cultivation in a defined medium. Journal of General Microbiology, 1991, 137, 1401-1408.	2.3	100
53	Microbial Transformations of Nitrogen, Sulfur, and Iron Dictate Vegetation Composition in Wetlands: A Review. Frontiers in Microbiology, 2012, 3, 156.	1.5	100
54	Mimicking the oxygen minimum zones: stimulating interaction of aerobic archaeal and anaerobic bacterial ammonia oxidizers in a laboratoryâ€scale model system. Environmental Microbiology, 2012, 14, 3146-3158.	1.8	100

#	Article	IF	Citations
55	Genome Sequence of the Obligate Methanotroph Methylosinus trichosporium Strain OB3b. Journal of Bacteriology, 2010, 192, 6497-6498.	1.0	98
56	Detection, Isolation, and Characterization of Acidophilic Methanotrophs from Sphagnum Mosses. Applied and Environmental Microbiology, 2011, 77, 5643-5654.	1.4	93
57	Evolution of a new enzyme for carbon disulphide conversion by an acidothermophilic archaeon. Nature, 2011, 478, 412-416.	13.7	91
58	Bifidobacterial Lipoglycan as a New Cause for False-Positive Platelia Aspergillus Enzyme-Linked Immunosorbent Assay Reactivity. Journal of Clinical Microbiology, 2005, 43, 3925-3931.	1.8	90
59	Improved nitrogen removal by application of new nitrogen-cycle bacteria. Reviews in Environmental Science and Biotechnology, 2002, 1, 51-63.	3.9	88
60	Current perspectives on the application of N-damo and anammox in wastewater treatment. Current Opinion in Biotechnology, 2018, 50, 222-227.	3.3	88
61	Methanosarcina semesiae sp. nov., a dimethylsulfide-utilizing methanogen from mangrove sediment.. International Journal of Systematic and Evolutionary Microbiology, 2000, 50, 171-178.	0.8	87
62	Iron Sulfide and Pyrite as Potential Electron Donors for Microbial Nitrate Reduction in Freshwater Wetlands. Geomicrobiology Journal, 2007, 24, 391-401.	1.0	87
63	Bacteria associated with iron seeps in a sulfur-rich, neutral pH, freshwater ecosystem. ISME Journal, 2008, 2, 1231-1242.	4.4	86
64	16S rRNA gene and lipid biomarker evidence for anaerobic ammonium-oxidizing bacteria (anammox) in California and Nevada hot springs. FEMS Microbiology Ecology, 2009, 67, 343-350.	1.3	86
65	Mutations in SELENBP1, encoding a novel human methanethiol oxidase, cause extraoral halitosis. Nature Genetics, 2018, 50, 120-129.	9.4	86
66	Promicromonospora pachnodae sp. nov., a member of the (hemi)cellulolytic hindgut flora of larvae of the scarab beetle Pachnoda marginata. Antonie Van Leeuwenhoek, 2003, 83, 135-148.	0.7	84
67	Bacteriohopanepolyol signatures as markers for methanotrophic bacteria in peat moss. Geochimica Et Cosmochimica Acta, 2012, 77, 52-61.	1.6	83
68	Plasmids from the gut microbiome of cabbage root fly larvae encode <scp>SaxA</scp> that catalyses the conversion of the plant toxin 2â€phenylethyl isothiocyanate. Environmental Microbiology, 2016, 18, 1379-1390.	1.8	83
69	Ladderane phospholipids in anammox bacteria comprise phosphocholine and phosphoethanolamine headgroups. FEMS Microbiology Letters, 2006, 258, 297-304.	0.7	82
70	Interactions between anaerobic ammonium and sulfurâ€oxidizing bacteria in a laboratory scale model system. Environmental Microbiology, 2014, 16, 3487-3498.	1.8	81
71	New Methyloceanibacter diversity from North Sea sediments includes methanotroph containing solely the soluble methane monooxygenase. Environmental Microbiology, 2016, 18, 4523-4536.	1.8	81
72	Methylacidiphilum fumariolicum SolV, a thermoacidophilic â€˜Knallgasâ€™ methanotroph with both an oxygen-sensitive and -insensitive hydrogenase. ISME Journal, 2017, 11, 945-958.	4.4	80

#	Article	IF	Citations
73	Anaerobic Ammonia Oxidation in the Presence of Nitrogen Oxides (NO x) by Two Different Lithotrophs. Applied and Environmental Microbiology, 2002, 68, 5351-5357.	1.4	79
74	Several ways one goalâ€"methanogenesis from unconventional substrates. Applied Microbiology and Biotechnology, 2020, 104, 6839-6854.	1.7	79
75	Global impact and application of the anaerobic ammonium-oxidizing (anammox) bacteria. Biochemical Society Transactions, 2006, 34, 174-178.	1.6	77
76	Coexistence of nitrifying, anammox and denitrifying bacteria in a sequencing batch reactor. Frontiers in Microbiology, 2014, 5, 28.	1.5	76
77	XoxF-Type Methanol Dehydrogenase from the Anaerobic Methanotroph â€œCandidatus Methylomirabilis oxyferaâ€. Applied and Environmental Microbiology, 2015, 81, 1442-1451.	1.4	75
78	Role of rare earth elements in methanol oxidation. Current Opinion in Chemical Biology, 2019, 49, 39-44.	2.8	75
79	Isolation of a dimethylsulfide-utilizingHyphomicrobium species and its application in biofiltration of polluted air. Biodegradation, 1994, 5, 105-112.	1.5	73
80	Purification and characterization of trehalose phosphorylase from the commercial mushroom Agaricus bisporus. Biochimica Et Biophysica Acta - General Subjects, 1998, 1425, 177-188.	1.1	72
81	Genome Sequence of the Haloalkaliphilic Methanotrophic Bacterium Methylomicrobium alcaliphilum 20Z. Journal of Bacteriology, 2012, 194, 551-552.	1.0	72
