

Caroline M Plugge

List of Publications by Year in descending order

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papers

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36203

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149
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#	ARTICLE	IF	CITATIONS
1	How microbial glycosyl hydrolase activity in the gut mucosa initiates microbial cross-feeding. <i>Glycobiology</i> , 2022, 32, 182-200.	1.3	14
2	Comparative analysis of microbial communities from different full-scale haloalkaline biodesulfurization systems. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 1759-1776.	1.7	10
3	Functional Insights of Salinity Stress-Related Pathways in Metagenome-Resolved <i>Methanotherix</i> Genomes. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0244921.	1.4	8
4	Comparative proteomics of <i>Geobacter sulfurreducens</i> PCA ^T in response to acetate, formate and/or hydrogen as electron donor. <i>Environmental Microbiology</i> , 2021, 23, 299-315.	1.8	25
5	Microbial catabolism-based grouping enables read-across of non-persistence for all constituents of hexyl glucoside and 2-ethylhexyl glucoside. <i>International Biodeterioration and Biodegradation</i> , 2021, 159, 105209.	1.9	2
6	Biofouling control: the impact of biofilm dispersal and membrane flushing. <i>Water Research</i> , 2021, 198, 117163.	5.3	32
7	<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.	1.2	8
8	Special Issue "Anaerobes in Biogeochemical Cycles". <i>Microorganisms</i> , 2021, 9, 23.	1.6	0
9	Proteomic Analysis of a Syntrophic Coculture of <i>Syntrophobacter fumaroxidans</i> MPOBT and <i>Geobacter sulfurreducens</i> PCAT. <i>Frontiers in Microbiology</i> , 2021, 12, 708911.	1.5	3
10	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.	3.8	9
11	Calcium effect on microbial activity and biomass aggregation during anaerobic digestion at high salinity. <i>New Biotechnology</i> , 2020, 56, 114-122.	2.4	27
12	Syngas as Electron Donor for Sulfate and Thiosulfate Reducing Haloalkaliphilic Microorganisms in a Gas-Lift Bioreactor. <i>Microorganisms</i> , 2020, 8, 1451.	1.6	2
13	Immobilization of sulfate and thiosulfate-reducing biomass on sand under haloalkaline conditions. <i>Science of the Total Environment</i> , 2020, 745, 141017.	3.9	3
14	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.	1.5	8
15	Microbial Community Drivers in Anaerobic Granulation at High Salinity. <i>Frontiers in Microbiology</i> , 2020, 11, 235.	1.5	30
16	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.	1.6	9
17	Characterization of dairy cow rumen bacterial and archaeal communities associated with grass silage and maize silage based diets. <i>PLoS ONE</i> , 2020, 15, e0229887.	1.1	5
18	Biodiversity and ecology of microorganisms in high pressure membrane filtration systems. <i>Water Research</i> , 2020, 172, 115511.	5.3	29

