

Caroline M Plugge

List of Publications by Year in descending order

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141
papers

12,211
citations

36303
51
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27406
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149
all docs

149
docs citations

149
times ranked

13404
citing authors

#	ARTICLE	IF	CITATIONS
1	Akkermansia muciniphila gen. nov., sp. nov., a human intestinal mucin-degrading bacterium. International Journal of Systematic and Evolutionary Microbiology, 2004, 54, 1469-1476.	1.7	1,566
2	Electron transfer in syntrophic communities of anaerobic bacteria and archaea. Nature Reviews Microbiology, 2009, 7, 568-577.	28.6	1,097
3	Reversible interconversion of carbon dioxide and formate by an electroactive enzyme. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 10654-10658.	7.1	472
4	The Mouse Intestinal Bacterial Collection (miBC) provides host-specific insight into cultured diversity and functional potential of the gut microbiota. Nature Microbiology, 2016, 1, 16131.	13.3	465
5	Chain Elongation with Reactor Microbiomes: Open-Culture Biotechnology To Produce Biochemicals. Environmental Science & Technology, 2016, 50, 2796-2810.	10.0	426
6	Exocellular electron transfer in anaerobic microbial communities. Environmental Microbiology, 2006, 8, 371-382.	3.8	343
7	Biological formation of caproate and caprylate from acetate: fuel and chemical production from low grade biomass. Energy and Environmental Science, 2011, 4, 216-224.	30.8	342
8	The Genome of Akkermansia muciniphila, a Dedicated Intestinal Mucin Degrader, and Its Use in Exploring Intestinal Metagenomes. PLoS ONE, 2011, 6, e16876.	2.5	328
9	Growth of Syntrophic Propionate-Oxidizing Bacteria with Fumarate in the Absence of Methanogenic Bacteria. Applied and Environmental Microbiology, 1993, 59, 1114-1119.	3.1	308
10	Biomethanation and Its Potential. Methods in Enzymology, 2011, 494, 327-351.	1.0	277
11	Metabolic Flexibility of Sulfate-Reducing Bacteria. Frontiers in Microbiology, 2011, 2, 81.	3.5	274
12	Interspecies electron transfer in methanogenic propionate degrading consortia. Water Research, 2004, 38, 1368-1375.	11.3	255
13	Reverse Methanogenesis and Respiration in Methanotrophic Archaea. Archaea, 2017, 2017, 1-22.	2.3	240
14	Syntrophic butyrate and propionate oxidation processes: from genomes to reaction mechanisms. Environmental Microbiology Reports, 2010, 2, 489-499.	2.4	238
15	Production of butyrate from lysine and the Amadori product fructoselysine by a human gut commensal. Nature Communications, 2015, 6, 10062.	12.8	199
16	Advancing microbial sciences by individual-based modelling. Nature Reviews Microbiology, 2016, 14, 461-471.	28.6	193
17	Presence and Role of Anaerobic Hydrolytic Microbes in Conversion of Lignocellulosic Biomass for Biogas Production. Critical Reviews in Environmental Science and Technology, 2015, 45, 2523-2564.	12.8	156
18	The first true obligately syntrophic propionate-oxidizing bacterium, Pelotomaculum schinkii sp. nov., co-cultured with Methanospirillum hungatei, and emended description of the genus Pelotomaculum. International Journal of Systematic and Evolutionary Microbiology, 2005, 55, 1697-1703.	1.7	139