82	A hydrogenosome with pyruvate formate-lyase: anaerobic chytrid fungi use an alternative route for pyruvate catabolism. Molecular Microbiology, 1999, 32, 1103-1114.	1.2	71
83	Application, eco-physiology and biodiversity of anaerobic ammonium-oxidizing bacteria. Reviews in Environmental Science and Biotechnology, 2004, 3, 255-264.	3.9	71
84	Intracellular localization of membraneâ€bound ATPases in the compartmentalized anammox bacterium â€˜Candidatus Kuenenia stuttgartiensisâ€™. Molecular Microbiology, 2010, 77, 701-715.	1.2	71
85	Impact of the lanthanide contraction on the activity of a lanthanide-dependent methanol dehydrogenase â€“ a kinetic and DFT study. Dalton Transactions, 2018, 47, 10463-10472.	1.6	69
86	Comparative Genomics of Candidatus Methylomirabilis Species and Description of Ca. Methylomirabilis Lanthanidiphila. Frontiers in Microbiology, 2018, 9, 1672.	1.5	67
87	Noncatalytic Docking Domains of Cellulosomes of Anaerobic Fungi. Journal of Bacteriology, 2001, 183, 5325-5333.	1.0	66
88	Obligate Sulfide-Dependent Degradation of Methoxylated Aromatic Compounds and Formation of Methanethiol and Dimethyl Sulfide by a Freshwater Sediment Isolate, Parasporobacterium paucivorans gen. nov., sp. nov. Applied and Environmental Microbiology, 2001, 67, 4017-4023.	1.4	64
89	Fibre Digestion in Arthropods. Comparative Biochemistry and Physiology A, Comparative Physiology, 1997, 118, 101-109.	0.7	63
90	A highly expressed family 1 Î²-glucosidase with transglycosylation capacity from the anaerobic fungus Piromyces sp. E2. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2002, 1574, 293-303.	2.4	63

#	Article	IF	Citations
91	Methanotrophic activity and diversity in different <i>Sphagnum magellanicum</i> dominated habitats in the southernmost peat bogs of Patagonia. Biogeosciences, 2012, 9, 47-55.	1.3	63
92	Bacterial SBP56 identified as a Cu-dependent methanethiol oxidase widely distributed in the biosphere. ISME Journal, 2018, 12, 145-160.	4.4	62
93	Genomic and Physiological Analysis of Carbon Storage in the Verrucomicrobial Methanotroph â€œCa. Methylacidiphilum Fumariolicumâ€•SolV. Frontiers in Microbiology, 2012, 3, 345.	1.5	61
94	Similar but Not the Same: First Kinetic and Structural Analyses of a Methanol Dehydrogenase Containing a Europium Ion in the Active Site. ChemBioChem, 2018, 19, 1147-1153.	1.3	61
95	Diversity of methanogenic archaea in a mangrove sediment and isolation of a newMethanococcoidesstrain. FEMS Microbiology Letters, 2009, 291, 247-253.	0.7	60
96	Mimicking microbial interactions under nitrateâ€•reducing conditions in an anoxic bioreactor: enrichment of novel Nitrospirae bacteria distantly related to Thermodesulfovibrio. Environmental Microbiology, 2017, 19, 4965-4977.	1.8	60
97	The enzymes of the ammonia assimilation in Pseudomonas aeruginosa. Archives of Microbiology, 1980, 124-124, 197-203.	1.0	58
98	Production of cellulolytic and xylanolytic enzymes during growth of the anaerobic fungus Piromyces sp. on different substrates. Journal of General Microbiology, 1992, 138, 1657-1664.	2.3	58
99	Ultra-deep pyrosequencing of pmoA amplicons confirms the prevalence of Methylomonas and Methylocystis in Sphagnum mosses from a Dutch peat bog. Environmental Microbiology Reports, 2011, 3, 667-673.	1.0	58
100	Biodiversity of N-cycle bacteria in nitrogen removing moving bed biofilters for freshwater recirculating aquaculture systems. Aquaculture, 2010, 306, 177-184.	1.7	57
101	Effect of coculture of anaerobic fungi isolated from ruminants and non-ruminants with methanogenic bacteria on cellulolytic and xylanolytic enzyme activities. Archives of Microbiology, 1992, 157, 176-182.	1.0	56
102	Sulfate Reduction and Methanogenesis in Sediments of Mtoni Mangrove Forest, Tanzania. Ambio, 2002, 31, 614-616.	2.8	56
103	Biogeochemical interactions between iron and sulphate in freshwater wetlands and their implications for interspecific competition between aquatic macrophytes. Freshwater Biology, 2007, 52, 434-447.	1.2	56
104	Fermentation of cellulose and production of cellulolytic and xylanolytic enzymes by anaerobic fungi from ruminant and non-ruminant herbivores. Archives of Microbiology, 1991, 156, 290-296.	1.0	55
105	Microbial Populations Involved in Cycling of Dimethyl Sulfide and Methanethiol in Freshwater Sediments. Applied and Environmental Microbiology, 2001, 67, 1044-1051.	1.4	55
106	Genome Sequence of the Methanotrophic Alphaproteobacterium Methylocystis sp. Strain Rockwell (ATCC 49242). Journal of Bacteriology, 2011, 193, 2668-2669.	1.0	55
107	Nonlegume Parasponia andersonii Deploys a Broad Rhizobium Host Range Strategy Resulting in Largely Variable Symbiotic Effectiveness. Molecular Plant-Microbe Interactions, 2012, 25, 954-963.	1.4	55
108	Anaerobic fungi and their cellulolytic and xylanolytic enzymes. Antonie Van Leeuwenhoek, 1993, 63, 63-76.	0.7	53