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19	Butyrate Conversion by Sulfate-Reducing and Methanogenic Communities from Anoxic Sediments of Aarhus Bay, Denmark. <i>Microorganisms</i> , 2020, 8, 606.	1.6	10
20	Methanogens: Syntrophic Metabolism. , 2019, , 179-209.		1
21	Mutual Metabolic Interactions in Co-cultures of the Intestinal <i>Anaerostipes rhamnosivorans</i> With an Acetogen, Methanogen, or Pectin-Degrader Affecting Butyrate Production. <i>Frontiers in Microbiology</i> , 2019, 10, 2449.	1.5	43
22	Isolation and characterization of Sphingomonadaceae from fouled membranes. <i>Npj Biofilms and Microbiomes</i> , 2019, 5, 6.	2.9	35
23	Microbial Diversity and Organic Acid Production of Guinea Pig Faecal Samples. <i>Current Microbiology</i> , 2019, 76, 425-434.	1.0	2
24	Ethyl tert-butyl ether (EtBE) degradation by an algal-bacterial culture obtained from contaminated groundwater. <i>Water Research</i> , 2019, 148, 314-323.	5.3	23
25	<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.	0.8	9
26	Comparative proteome analysis of propionate degradation by <i>Syntrophobacter fumaroxidans</i> in pure culture and in coculture with methanogens. <i>Environmental Microbiology</i> , 2018, 20, 1842-1856.	1.8	50
27	Controlling Ethanol Use in Chain Elongation by CO ₂ Loading Rate. <i>Environmental Science & Technology</i> , 2018, 52, 1496-1505.	4.6	127
28	Methanogens: Syntrophic Metabolism. , 2018, , 1-31.		4
29	Fast anaerobic sludge granulation at elevated salinity. <i>Water Research</i> , 2018, 128, 293-303.	5.3	66
30	Syntrophy in Methanogenic Degradation. <i>Microbiology Monographs</i> , 2018, , 153-192.	0.3	5
31	Metabolism and Occurrence of Methanogenic and Sulfate-Reducing Syntrophic Acetate Oxidizing Communities in Haloalkaline Environments. <i>Frontiers in Microbiology</i> , 2018, 9, 3039.	1.5	48
32	The potential of osmolytes and their precursors to alleviate osmotic stress of anaerobic granular sludge.. <i>Water Research</i> , 2018, 147, 142-151.	5.3	26
33	EPS Glycoconjugate Profiles Shift as Adaptive Response in Anaerobic Microbial Granulation at High Salinity. <i>Frontiers in Microbiology</i> , 2018, 9, 1423.	1.5	28
34	The Effect of DNA Extraction Methods on Observed Microbial Communities from Fibrous and Liquid Rumen Fractions of Dairy Cows. <i>Frontiers in Microbiology</i> , 2018, 9, 92.	1.5	46
35	Organic acid production from potato starch waste fermentation by rumen microbial communities from Dutch and Thai dairy cows. <i>Biotechnology for Biofuels</i> , 2018, 11, 13.	6.2	30
36	Effect of humic acids on the activity of pure and mixed methanogenic cultures. <i>Biomass and Bioenergy</i> , 2017, 99, 21-30.	2.9	44

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37	Inhibitory Effect of Coumarin on Syntrophic Fatty Acid-Oxidizing and Methanogenic Cultures and Biogas Reactor Microbiomes. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	37
38	Biofilm formation and granule properties in anaerobic digestion at high salinity. <i>Water Research</i> , 2017, 121, 61-71.	5.3	105
39	Read-across of ready biodegradability based on the substrate specificity of N-alkyl polypropylene polyamine-degrading microorganisms. <i>SAR and QSAR in Environmental Research</i> , 2017, 28, 311-323.	1.0	1
40	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.. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 889-901.	1.7	87
41	Draft Genome Sequence of <i>Actinomyces glycerinitolerans</i> Strain G10 T , Isolated from Sheep Rumen Fluid. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
42	Sodium lauryl ether sulfate (SLES) degradation by nitrate-reducing bacteria. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 5163-5173.	1.7	26
43	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.	4.6	8
44	Biogas. <i>Microbial Biotechnology</i> , 2017, 10, 1128-1130.	2.0	36
45	Draft Genome Sequence of <i>Actinomyces succiniciruminis</i> Strain Am4 T , Isolated from Cow Rumen Fluid. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
46	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.	1.7	8
47	Draft Genome Sequence of <i>Sphingomonas</i> sp. Strain Sph1(2015), Isolated from a Fouled Membrane Filter Used to Produce Drinking Water. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
48	Draft Genome Sequence of <i>Streptococcus caviae</i> Strain Cavy grass 6 T , Isolated from Domesticated Guinea Pig Fecal Samples. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
49	Diurnal Dynamics of Gaseous and Dissolved Metabolites and Microbiota Composition in the Bovine Rumen. <i>Frontiers in Microbiology</i> , 2017, 8, 425.	1.5	67
50	From Genes to Ecosystems in Microbiology: Modeling Approaches and the Importance of Individuality. <i>Frontiers in Microbiology</i> , 2017, 8, 2299.	1.5	37
51	Reverse Methanogenesis and Respiration in Methanotrophic Archaea. <i>Archaea</i> , 2017, 2017, 1-22.	2.3	240
52	Membrane Fouling and Chemical Cleaning in Three Full-Scale Reverse Osmosis Plants Producing Demineralized Water. <i>Journal of Engineering (United States)</i> , 2017, 2017, 1-14.	0.5	28
53	<i>Streptococcus caviae</i> sp. nov., isolated from guinea pig faecal samples. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 1551-1556.	0.8	10
54	Comparative Analysis of Carbon Monoxide Tolerance among <i>Thermoanaerobacter</i> Species. <i>Frontiers in Microbiology</i> , 2016, 7, 1330.	1.5	7