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19	Application of bacteria involved in the biological sulfur cycle for paper mill effluent purification. Science of the Total Environment, 2009, 407, 1333-1343.	8.0	130
20	Anaerobic Degradation of Propionate by a Mesophilic Acetogenic Bacterium in Coculture and Triculture with Different Methanogens. Applied and Environmental Microbiology, 1994, 60, 2834-2838.	3.1	129
21	Controlling Ethanol Use in Chain Elongation by CO ₂ Loading Rate. Environmental Science & Technology, 2018, 52, 1496-1505.	10.0	127
22	Victivallis vadensis gen. nov., sp. nov., a sugar-fermenting anaerobe from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2003, 53, 211-215.	1.7	117
23	Desulfotomaculum thermobenzoicum subsp. thermosyntrophicum subsp. nov., a thermophilic, syntrophic, propionate-oxidizing, spore-forming bacterium.. International Journal of Systematic and Evolutionary Microbiology, 2002, 52, 391-399.	1.7	115
24	Metabolic interactions in methanogenic and sulfate-reducing bioreactors. Water Science and Technology, 2005, 52, 13-20.	2.5	115
25	Variation of carbon isotope fractionation in hydrogenotrophic methanogenic microbial cultures and environmental samples at different energy status. Global Change Biology, 2005, 11, 2103-2113.	9.5	113
26	Role of syntrophic microbial communities in high-rate methanogenic bioreactors. Water Science and Technology, 2012, 66, 352-362.	2.5	112
27	A genomic view on syntrophic versus non-syntrophic lifestyle in anaerobic fatty acid degrading communities. Biochimica Et Biophysica Acta - Bioenergetics, 2014, 1837, 2004-2016.	1.0	107
28	Methanogenic archaea and sulfate reducing bacteria co-cultured on acetate: teamwork or coexistence?. Frontiers in Microbiology, 2015, 6, 492.	3.5	107
29	Analysis of the mechanisms of bioelectrochemical methane production by mixed cultures. Journal of Chemical Technology and Biotechnology, 2015, 90, 963-970.	3.2	107
30	Biofilm formation and granule properties in anaerobic digestion at high salinity. Water Research, 2017, 121, 61-71.	11.3	105
31	Comparative genomics and physiology of the butyrate-producing bacterium <i>Intestinimonas butyriciproducens</i> . Environmental Microbiology Reports, 2016, 8, 1024-1037.	2.4	104
32	Anaerobic benzene degradation under denitrifying conditions: <i>Peptococcaceae</i> as dominant benzene degraders and evidence for a syntrophic process. Environmental Microbiology, 2012, 14, 1171-1181.	3.8	100
33	Microbial Community Analysis of a Methane-Producing Biocathode in a Bioelectrochemical System. Archaea, 2013, 2013, 1-12.	2.3	98
34	Intestinimonas butyriciproducens gen. nov., sp. nov., a butyrate-producing bacterium from the mouse intestine. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 4606-4612.	1.7	95
35	Syntrophic Growth on Formate: a New Microbial Niche in Anoxic Environments. Applied and Environmental Microbiology, 2008, 74, 6126-6131.	3.1	94
36	Role of substrate concentration in particle size distribution of methanogenic granular sludge in UASB reactors. Water Research, 1991, 25, 21-27.	11.3	91

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37	Anaerobic oxidation of methane associated with sulfate reduction in a natural freshwater gas source. ISME Journal, 2016, 10, 1400-1412.	9.8	90
38	The Rhizosphere Selects for Particular Groups of Acidobacteria and Verrucomicrobia. PLoS ONE, 2013, 8, e82443.	2.5	87
39	Effect of humic acid on anaerobic digestion of cellulose and xylan in completely stirred tank reactors: inhibitory effect, mitigation of the inhibition and the dynamics of the microbial communities.. Applied Microbiology and Biotechnology, 2017, 101, 889-901.	3.6	87
40	Acetyl-CoA cleavage pathway in a syntrophic propionate oxidizing bacterium growing on fumarate in the absence of methanogens. FEMS Microbiology Letters, 1993, 110, 71-76.	1.8	76
41	Identification of glucose-fermenting bacteria present in an in vitro model of the human intestine by RNA-stable isotope probing. FEMS Microbiology Ecology, 2007, 60, 126-135.	2.7	74
42	Anoxic Media Design, Preparation, and Considerations. Methods in Enzymology, 2005, 397, 3-16.	1.0	71
43	Growth of Anaerobic Methane-Oxidizing Archaea and Sulfate-Reducing Bacteria in a High-Pressure Membrane Capsule Bioreactor. Applied and Environmental Microbiology, 2015, 81, 1286-1296.	3.1	71
44	Diurnal Dynamics of Gaseous and Dissolved Metabolites and Microbiota Composition in the Bovine Rumen. Frontiers in Microbiology, 2017, 8, 425.	3.5	67
45	Formate Formation and Formate Conversion in Biological Fuels Production. Enzyme Research, 2011, 2011, 1-8.	1.8	66
46	Fast anaerobic sludge granulation at elevated salinity. Water Research, 2018, 128, 293-303.	11.3	66
47	Growth- and substrate-dependent transcription of formate dehydrogenase and hydrogenase coding genes in Syntrophobacter fumaroxidans and Methanospirillum hungatei. Microbiology (United Kingdom), 2014, 154, 1481-1491.	1.0	66
48	Anaerostipes rhamnosivorans sp. nov., a human intestinal, butyrate-forming bacterium. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 787-793.	1.7	62
49	Decreased activity of a propionate degrading community in a UASB reactor fed with synthetic medium without molybdenum, tungsten and selenium. Enzyme and Microbial Technology, 2009, 45, 139-145.	3.2	60
50	Influence of setup and carbon source on the bacterial community of biocathodes in microbial electrolysis cells. Enzyme and Microbial Technology, 2014, 61-62, 67-75.	3.2	58
51	Complete genome sequence of Syntrophobacter fumaroxidans strain (MPOBT). Standards in Genomic Sciences, 2012, 7, 91-106.	1.5	55
52	Mighty small: Observing and modeling individual microbes becomes big science. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18027-18028.	7.1	54
53	Selenomonas acidaminovorans sp. nov., a versatile thermophilic proton-reducing anaerobe able to grow by decarboxylation of succinate to propionate. Archives of Microbiology, 1992, 157, 169-175.	2.2	51
54	Long-term performance and fouling analysis of full-scale direct nanofiltration (NF) installations treating anoxic groundwater. Journal of Membrane Science, 2014, 468, 339-348.	8.2	51