#	Article	IF	Citations
109	Cell division ring, a new cell division protein and vertical inheritance of a bacterial organelle in anammox planctomycetes. Molecular Microbiology, 2009, 73, 1009-1019.	1.2	53
110	Metagenomic profiling of ammonia- and methane-oxidizing microorganisms in two sequential rapid sand filters. Water Research, 2020, 185, 116288.	5.3	52
111	A New Addition to the Cell Plan of Anammox Bacteria: "Candidatus Kuenenia stuttgartiensis" Has a Protein Surface Layer as the Outermost Layer of the Cell. Journal of Bacteriology, 2014, 196, 80-89.	1.0	50
112	Role of Methanogens and Other Bacteria in Degradation of Dimethyl Sulfide and Methanethiol in Anoxic Freshwater Sediments. Applied and Environmental Microbiology, 1999, 65, 2116-2121.	1.4	50
113	Nitrite-dependent anaerobic methane oxidizing bacteria along the water level fluctuation zone of the Three Gorges Reservoir. Applied Microbiology and Biotechnology, 2016, 100, 1977-1986.	1.7	49
114	Verrucomicrobial methanotrophs: ecophysiology of metabolically versatile acidophiles. FEMS Microbiology Reviews, 2021, 45, .	3.9	49
115	Resolving the complete genome of Kuenenia stuttgartiensis from a membrane bioreactor enrichment using Single-Molecule Real-Time sequencing. Scientific Reports, 2018, 8, 4580.	1.6	48
116	The thermoacidophilic methanotroph Methylacidiphilum fumariolicum SolV oxidizes subatmospheric H2 with a high-affinity, membrane-associated [NiFe] hydrogenase. ISME Journal, 2020, 14, 1223-1232.	4.4	47
117	The role of endophytic methane-oxidizing bacteria in submerged <I>Sphagnum</I> in determining methane emissions of Northeastern Siberian tundra. Biogeosciences, 2011, 8, 1267-1278.	1.3	46
118	Draft Genome Sequence of Anammox Bacterium â€œCandidatus Scalindua brodae,â€•Obtained Using Differential Coverage Binning of Sequencing Data from Two Reactor Enrichments. Genome Announcements, 2015, 3, .	0.8	46
119	Evidence that unrestricted legumain activity is involved in disturbed epidermal cornification in cystatin M/E deficient mice. Human Molecular Genetics, 2004, 13, 1069-1079.	1.4	45
120	Ammonia Oxidation and Nitrite Reduction in the Verrucomicrobial Methanotroph Methylacidiphilum fumariolicum SolV. Frontiers in Microbiology, 2017, 8, 1901.	1.5	45
121	Biomass and Biological Activity during the Production of Compost Used as a Substrate in Mushroom Cultivation. Applied and Environmental Microbiology, 1990, 56, 3029-3034.	1.4	45
122	beta-Glucosidase in cellulosome of the anaerobic fungus Piromyces sp. strain E2 is a family 3 glycoside hydrolase. Biochemical Journal, 2003, 370, 963-970.	1.7	44
123	De novo transcriptome characterization and development of genomic tools for Scabiosa columbaria L. using nextâ€generation sequencing techniques. Molecular Ecology Resources, 2011, 11, 662-674.	2.2	44
124	Effects of nitrogen fertilization on diazotrophic activity of microorganisms associated with Sphagnum magellanicum. Plant and Soil, 2016, 406, 83-100.	1.8	44
125	Anaerobic versus Aerobic Degradation of Dimethyl Sulfide and Methanethiol in Anoxic Freshwater Sediments. Applied and Environmental Microbiology, 1999, 65, 438-443.	1.4	44
126	Lipids of symbiotic methane-oxidizing bacteria in peat moss studied using stable carbon isotopic labelling. Organic Geochemistry, 2010, 41, 1040-1044.	0.9	43

#	Article	IF	Citations
127	Draft Genome Sequence of the Volcano-Inhabiting Thermoacidophilic Methanotroph Methylacidiphilum fumariolicum Strain SolV. Journal of Bacteriology, 2012, 194, 3729-3730.	1.0	43
128	Effects of lignin on the anaerobic degradation of (ligno) cellulosic wastes by rumen microorganisms. Applied Microbiology and Biotechnology, 1988, 29, 408-412.	1.7	42
129	FACIL: Fast and Accurate Genetic Code Inference and Logo. Bioinformatics, 2011, 27, 1929-1933.	1.8	42
130	Response of the Anaerobic Methanotroph â€œ Candidatus Methanoperedens nitroreducensâ€•to Oxygen Stress. Applied and Environmental Microbiology, 2018, 84, .	1.4	42
131	Nitrogen assimilating enzymes in the white button mushroom Agaricus bisporus. Microbiology (United Kingdom), 1994, 140, 1161-1168.	0.7	41
132	HPLC Detection of Soluble Carbohydrates Involved in Mannitol and Trehalose Metabolism in the Edible MushroomAgaricusbisporus. Journal of Agricultural and Food Chemistry, 2000, 48, 287-291.	2.4	41
133	Enrichment of an anammox bacterial community from a flooded paddy soil. Environmental Microbiology Reports, 2013, 5, 483-489.	1.0	41
134	Presence and diversity of anammox bacteria in cold hydrocarbon-rich seeps and hydrothermal vent sediments of the Guaymas Basin. Frontiers in Microbiology, 2013, 4, 219.	1.5	41
135	Draft Genomes of Gammaproteobacterial Methanotrophs Isolated from Terrestrial Ecosystems. Genome Announcements, 2015, 3, .	0.8	41
136	Physiological role of the respiratory quinol oxidase in the anaerobic nitrite-reducing methanotroph â€˜Candidatus Methylomirabilis oxyferaâ€™. Microbiology (United Kingdom), 2011, 157, 890-898.	0.7	40