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55	Thermodynamic Driving Force of Hydrogen on Rumen Microbial Metabolism: A Theoretical Investigation. <i>PLoS ONE</i> , 2016, 11, e0161362.	1.1	51
56	Genome and proteome analysis of <i>Pseudomonas chloritidismutans</i> AW-1 ^T that grows on n-decane with chlorate or oxygen as electron acceptor. <i>Environmental Microbiology</i> , 2016, 18, 3247-3257.	1.8	21
57	Anaerobic oxidation of methane associated with sulfate reduction in a natural freshwater gas source. <i>ISME Journal</i> , 2016, 10, 1400-1412.	4.4	90
58	<i>Actinomyces succiniciruminis</i> sp. nov. and <i>Actinomyces glycerinitolerans</i> sp. nov., two novel organic acid-producing bacteria isolated from rumen. <i>Systematic and Applied Microbiology</i> , 2016, 39, 445-452.	1.2	17
59	Comparative genomics and physiology of the butyrate-producing bacterium <i>Intestinimonas butyriciproducens</i> . <i>Environmental Microbiology Reports</i> , 2016, 8, 1024-1037.	1.0	104
60	The Mouse Intestinal Bacterial Collection (miBC) provides host-specific insight into cultured diversity and functional potential of the gut microbiota. <i>Nature Microbiology</i> , 2016, 1, 16131.	5.9	465
61	Piezo-tolerant natural gas-producing microbes under accumulating pCO ₂ . <i>Biotechnology for Biofuels</i> , 2016, 9, 236.	6.2	22
62	Advancing microbial sciences by individual-based modelling. <i>Nature Reviews Microbiology</i> , 2016, 14, 461-471.	13.6	193
63	Chain Elongation with Reactor Microbiomes: Open-Culture Biotechnology To Produce Biochemicals. <i>Environmental Science & Technology</i> , 2016, 50, 2796-2810.	4.6	426
64	Thiosulphate conversion in a methane and acetate fed membrane bioreactor. <i>Environmental Science and Pollution Research</i> , 2016, 23, 2467-2478.	2.7	10
65	<i>Lachnotalea glycerini</i> gen. nov., sp. nov., an anaerobe isolated from a nanofiltration unit treating anoxic groundwater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 774-779.	0.8	13
66	Production of butyrate from lysine and the Amadori product fructoselysine by a human gut commensal. <i>Nature Communications</i> , 2015, 6, 10062.	5.8	199
67	Mitigation of Humic Acid Inhibition in Anaerobic Digestion of Cellulose by Addition of Various Salts. <i>Bioengineering</i> , 2015, 2, 54-65.	1.6	47
68	Methanogenic archaea and sulfate reducing bacteria co-cultured on acetate: teamwork or coexistence?. <i>Frontiers in Microbiology</i> , 2015, 6, 492.	1.5	107
69	Growth and activity of ANME clades with different sulfate and sulfide concentrations in the presence of methane. <i>Frontiers in Microbiology</i> , 2015, 6, 988.	1.5	36
70	Proteomic analysis of nitrate-dependent acetone degradation by <i>Alicyclophilus denitrificans</i> strain BC. <i>FEMS Microbiology Letters</i> , 2015, 362, .	0.7	9
71	Growth of Anaerobic Methane-Oxidizing Archaea and Sulfate-Reducing Bacteria in a High-Pressure Membrane Capsule Bioreactor. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1286-1296.	1.4	71
72	Analysis of the mechanisms of bioelectrochemical methane production by mixed cultures. <i>Journal of Chemical Technology and Biotechnology</i> , 2015, 90, 963-970.	1.6	107