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55	Thermodynamic Driving Force of Hydrogen on Rumen Microbial Metabolism: A Theoretical Investigation. PLoS ONE, 2016, 11, e0161362.	2.5	51
56	Comparative proteome analysis of propionate degradation by <i>Syntrophobacter fumaroxidans</i> in pure culture and in coculture with methanogens. Environmental Microbiology, 2018, 20, 1842-1856.	3.8	50
57	Enrichment of anaerobic syngas-converting bacteria from thermophilic bioreactor sludge. FEMS Microbiology Ecology, 2013, 86, 590-597.	2.7	48
58	Metabolism and Occurrence of Methanogenic and Sulfate-Reducing Syntrophic Acetate Oxidizing Communities in Haloalkaline Environments. Frontiers in Microbiology, 2018, 9, 3039.	3.5	48
59	Mitigation of Humic Acid Inhibition in Anaerobic Digestion of Cellulose by Addition of Various Salts. Bioengineering, 2015, 2, 54-65.	3.5	47
60	The Effect of DNA Extraction Methods on Observed Microbial Communities from Fibrous and Liquid Rumen Fractions of Dairy Cows. Frontiers in Microbiology, 2018, 9, 92.	3.5	46
61	Effect of humic acids on the activity of pure and mixed methanogenic cultures. Biomass and Bioenergy, 2017, 99, 21-30.	5.7	44
62	Mutual Metabolic Interactions in Co-cultures of the Intestinal Anaerostipes rhamnosivorans With an Acetogen, Methanogen, or Pectin-Degrader Affecting Butyrate Production. Frontiers in Microbiology, 2019, 10, 2449.	3.5	43
63	Genome analysis of Desulfotomaculum kuznetsovii strain 17T reveals a physiological similarity with Pelotomaculum thermopropionicum strain SIT.. Standards in Genomic Sciences, 2013, 8, 69-87.	1.5	42
64	Title is missing!. Biodegradation, 1998, 9, 463-473.	3.0	41
65	Effect of tungsten and molybdenum on growth of a syntrophic coculture of Syntrophobacter fumaroxidans and Methanospirillum hungatei. Archives of Microbiology, 2009, 191, 55-61.	2.2	41
66	Global transcriptomics analysis of the Desulfovibrio vulgaris change from syntrophic growth with Methanosarcina barkeri to sulfidogenic metabolism. Microbiology (United Kingdom), 2010, 156, 2746-2756.	1.8	40
67	Inhibitory Effect of Coumarin on Syntrophic Fatty Acid-Oxidizing and Methanogenic Cultures and Biogas Reactor Microbiomes. Applied and Environmental Microbiology, 2017, 83, .	3.1	37
68	From Genes to Ecosystems in Microbiology: Modeling Approaches and the Importance of Individuality. Frontiers in Microbiology, 2017, 8, 2299.	3.5	37
69	Growth and activity of ANME clades with different sulfate and sulfide concentrations in the presence of methane. Frontiers in Microbiology, 2015, 6, 988.	3.5	36
70	Biogas. Microbial Biotechnology, 2017, 10, 1128-1130.	4.2	36
71	Isolation and characterization of Sphingomonadaceae from fouled membranes. Npj Biofilms and Microbiomes, 2019, 5, 6.	6.4	35
72	Biofouling control: the impact of biofilm dispersal and membrane flushing. Water Research, 2021, 198, 117163.	11.3	32