137	The genomic landscape of the verrucomicrobial methanotroph Methylacidiphilum fumariolicum SolV. BMC Genomics, 2014, 15, 914.	1.2	39
138	Genome Characteristics of Two Novel Type I Methanotrophs Enriched from North Sea Sediments Containing Exclusively a Lanthanide-Dependent XoxF5-Type Methanol Dehydrogenase. Microbial Ecology, 2016, 72, 503-509.	1.4	39
139	Key Physiology of a Nitrite-Dependent Methane-Oxidizing Enrichment Culture. Applied and Environmental Microbiology, 2019, 85, .	1.4	39
140	Ammonia oxidation at pH 2.5 by a new gammaproteobacterial ammonia-oxidizing bacterium. ISME Journal, 2021, 15, 1150-1164.	4.4	39
141	In vitro metabolism of fumonisin B1 by ruminal microflora. Veterinary Research Communications, 2000, 24, 379-387.	0.6	38
142	Inoculation of Scytalidium thermophilum in Button Mushroom Compost and Its Effect on Yield. Applied and Environmental Microbiology, 1994, 60, 3049-3054.	1.4	38
143	Increased susceptibility of serum amyloid A 1.1 to degradation by MMP-1: potential explanation for higher risk of type AA amyloidosis. Rheumatology, 2008, 47, 1651-1654.	0.9	37
144	Anaerobic oxidation of dimethylsulfide and methanethiol in mangrove sediments is dominated by sulfate-reducing bacteria. FEMS Microbiology Ecology, 2009, 70, 483-492.	1.3	36

#	Article	IF	Citations
145	Draft Genome Sequence of Methylomicrobium buryatense Strain 5G, a Haloalkaline-Tolerant Methanotrophic Bacterium. Genome Announcements, 2013, 1, .	0.8	36
146	Effect of Host Diet and Hindgut Microbial Composition on Cellulolytic Activity in the Hindgut of the American Cockroach, Periplaneta americana. Applied and Environmental Microbiology, 1994, 60, 1822-1826.	1.4	36
147	In vitro leishmanicidal activity of Tityus discrepans scorpion venom. Parasitology Research, 2006, 99, 167-173.	0.6	35
148	Metabolic Regulation of â€œCa. Methylacidiphilum Fumariolicumâ€•SolV Cells Grown Under Different Nitrogen and Oxygen Limitations. Frontiers in Microbiology, 2012, 3, 266.	1.5	35
149	Molecular and Biochemical Characterization of Two Xylanase-Encoding Genes from Cellulomonas pachnodae. Applied and Environmental Microbiology, 1999, 65, 4099-4107.	1.4	35
150	The Major Component of the Cellulosomes of Anaerobic Fungi from the Genus Piromyces is a Family 48 Glycoside Hydrolase. DNA Sequence, 2002, 13, 313-320.	0.7	34
151	A serpin in the cellulosome of the anaerobic fungus Piromyces sp. strain E2. Mycological Research, 2008, 112, 999-1006.	2.5	34
152	Branchial nitrogen cycle symbionts can remove ammonia in fish gills. Environmental Microbiology Reports, 2016, 8, 590-594.	1.0	34
153	Facile Arsenazo III-Based Assay for Monitoring Rare Earth Element Depletion from Cultivation Media for Methanotrophic and Methylotrophic Bacteria. Applied and Environmental Microbiology, 2018, 84, .	1.4	34
154	Understanding the chemistry of the artificial electron acceptors PES, PMS, DCPIP and Wursterâ€™s Blue in methanol dehydrogenase assays. Journal of Biological Inorganic Chemistry, 2020, 25, 199-212.	1.1	34
155	A new soluble 10 kDa monoheme cytochromec-552 from the anammox bacteriumCandidatusâ€œKuenenia stuttgartiensisâ€• FEMS Microbiology Letters, 2005, 252, 273-278.	0.7	33
156	Trehalose Phosphorylase Activity and Carbohydrate Levels During Axenic Fruiting in Three Agaricus bisporus Strains. Current Microbiology, 1999, 39, 205-210.	1.0	32
157	Spatial distribution of archaeal and bacterial ammonia oxidizers in the littoral buffer zone of a nitrogen-rich lake. Journal of Environmental Sciences, 2012, 24, 790-799.	3.2	32
158	Degradation of structural polysaccharides by the plant cell-wall degrading enzyme system from anaerobic fungi: An application study. Enzyme and Microbial Technology, 1997, 21, 130-136.	1.6	31
159	Diversity of long-chain toxins in Tityus zulianus and Tityus discrepans venoms (Scorpiones, Buthidae): Molecular, immunological, and mass spectral analyses. Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology, 2006, 142, 240-252.	1.3	31
160	A comparative genomics study of genetic products potentially encoding ladderane lipid biosynthesis. Biology Direct, 2009, 4, 8.	1.9	31
161	A novel marine nitrite-oxidizing Nitrospira species from Dutch coastal North Sea water. Frontiers in Microbiology, 2013, 4, 60.	1.5	30
162	Generation of soluble lignin-derived compounds during degradation of barley straw in an artificial rumen reactor. Applied Microbiology and Biotechnology, 1990, 33, 93-98.	1.7	29

#	Article	IF	Citations
163	Growth kinetics of Agaricus bisporus mycelium on solid substrate (mushroom compost). Journal of General Microbiology, 1991, 137, 1471-1477.	2.3	29
164	Induced cooperation between marine nitrifiers and anaerobic ammonium-oxidizing bacteria by incremental exposure to oxygen. Systematic and Applied Microbiology, 2010, 33, 407-415.	1.2	29
165	Evidence that the catenane form of CS2 hydrolase is not an artefact. Chemical Communications, 2013, 49, 7770.	2.2	29