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73	Presence and Role of Anaerobic Hydrolytic Microbes in Conversion of Lignocellulosic Biomass for Biogas Production. <i>Critical Reviews in Environmental Science and Technology</i> , 2015, 45, 2523-2564.	6.6	156
74	Influence of phenylacetic acid pulses on anaerobic digestion performance and archaeal community structure in WWTP sewage sludge digesters. <i>Water Science and Technology</i> , 2015, 71, 1790-1799.	1.2	10
75	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.	2.9	6
76	Characterization of the bacterial community involved in the bioflocculation process of wastewater organic matter in high-loaded MBRs. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 5327-5337.	1.7	11
77	Ecology and application of haloalkaliphilic anaerobic microbial communities. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 9331-9336.	1.7	16
78	Sulfate reduction in a hydrogen fed bioreactor operated at haloalkaline conditions. <i>Water Research</i> , 2015, 68, 67-76.	5.3	28
79	<i>Anaerostipes rhamnosivorans</i> sp. nov., a human intestinal, butyrate-forming bacterium. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 787-793.	0.8	62
80	Starch hydrolysis in autogenerative high pressure digestion: Gelatinisation and saccharification as rate limiting steps. <i>Biomass and Bioenergy</i> , 2014, 71, 256-265.	2.9	9
81	Influence of setup and carbon source on the bacterial community of biocathodes in microbial electrolysis cells. <i>Enzyme and Microbial Technology</i> , 2014, 61-62, 67-75.	1.6	58
82	Microorganisms hydrolyse amide bonds; knowledge enabling read-across of biodegradability of fatty acid amides. <i>Biodegradation</i> , 2014, 25, 605-14.	1.5	6
83	Long-term performance and fouling analysis of full-scale direct nanofiltration (NF) installations treating anoxic groundwater. <i>Journal of Membrane Science</i> , 2014, 468, 339-348.	4.1	51
84	A genomic view on syntrophic versus non-syntrophic lifestyle in anaerobic fatty acid degrading communities. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, 2004-2016.	0.5	107
85	Genome analyses of the carboxydrotrophic sulfate-reducers <i>Desulfotomaculum nigrificans</i> and <i>Desulfotomaculum carboxydvorans</i> and reclassification of <i>Desulfotomaculum caboxydivorans</i> as a later synonym of <i>Desulfotomaculum nigrificans</i> . <i>Standards in Genomic Sciences</i> , 2014, 9, 655-675.	1.5	25
86	Genome analysis of <i>Desulfotomaculum gibsoniae</i> strain GrollT a highly versatile Gram-positive sulfate-reducing bacterium. <i>Standards in Genomic Sciences</i> , 2014, 9, 821-839.	1.5	27
87	Enrichment of anaerobic syngas-converting bacteria from thermophilic bioreactor sludge. <i>FEMS Microbiology Ecology</i> , 2013, 86, 590-597.	1.3	48
88	Relating MEC population dynamics to anode performance from DGGE and electrical data. <i>Systematic and Applied Microbiology</i> , 2013, 36, 408-416.	1.2	17
89	Mighty small: Observing and modeling individual microbes becomes big science. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 18027-18028.	3.3	54
90	<i>Intestinimonas butyriciproducens</i> gen. nov., sp. nov., a butyrate-producing bacterium from the mouse intestine. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 4606-4612.	0.8	95