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73	Genome Analysis and Physiological Comparison of Alicyclophilus denitrificans Strains BC and K601T. PLoS ONE, 2013, 8, e66971.	2.5	32
74	Genome Sequences of Alicyclophilus denitrificans Strains BC and K601 ^T. Journal of Bacteriology, 2011, 193, 5028-5029.	2.2	31
75	Organic acid production from potato starch waste fermentation by rumen microbial communities from Dutch and Thai dairy cows. Biotechnology for Biofuels, 2018, 11, 13.	6.2	30
76	Microbial Community Drivers in Anaerobic Granulation at High Salinity. Frontiers in Microbiology, 2020, 11, 235.	3.5	30
77	Biodiversity and ecology of microorganisms in high pressure membrane filtration systems. Water Research, 2020, 172, 115511.	11.3	29
78	Syntrophy in Methanogenic Degradation. Microbiology Monographs, 2010, , 143-173.	0.6	28
79	Sulfate reduction in a hydrogen fed bioreactor operated at haloalkaline conditions. Water Research, 2015, 68, 67-76.	11.3	28
80	Membrane Fouling and Chemical Cleaning in Three Full-Scale Reverse Osmosis Plants Producing Demineralized Water. Journal of Engineering (United States), 2017, 2017, 1-14.	1.0	28
81	EPS Glycoconjugate Profiles Shift as Adaptive Response in Anaerobic Microbial Granulation at High Salinity. Frontiers in Microbiology, 2018, 9, 1423.	3.5	28
82	Genome analysis of Desulfotomaculum gibsoniae strain GrollT a highly versatile Gram-positive sulfate-reducing bacterium. Standards in Genomic Sciences, 2014, 9, 821-839.	1.5	27
83	Calcium effect on microbial activity and biomass aggregation during anaerobic digestion at high salinity. New Biotechnology, 2020, 56, 114-122.	4.4	27
84	Sodium lauryl ether sulfate (SLES) degradation by nitrate-reducing bacteria. Applied Microbiology and Biotechnology, 2017, 101, 5163-5173.	3.6	26
85	The potential of osmolytes and their precursors to alleviate osmotic stress of anaerobic granular sludge.. Water Research, 2018, 147, 142-151.	11.3	26
86	Genome analyses of the carboxydophilic sulfate-reducers Desulfotomaculum nigrificans and Desulfotomaculum carboxydovorans and reclassification of Desulfotomaculum carboxydovorans as a later synonym of Desulfotomaculum nigrificans. Standards in Genomic Sciences, 2014, 9, 655-675.	1.5	25
87	Comparative proteomics of <i>Geobacter sulfurreducens</i> PCA^T in response to acetate, formate and/or hydrogen as electron donor. Environmental Microbiology, 2021, 23, 299-315.	3.8	25
88	Transcription of <i>fdh</i> and <i>hyd</i> in <i>Syntrophobacter</i> spp. and <i>Methanospirillum</i> spp. as a diagnostic tool for monitoring anaerobic sludge deprived of molybdenum, tungsten and selenium. Environmental Microbiology, 2011, 13, 1228-1235.	3.8	24
89	Ethyl tert-butyl ether (EtBE) degradation by an algal-bacterial culture obtained from contaminated groundwater. Water Research, 2019, 148, 314-323.	11.3	23
90	Complete genome sequence of the sulfate-reducing firmicute Desulfotomaculum ruminis type strain (DLT). Standards in Genomic Sciences, 2012, 7, 304-319.	1.5	22