166	Structure of the lipoteichoic acids from Bifidobacterium bifidum spp. pennsylvanicum. Lipids and Lipid Metabolism, 1984, 795, 301-313.	2.6	28
167	Community Composition and Ultrastructure of a Nitrate-Dependent Anaerobic Methane-Oxidizing Enrichment Culture. Applied and Environmental Microbiology, 2018, 84, .	1.4	28
168	The Acidophilic Methanotroph Methylacidimicrobium tartarophylax 4AC Grows as Autotroph on H2 Under Microoxic Conditions. Frontiers in Microbiology, 2019, 10, 2352.	1.5	28
169	Evidence for the involvement of betaproteobacterial Thiobacilli in the nitrate-dependent oxidation of iron sulfide minerals. FEMS Microbiology Ecology, 2006, 58, 439-448.	1.3	27
170	Bacterial CS2 Hydrolases from Acidithiobacillus thiooxidans Strains Are Homologous to the Archaeal Catenane CS2 Hydrolase. Journal of Bacteriology, 2013, 195, 4046-4056.	1.0	27
171	Production of cellulolytic and xylanolytic enzymes during growth of anaerobic fungi from ruminant and nonruminant herbivores on different substrates. Applied Biochemistry and Biotechnology, 1993, 39-40, 177-189.	1.4	26
172	An intron-containing glycoside hydrolase family 9 cellulase gene encodes the dominant 90ÂkDa component of the cellulosome of the anaerobic fungus Piromyces sp. strain E2. Biochemical Journal, 2002, 365, 193-204.	1.7	26
173	Envenomation by the Scorpion Tityus breweri in the Guayana Shield, Venezuela: Report of a Case, Efficacy and Reactivity of Antivenom, and Proposal for a Toxinological Partitioning of the Venezuelan Scorpion Fauna. Wilderness and Environmental Medicine, 2010, 21, 282-290.	0.4	26
174	Interactions between anaerobic ammonium- and methane-oxidizing microorganisms in a laboratory-scale sequencing batch reactor. Applied Microbiology and Biotechnology, 2019, 103, 6783-6795.	1.7	26
175	Differences in sequencing technologies improve the retrieval of anammox bacterial genome from metagenomes. BMC Genomics, 2013, 14, 7.	1.2	25
176	Collembolan Transcriptomes Highlight Molecular Evolution of Hexapods and Provide Clues on the Adaptation to Terrestrial Life. PLoS ONE, 2015, 10, e0130600.	1.1	25
177	Characterization of a novel cytochrome c as the electron acceptor of XoxF-MDH in the thermoacidophilic methanotroph Methylacidiphilum fumariolicum SolV. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2019, 1867, 595-603.	1.1	25
178	Multiheme hydroxylamine oxidoreductases produce NO during ammonia oxidation in methanotrophs. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 24459-24463.	3.3	25
179	Bioconversion of cereal straw into mushroom compost. Canadian Journal of Botany, 1995, 73, 1019-1024.	1.2	24
180	The role of the cellulolytic high molecular mass (HMM) complex of the anaerobic fungus Piromyces sp. strain E2 in the hydrolysis of microcrystalline cellulose. Archives of Microbiology, 1997, 167, 137-142.	1.0	24

#	Article	IF	Citations
181	Cel6A, a major exoglucanase from the cellulosome of the anaerobic fungi Piromyces sp. E2 and Piromyces equi. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2003, 1628, 30-39.	2.4	24
182	Isolation of a carbon disulfide utilizing Thiomonas sp. and its application in a biotrickling filter. Applied Microbiology and Biotechnology, 2007, 74, 439-446.	1.7	24
183	Impact of the invasive alien topmouth gudgeon (Pseudorasbora parva) and its associated parasite Sphaerothecum destruens on native fish species. Biological Invasions, 2020, 22, 587-601.	1.2	24
184	Improved method for simultaneous determination of alcohols, volatile fatty acids, lactic acid or 2,3-butanediol in biological samples. Journal of Microbiological Methods, 1989, 10, 247-254.	0.7	23
185	The ornithine cycle enzyme arginase from Agaricus bisporus and its role in urea accumulation in fruit bodies. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2005, 1681, 107-115.	2.4	23
186	Challenging protein purification from anammox bacteria. International Journal of Biological Macromolecules, 2006, 39, 88-94.	3.6	23
187	Anoxic Iron Cycling Bacteria from an Iron Sulfide- and Nitrate-Rich Freshwater Environment. Frontiers in Microbiology, 2012, 3, 26.	1.5	23
188	Genome analysis and heterologous expression of acetate-activating enzymes in the anammox bacterium Kuenenia stuttgartiensis. Archives of Microbiology, 2012, 194, 943-948.	1.0	23
189	Identification of the type II cytochrome cmaturation pathway in anammox bacteria by comparative genomics. BMC Microbiology, 2013, 13, 265.	1.3	23
190	Genome Sequence of the Obligate Gammaproteobacterial Methanotroph Methylomicrobium album Strain BG8. Genome Announcements, 2013, 1, e0017013.	0.8	23
191	Draft Genome Sequences of Gammaproteobacterial Methanotrophs Isolated from Marine Ecosystems. Genome Announcements, 2016, 4, .	0.8	23
192	Diversity of isoprene-degrading bacteria in phyllosphere and soil communities from a high isoprene-emitting environment: a Malaysian oil palm plantation. Microbiome, 2020, 8, 81.	4.9	23