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91	Anaerobic degradation of sodium dodecyl sulfate (SDS) by denitrifying bacteria. International Biodeterioration and Biodegradation, 2013, 84, 14-20.	1.9	22
92	Metabolic response of <i>Alicyclophilus denitrificans</i> strain BC toward electron acceptor variation. Proteomics, 2013, 13, 2886-2894.	1.3	13
93	Genome analysis of <i>Desulfotomaculum kuznetsovii</i> strain 17T reveals a physiological similarity with <i>Pelotomaculum thermopropionicum</i> strain SIT.. Standards in Genomic Sciences, 2013, 8, 69-87.	1.5	42
94	The Rhizosphere Selects for Particular Groups of Acidobacteria and Verrucomicrobia. PLoS ONE, 2013, 8, e82443.	1.1	87
95	Microbial Community Analysis of a Methane-Producing Biocathode in a Bioelectrochemical System. Archaea, 2013, 2013, 1-12.	2.3	98
96	Genome Analysis and Physiological Comparison of <i>Alicyclophilus denitrificans</i> Strains BC and K601T. PLoS ONE, 2013, 8, e66971.	1.1	32
97	Role of syntrophic microbial communities in high-rate methanogenic bioreactors. Water Science and Technology, 2012, 66, 352-362.	1.2	112
98	Complete genome sequence of <i>Syntrophobacter fumaroxidans</i> strain (MPOBT). Standards in Genomic Sciences, 2012, 7, 91-106.	1.5	55
99	Complete genome sequence of the sulfate-reducing firmicute <i>Desulfotomaculum ruminis</i> type strain (DLT). Standards in Genomic Sciences, 2012, 7, 304-319.	1.5	22
100	Syntrophic Degradation of Fatty Acids by Methanogenic Communities. , 2012, , 127-142.		7
101	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.	1.8	100
102	Biological formation of caproate and caprylate from acetate: fuel and chemical production from low grade biomass. Energy and Environmental Science, 2011, 4, 216-224.	15.6	342
103	Nitrate and (per)chlorate reduction pathways in (per)chlorate-reducing bacteria. Biochemical Society Transactions, 2011, 39, 230-235.	1.6	21
104	Biomethanation and Its Potential. Methods in Enzymology, 2011, 494, 327-351.	0.4	277
105	Metabolic Flexibility of Sulfate-Reducing Bacteria. Frontiers in Microbiology, 2011, 2, 81.	1.5	274
106	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.	1.8	24
107	Growth- and substrate-dependent transcription of formate dehydrogenase and hydrogenase coding genes in <i>Syntrophobacter fumaroxidans</i> and <i>Methanospirillum hungatei</i> . Microbiology (United Kingdom), 2011, 151, 147-155.	1.7	10
108	Formate Formation and Formate Conversion in Biological Fuels Production. Enzyme Research, 2011, 2011, 1-8.	1.8	66

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109	Genome Sequences of Alicyclophilus denitrificans Strains BC and K601 ^T. Journal of Bacteriology, 2011, 193, 5028-5029.	1.0	31
110	The Genome of Akkermansia muciniphila, a Dedicated Intestinal Mucin Degradator, and Its Use in Exploring Intestinal Metagenomes. PLoS ONE, 2011, 6, e16876.	1.1	328
111	Global transcriptomics analysis of the Desulfovibrio vulgaris change from syntrophic growth with Methanosarcina barkeri to sulfidogenic metabolism. Microbiology (United Kingdom), 2010, 156, 2746-2756.	0.7	40
112	Syntrophy in Methanogenic Degradation. Microbiology Monographs, 2010, , 143-173.	0.3	28
113	Syntrophic butyrate and propionate oxidation processes: from genomes to reaction mechanisms. Environmental Microbiology Reports, 2010, 2, 489-499.	1.0	238
114	Syntrophic Communities in Methane Formation from High Strength Wastewaters. , 2010, , 59-77.		3
115	Application of bacteria involved in the biological sulfur cycle for paper mill effluent purification. Science of the Total Environment, 2009, 407, 1333-1343.	3.9	130
116	Effect of tungsten and molybdenum on growth of a syntrophic coculture of Syntrophobacter fumaroxidans and Methanospirillum hungatei. Archives of Microbiology, 2009, 191, 55-61.	1.0	41
117	Electron transfer in syntrophic communities of anaerobic bacteria and archaea. Nature Reviews Microbiology, 2009, 7, 568-577.	13.6	1,097
118	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.	1.6	60
119	Biodegradation pathway of l-glutamatediacetate by Rhizobium radiobacter strain BG-1. International Biodeterioration and Biodegradation, 2008, 62, 31-37.	1.9	6
120	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.	3.3	472
121	Anaerobic degradation of long-chain alkylamines by a denitrifying Pseudomonas stutzeri. FEMS Microbiology Ecology, 2008, 66, 136-142.	1.3	7
122	Syntrophic Growth on Formate: a New Microbial Niche in Anoxic Environments. Applied and Environmental Microbiology, 2008, 74, 6126-6131.	1.4	94
123	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.	1.3	74
124	Exocellular electron transfer in anaerobic microbial communities. Environmental Microbiology, 2006, 8, 371-382.	1.8	343
125	Variation of carbon isotope fractionation in hydrogenotrophic methanogenic microbial cultures and environmental samples at different energy status. Global Change Biology, 2005, 11, 2103-2113.	4.2	113
126	Metabolic interactions in methanogenic and sulfate-reducing bioreactors. Water Science and Technology, 2005, 52, 13-20.	1.2	115