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91	Anaerobic degradation of sodium dodecyl sulfate (SDS) by denitrifying bacteria. International Biodeterioration and Biodegradation, 2013, 84, 14-20.	3.9	22
92	Piezo-tolerant natural gas-producing microbes under accumulating pCO ₂ . Biotechnology for Biofuels, 2016, 9, 236.	6.2	22
93	Elucidation of the pathways of catabolic glutamate conversion in three thermophilic anaerobic bacteria. Archives of Microbiology, 2001, 176, 29-36.	2.2	21
94	Nitrate and (per)chlorate reduction pathways in (per)chlorate-reducing bacteria. Biochemical Society Transactions, 2011, 39, 230-235.	3.4	21
95	Genome and proteome analysis of <i>Pseudomonas chloritidismutans</i> AW ^T that grows on n-decane with chlorate or oxygen as electron acceptor. Environmental Microbiology, 2016, 18, 3247-3257.	3.8	21
96	Relating MEC population dynamics to anode performance from DGGE and electrical data. Systematic and Applied Microbiology, 2013, 36, 408-416.	2.8	17
97	<i>Actinomyces succiniciruminis</i> sp. nov. and <i>Actinomyces glycerinitolerans</i> sp. nov., two novel organic acid-producing bacteria isolated from rumen. Systematic and Applied Microbiology, 2016, 39, 445-452.	2.8	17
98	Ecology and application of haloalkaliphilic anaerobic microbial communities. Applied Microbiology and Biotechnology, 2015, 99, 9331-9336.	3.6	16
99	How microbial glycosyl hydrolase activity in the gut mucosa initiates microbial cross-feeding. Glycobiology, 2022, 32, 182-200.	2.5	14
100	Metabolic response of <i>Alicyclophilus denitrificans</i> strain BC toward electron acceptor variation. Proteomics, 2013, 13, 2886-2894.	2.2	13
101	<i>Lachnotalea glycerini</i> gen. nov., sp. nov., an anaerobe isolated from a nanofiltration unit treating anoxic groundwater. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 774-779.	1.7	13
102	Arginine catabolism by <i>Thermanaerovibrio acidaminovorans</i> . FEMS Microbiology Letters, 2001, 195, 259-262.	1.8	12
103	Characterization of the bacterial community involved in the bioflocculation process of wastewater organic matter in high-loaded MBRs. Applied Microbiology and Biotechnology, 2015, 99, 5327-5337.	3.6	11
104	Influence of phenylacetic acid pulses on anaerobic digestion performance and archaeal community structure in WWTP sewage sludge digesters. Water Science and Technology, 2015, 71, 1790-1799.	2.5	10
105	Thiosulphate conversion in a methane and acetate fed membrane bioreactor. Environmental Science and Pollution Research, 2016, 23, 2467-2478.	5.3	10
106	Butyrate Conversion by Sulfate-Reducing and Methanogenic Communities from Anoxic Sediments of Aarhus Bay, Denmark. Microorganisms, 2020, 8, 606.	3.6	10
107	<i>Streptococcus caviae</i> sp. nov., isolated from guinea pig faecal samples. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 1551-1556.	1.7	10
108	Comparative analysis of microbial communities from different full-scale haloalkaline biodesulfurization systems. Applied Microbiology and Biotechnology, 2022, 106, 1759-1776.	3.6	10

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109	Starch hydrolysis in autogenerative high pressure digestion: Gelatinisation and saccharification as rate limiting steps. <i>Biomass and Bioenergy</i> , 2014, 71, 256-265.	5.7	9
110	Proteomic analysis of nitrate-dependent acetone degradation by <i>Alicyclophilus denitrificans</i> strain BC. <i>FEMS Microbiology Letters</i> , 2015, 362, .	1.8	9
111	Concurrent use of methanol and ethanol for chain-elongating short chain fatty acids into caproate and isobutyrate. <i>Journal of Environmental Management</i> , 2020, 258, 110008.	7.8	9
112	Propionate Converting Anaerobic Microbial Communities Enriched from Distinct Biogeochemical Zones of Aarhus Bay, Denmark under Sulfidogenic and Methanogenic Conditions. <i>Microorganisms</i> , 2020, 8, 394.	3.6	9
113	<i>Propionibacterium ruminifibrarum</i> sp. nov., isolated from cow rumen fibrous content. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2584-2590.	1.7	9
114	Enrichment of Thermophilic Syntrophic Anaerobic Glutamate-Degrading Consortia using a Dialysis Membrane Reactor. <i>Microbial Ecology</i> , 2002, 43, 378-387.	2.8	8
115	Thiosulfate Conversion to Sulfide by a Haloalkaliphilic Microbial Community in a Bioreactor Fed with H_2 Gas. <i>Environmental Science & Technology</i> , 2017, 51, 914-923.	10.0	8
116	Evaluation and optimization of PCR primers for selective and quantitative detection of marine ANME subclusters involved in sulfate-dependent anaerobic methane oxidation. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 5847-5859.	3.6	8
117	Effect of Sulfate on Carbon Monoxide Conversion by a Thermophilic Syngas-Fermenting Culture Dominated by a <i>Desulfofundulus</i> Species. <i>Frontiers in Microbiology</i> , 2020, 11, 588468.	3.5	8
118	<i>Pelorhabdus rhamnosifermentans</i> gen. nov., sp. nov., a strictly anaerobic rhamnose degrader from freshwater lake sediment. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126225.	2.8	8
119	Functional Insights of Salinity Stress-Related Pathways in Metagenome-Resolved <i>Methanotrix</i> Genomes. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0244921.	3.1	8
120	Anaerobic degradation of long-chain alkylamines by a denitrifying <i>Pseudomonas stutzeri</i> . <i>FEMS Microbiology Ecology</i> , 2008, 66, 136-142.	2.7	7
121	Syntrophic Degradation of Fatty Acids by Methanogenic Communities. , 2012, , 127-142.		7
122	Comparative Analysis of Carbon Monoxide Tolerance among <i>Thermoanaerobacter</i> Species. <i>Frontiers in Microbiology</i> , 2016, 7, 1330.	3.5	7
123	Biodegradation pathway of l-glutamatediacetate by <i>Rhizobium radiobacter</i> strain BG-1. <i>International Biodeterioration and Biodegradation</i> , 2008, 62, 31-37.	3.9	6
124	Microorganisms hydrolyse amide bonds; knowledge enabling read-across of biodegradability of fatty acid amides. <i>Biodegradation</i> , 2014, 25, 605-14.	3.0	6
125	Accurate assessment of the biodegradation of cationic surfactants in activated sludge reactors (OECD TG 303A). <i>Ecotoxicology and Environmental Safety</i> , 2015, 118, 83-89.	6.0	6
126	Syntrophy in Methanogenic Degradation. <i>Microbiology Monographs</i> , 2018, , 153-192.	0.6	5