193	Molecular characterization of the. Molecular Genetics and Genomics, 1997, 256, 179.	2.4	23
194	Purification and characterization of NADP-dependent glutamate dehydrogenase from the commercial mushroom Agaricus bisporus. Current Microbiology, 1995, 30, 211-217.	1.0	22
195	Complete conversion of nitrate into dinitrogen gas in co-cultures of denitrifying bacteria. Biochemical Society Transactions, 2005, 33, 205-209.	1.6	21
196	Shifts of archaeal community structure in soil along an elevation gradient in a reservoir water level fluctuation zone. Journal of Soils and Sediments, 2016, 16, 2728-2739.	1.5	21
197	The Anaerobic Fungus Neocallimastix sp. Strain L2: Growth and Production of (Hemi)Cellulolytic Enzymes on a Range of Carbohydrate Substrates. Current Microbiology, 1997, 34, 91-96.	1.0	20
198	More Than a Methanotroph: A Broader Substrate Spectrum for Methylacidiphilum fumariolicum SolV. Frontiers in Microbiology, 2020, 11, 604485.	1.5	20

#	Article	IF	Citations
199	High prevalence of the parasite Sphaerothecum destruens in the invasive topmouth gudgeon Pseudorasbora parva in the Netherlands, a potential threat to native freshwater fish. Aquatic Invasions, 2013, 8, 355-360.	0.6	20
200	Styrene Removal from Waste Gas with a Bacterial Biotrickling Filter. Biotechnology Letters, 1998, 20, 407-410.	1.1	19
201	Genomic DNA analysis of genes encoding (hemi-)cellulolytic enzymes of the anaerobic fungus Piromyces sp. E2. Gene, 2003, 314, 73-80.	1.0	19
202	Argininosuccinate synthetase and argininosuccinate lyase: two ornithine cycle enzymes from Agaricus bisporus. Mycological Research, 2007, 111, 493-502.	2.5	19
203	Methanol Production by â€œ Methylacidiphilum fumariolicum â€•SolV under Different Growth Conditions. Applied and Environmental Microbiology, 2020, 86, .	1.4	19
204	A Î²-1,4-endoglucanase-encoding gene from Cellulomonas pachnodae. Applied Microbiology and Biotechnology, 1999, 52, 232-239.	1.7	18
205	Expression of the urease gene of Agaricus bisporus: a tool for studying fruit body formation and post-harvest development. Applied Microbiology and Biotechnology, 2006, 71, 486-492.	1.7	18
206	Different Recovery Processes of Soil Ammonia Oxidizers from Flooding Disturbance. Microbial Ecology, 2018, 76, 1041-1052.	1.4	18
207	Hydrogen and Carbon Monoxide-Utilizing Kyrpidia spormannii Species From Pantelleria Island, Italy. Frontiers in Microbiology, 2020, 11, 951.	1.5	18
208	15N-NMR study of ammonium assimilation in Agaricus bisporus. Biochimica Et Biophysica Acta - Molecular Cell Research, 1996, 1310, 74-80.	1.9	17
209	The role of ornithine aminotransferase in fruiting body formation of the mushroom Agaricus bisporus. Mycological Research, 2007, 111, 909-918.	2.5	17
210	Unusual Members of the PVC Superphylum: The Methanotrophic Verrucomicrobia Genus â€œMethylacidiphilumâ€• , 2013, , 211-227.		17
211	Transport of amino acids and ammonium in mycelium of Agaricus bisporus. Biochimica Et Biophysica Acta - General Subjects, 1999, 1428, 260-272.	1.1	16
212	The structure of a mannitol teichoic acid from Bifidobacterium bifidum ssp. Pennsylvanicum. Biochimica Et Biophysica Acta - General Subjects, 1983, 755, 439-451.	1.1	15
213	Cell surface hydrophobicity ofBifidobacterium bifidum subsp.pennsylvanicum. Antonie Van Leeuwenhoek, 1985, 51, 303-312.	0.7	15
214	Application of rumen microorganisms in the anaerobic fermentation of an organic fraction of domestic refuse. Biological Wastes, 1989, 30, 309-316.	0.3	15
215	Hyphal and mycelial interactions betweenAgaricus bisporus andScytalidium thermophilum on agar media. Microbial Ecology, 1990, 19, 303-309.	1.4	15
216	A semi-continuous culture system for production of cellulolytic and xylanolytic enzymes by the anaerobic fungus Piromyces sp. strain E2. Applied Microbiology and Biotechnology, 1992, 38, 28-33.	1.7	15

#	Article	IF	Citations
217	Conversion of cereal residues into biogas in a rumen-derived process. World Journal of Microbiology and Biotechnology, 1992, 8, 428-433.	1.7	15
218	Anammox bacteria in different compartments of recirculating aquaculture systems. Biochemical Society Transactions, 2011, 39, 1817-1821.	1.6	15
219	Methanethiol Consumption and Hydrogen Sulfide Production by the Thermoacidophilic Methanotroph Methylacidiphilum fumariolicum SolV. Frontiers in Microbiology, 2022, 13, 857442.	1.5	15
220	Expression and characterisation of a major c-type cytochrome encoded by gene kustc0563 from Kuenenia stuttgartiensis as a recombinant protein in Escherichia coli. Protein Expression and Purification, 2007, 51, 28-33.	0.6	14
221	Draft Genome Sequence of the Moderately Halophilic Methanotroph Methylohalobius crimeensis Strain 10Ki. Genome Announcements, 2015, 3, .	0.8	14
222	Nutrient Limitation Causes Differential Expression of Transport- and Metabolism Genes in the Compartmentalized Anammox Bacterium Kuenenia stuttgartiensis. Frontiers in Microbiology, 2020, 11, 1959.	1.5	14