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127	Characterization of dairy cow rumen bacterial and archaeal communities associated with grass silage and maize silage based diets. PLoS ONE, 2020, 15, e0229887.	2.5	5
128	Methanogens: Syntrophic Metabolism. , 2018, , 1-31.		4
129	Immobilization of sulfate and thiosulfate-reducing biomass on sand under haloalkaline conditions. Science of the Total Environment, 2020, 745, 141017.	8.0	3
130	Syntrophic Communities in Methane Formation from High Strength Wastewaters. , 2010, , 59-77.		3
131	Proteomic Analysis of a Syntrophic Coculture of Syntrophobacter fumaroxidans MPOBT and Geobacter sulfurreducens PCAT. Frontiers in Microbiology, 2021, 12, 708911.	3.5	3
132	Microbial Diversity and Organic Acid Production of Guinea Pig Faecal Samples. Current Microbiology, 2019, 76, 425-434.	2.2	2
133	Syngas as Electron Donor for Sulfate and Thiosulfate Reducing Haloalkaliphilic Microorganisms in a Gas-Lift Bioreactor. Microorganisms, 2020, 8, 1451.	3.6	2
134	Microbial catabolism-based grouping enables read-across of non-persistence for all constituents of hexyl glucoside and 2-ethylhexyl glucoside. International Biodeterioration and Biodegradation, 2021, 159, 105209.	3.9	2
135	Read-across of ready biodegradability based on the substrate specificity of N-alkyl polypropylene polyamine-degrading microorganisms. SAR and QSAR in Environmental Research, 2017, 28, 311-323.	2.2	1
136	Draft Genome Sequence of Actinomyces glycerinitolerans Strain G10 T , Isolated from Sheep Rumen Fluid. Genome Announcements, 2017, 5, .	0.8	1
137	Draft Genome Sequence of Actinomyces succiniciruminis Strain Am4 T , Isolated from Cow Rumen Fluid. Genome Announcements, 2017, 5, .	0.8	1
138	Methanogens: Syntrophic Metabolism. , 2019, , 179-209.		1
139	Draft Genome Sequence of <i>Sphingomonas</i> sp. Strain Sph1(2015), Isolated from a Fouled Membrane Filter Used to Produce Drinking Water. Genome Announcements, 2017, 5, .	0.8	0
140	Draft Genome Sequence of Streptococcus caviae Strain Cavy grass 6 ^T , Isolated from Domesticated Guinea Pig Fecal Samples. Genome Announcements, 2017, 5, .	0.8	0
141	Special Issue “Anaerobes in Biogeochemical Cycles”, Microorganisms, 2021, 9, 23.	3.6	0