223	Methylacidimicrobium thermophilum AP8, a Novel Methane- and Hydrogen-Oxidizing Bacterium Isolated From Volcanic Soil on Pantelleria Island, Italy. Frontiers in Microbiology, 2021, 12, 637762.	1.5	14
224	Proteomic analysis of the outer membrane of Protochlamydia amoebophila elementary bodies. Proteomics, 2010, 10, 4363-4376.	1.3	13
225	Ultrastructure and Viral Metagenome of Bacteriophages from an Anaerobic Methane Oxidizing Methylomirabilis Bioreactor Enrichment Culture. Frontiers in Microbiology, 2016, 7, 1740.	1.5	13
226	Electrocatalysis of a Europiumâ€Dependent Bacterial Methanol Dehydrogenase with Its Physiological Electronâ€Acceptor Cytochromeâ€…c_{GJ}. Chemistry - A European Journal, 2019, 25, 8760-8768.	1.7	13
227	Contaminations in (meta)genome data: An open issue for the scientific community. IUBMB Life, 2020, 72, 698-705.	1.5	13
228	Geothermal Gases Shape the Microbial Community of the Volcanic Soil of Pantelleria, Italy. MSystems, 2020, 5, .	1.7	13
229	Metagenome Assembled Genome of a Novel Verrucomicrobial Methanotroph From Pantelleria Island. Frontiers in Microbiology, 2021, 12, 666929.	1.5	13
230	Regulation of nitrogen-metabolizing enzymes in the commercial Mushroom Agaricus bisporus. Current Microbiology, 1995, 31, 345-350.	1.0	12
231	Cultivation of anaerobic fungi in a 10-l fermenter system for the production of (hemi-)cellulolytic enzymes. Applied Microbiology and Biotechnology, 1996, 46, 85-91.	1.7	12
232	NAD+-dependent glutamate dehydrogenase of the edible mushroom Agaricus bisporus: biochemical and molecular characterization. Molecular Genetics and Genomics, 1999, 261, 452-462.	2.4	12
233	Purification and characterization of an acid phosphatase from the commercial mushroom Agaricus bisporus. Antonie Van Leeuwenhoek, 2000, 77, 215-222.	0.7	12
234	Specific activation of human neutrophils by scorpion venom: A flow cytometry assessment. Toxicology in Vitro, 2011, 25, 358-367.	1.1	12

#	Article	IF	Citations
235	Proteomic analysis reveals a virtually complete set of proteins for translation and energy generation in elementary bodies of the amoeba symbiont Protochlamydia amoebophila. Proteomics, 2011, 11, 1868-1892.	1.3	12
236	Draft genome of a novel methanotrophic Methylobacter sp. from the volcanic soils of Pantelleria Island. Antonie Van Leeuwenhoek, 2021, 114, 313-324.	0.7	12
237	Interactions of anaerobic ammonium oxidizers and sulfide-oxidizing bacteria in a substrate-limited model system mimicking the marine environment. FEMS Microbiology Ecology, 2019, 95, .	1.3	11
238	Artificial ponds as hotspots of nitrogen removal in agricultural watershed. Biogeochemistry, 2022, 159, 283-301.	1.7	11
239	Purification and characterization of the NADP-dependent glutamate dehydrogenase from Bacillus fastidiosus. Antonie Van Leeuwenhoek, 1989, 55, 303-311.	0.7	10
240	Purification and characterization of glutamine synthetase from the commerical mushroom Agaricus bisporus. Current Microbiology, 1995, 31, 108-113.	1.0	10
241	Anammox. , 2007, , 245-262.		10
242	PREDICTING METAL UPTAKE BY WETLAND PLANTS UNDER AEROBIC AND ANAEROBIC CONDITIONS. Environmental Toxicology and Chemistry, 2007, 26, 686.	2.2	10
243	RNA Sequencing Elucidates Drug-Specific Mechanisms of Antibiotic Tolerance and Resistance in Mycobacterium abscessus. Antimicrobial Agents and Chemotherapy, 2022, 66, AAC0150921.	1.4	10
244	Dibenzo Crown Ether Layer Formation on Muscovite Mica. Langmuir, 2014, 30, 12570-12577.	1.6	9
245	Diversity, enrichment, and genomic potential of anaerobic methane- and ammonium-oxidizing microorganisms from a brewery wastewater treatment plant. Applied Microbiology and Biotechnology, 2020, 104, 7201-7212.	1.7	9
246	Neodymium as Metal Cofactor for Biological Methanol Oxidation: Structure and Kinetics of an XoxF1-Type Methanol Dehydrogenase. MBio, 2021, 12, e0170821.	1.8	9
247	Differences in venom toxicity and antigenicity between females and males Tityus nororientalis (Buthidae) scorpions. Journal of Venom Research, 2010, 1, 61-70.	0.6	9
248	Diversity and Ecophysiology of New Isolates of Extremely Acidophilic CS ₂ -Converting Acidithiobacillus Strains. Applied and Environmental Microbiology, 2013, 79, 6784-6794.	1.4	8
249	Draft Genome Sequences of Two Gammaproteobacterial Methanotrophs Isolated from Rice Ecosystems. Genome Announcements, 2017, 5, .	0.8	8
250	Amsterdam urban canals contain novel niches for methaneâ€cycling microorganisms. Environmental Microbiology, 2022, 24, 82-97.	1.8	8
251	Hepatocystin Is Not Secreted in Cyst Fluid of Hepatocystin Mutant Polycystic Liver Patients. Journal of Proteome Research, 2008, 7, 2490-2495.	1.8	7
252	Anthropogenic Pollution Intervenes the Recovery Processes of Soil Archaeal Community Composition and Diversity From Flooding. Frontiers in Microbiology, 2019, 10, 2285.	1.5	7

#	Article	IF	Citations
253	Immune recognition of putative alien microbial structures: Hostâ€“pathogen interactions in the age of space travel. PLoS Pathogens, 2020, 16, e1008153.	2.1	7
254	Growth of Bacillus fastidiosus on glycerol and the enzymes of ammonia assimilation. Archives of Microbiology, 1986, 146, 292-294.	1.0	6
255	Purification and Characterization of Glutamine Synthetase from the Basidiomycete Pleurotus ostreatus. Current Microbiology, 1996, 33, 181-186.	1.0	5
256	Purine degradation in the edible mushroomAgaricus bisporus. Folia Microbiologica, 2002, 47, 672-676.	1.1	5
257	Close relationship of RNase P RNA in Gemmata and anammox planctomycete bacteria. FEMS Microbiology Letters, 2007, 268, 244-253.	0.7	5
258	Complete Genome Sequence of the Aerobic Facultative Methanotroph Methylocella tundrae Strain T4. Microbiology Resource Announcements, 2019, 8, .	0.3	5
259	Horizontal Gene Transfer of Genes Encoding Copper-Containing Membrane-Bound Monooxygenase (CuMMO) and Soluble Di-iron Monooxygenase (SDIMO) in Ethane- and Propane-Oxidizing Rhodococcus Bacteria. Applied and Environmental Microbiology, 2021, 87, e0022721.	1.4	5
260	The level of enzymes involved in the allantoin metabolism of Bacillus fastidiosus grown under different conditions. Current Microbiology, 1995, 30, 45-47.	1.0	4
261	The anaerobic fungusPiromyces sp. strain E2: nitrogen requirement and enzymes involved in primary nitrogen metabolism. Archives of Microbiology, 1996, 166, 399-404.	1.0	4
262	The anaerobic fungus Piromyces sp. strain E2: nitrogen requirement and enzymes involved in primary nitrogen metabolism. Archives of Microbiology, 1997, 166, 399-404.	1.0	4
263	Regulation of Glutamine Synthetase from the White Button MushroomAgaricus bisporus. Archives of Biochemistry and Biophysics, 1999, 364, 228-234.	1.4	4
264	Extremely acidophilic sulfur-oxidizing bacteria applied in biotechnological processes for gas purification. Journal of Environmental Science and Health - Part A Toxic/Hazardous Substances and Environmental Engineering, 2012, 47, 964-969.	0.9	4
265	Verrucomicrobial Methanotrophs. , 2018, , 43-55.		4
266	Structure of the 4-hydroxy-tetrahydrodipicolinate synthase from the thermoacidophilic methanotroph Methylacidiphilum fumariolicum SolV and the phylogeny of the aminotransferase pathway. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 199-208.	0.4	4
267	Studies of pyrroloquinoline quinone species in solution and in lanthanide-dependent methanol dehydrogenases. Physical Chemistry Chemical Physics, 2022, 24, 15397-15405.	1.3	4
268	Quantification of coenzyme F420 analogues from methanogenic bacteria by HPLC and fluorimetry. Biotechnology Letters, 1989, 3, 239-244.	0.5	3
269	Novel nitrogen sources for growth ofBacillus fastidiosusand their effect on the activity of NADP-dependent glutamate dehydrogenase. FEMS Microbiology Letters, 1993, 114, 195-199.	0.7	3
270	Growth on Carbohydrates from Carbonaceous Meteorites Alters the Immunogenicity of Environment-Derived Bacterial Pathogens. Astrobiology, 2020, 20, 1353-1362.	1.5	3

#	Article	IF	Citations
271	A Novel Laboratory-Scale Mesocosm Setup to Study Methane Emission Mitigation by Sphagnum Mosses and Associated Methanotrophs. Frontiers in Microbiology, 2021, 12, 652486.	1.5	3
272	Simultaneous Anaerobic and Aerobic Ammonia and Methane Oxidation under Oxygen Limitation Conditions. Applied and Environmental Microbiology, 2021, 87, e0004321.	1.4	3
273	Nucleotide sequence and expression of the gene encoding NADP. Molecular Genetics and Genomics, 1996, 250, 339.	2.4	3
274	Bioreactor virome metagenomics sequencing using DNA spike-ins. PeerJ, 2018, 6, e4351.	0.9	3
275	Metascan: METabolic Analysis, SCreening and ANnotation of Metagenomes. Frontiers in Bioinformatics, 0, 2, .	1.0	3
276	Methane-munching microbes. Nature Geoscience, 2010, 3, 660-660.	5.4	2
277	Unraveling Nitrogen, Sulfur, and Carbon Metabolic Pathways and Microbial Community Transcriptional Responses to Substrate Deprivation and Toxicity Stresses in a Bioreactor Mimicking Anoxic Brackish Coastal Sediment Conditions. Frontiers in Microbiology, 2022, 13, 798906.	1.5	2
278	Rapid purification of uricase from Bacillus fastidiosus. Biotechnology Letters, 1996, 10, 709-712.	0.5	1
279	Draft Genome Sequences of Two Acidophilic, Mesophilic Verrucomicrobial Methanotrophs Contain Only One pmoCAB Operon. Microbiology Resource Announcements, 2020, 9, .	0.3	1
280	Degradation of Lâ€5â€vinyloxazolidineâ€2â€thione, a goitrogenic product from rapeseed, by rumen microorganisms. Journal of Environmental Science and Health Part A: Environmental Science and Engineering, 1994, 29, 2009-2021.	0.1	0
281	Rope from the Rutten cog, a 13th Century Seagoing Vessel found in The Netherlands. Journal of Archaeological Science, 1995, 22, 551-559.	1.2	0
282	Draft Genome Sequence of a Novel Methylobacterium brachiatum Strain Isolated from Human Skin. Microbiology Resource Announcements, 2020, 9, .	0.3	0