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127	The first true obligately syntrophic propionate-oxidizing bacterium, <i>Pelotomaculum schinkii</i> sp. nov., co-cultured with <i>Methanospirillum hungatei</i> , and emended description of the genus <i>Pelotomaculum</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2005, 55, 1697-1703.	0.8	139
128	Anoxic Media Design, Preparation, and Considerations. <i>Methods in Enzymology</i> , 2005, 397, 3-16.	0.4	71
129	<i>Akkermansia muciniphila</i> gen. nov., sp. nov., a human intestinal mucin-degrading bacterium. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004, 54, 1469-1476.	0.8	1,566
130	Interspecies electron transfer in methanogenic propionate degrading consortia. <i>Water Research</i> , 2004, 38, 1368-1375.	5.3	255
131	<i>Victivallis vadensis</i> gen. nov., sp. nov., a sugar-fermenting anaerobe from human faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003, 53, 211-215.	0.8	117
132	<i>Desulfotomaculum thermobenzoicum</i> subsp. <i>thermosyntrophicum</i> subsp. nov., a thermophilic, syntrophic, propionate-oxidizing, spore-forming bacterium.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2002, 52, 391-399.	0.8	115
133	Enrichment of Thermophilic Syntrophic Anaerobic Glutamate-Degrading Consortia using a Dialysis Membrane Reactor. <i>Microbial Ecology</i> , 2002, 43, 378-387.	1.4	8
134	Elucidation of the pathways of catabolic glutamate conversion in three thermophilic anaerobic bacteria. <i>Archives of Microbiology</i> , 2001, 176, 29-36.	1.0	21
135	Arginine catabolism by <i>Thermanaerovibrio acidaminovorans</i> . <i>FEMS Microbiology Letters</i> , 2001, 195, 259-262.	0.7	12
136	Title is missing!. <i>Biodegradation</i> , 1998, 9, 463-473.	1.5	41
137	Anaerobic Degradation of Propionate by a Mesophilic Acetogenic Bacterium in Coculture and Triculture with Different Methanogens. <i>Applied and Environmental Microbiology</i> , 1994, 60, 2834-2838.	1.4	129
138	Acetyl-CoA cleavage pathway in a syntrophic propionate oxidizing bacterium growing on fumarate in the absence of methanogens. <i>FEMS Microbiology Letters</i> , 1993, 110, 71-76.	0.7	76
139	Growth of Syntrophic Propionate-Oxidizing Bacteria with Fumarate in the Absence of Methanogenic Bacteria. <i>Applied and Environmental Microbiology</i> , 1993, 59, 1114-1119.	1.4	308
140	<i>Selenomonas acidaminovorans</i> sp. nov., a versatile thermophilic proton-reducing anaerobe able to grow by decarboxylation of succinate to propionate. <i>Archives of Microbiology</i> , 1992, 157, 169-175.	1.0	51
141	Role of substrate concentration in particle size distribution of methanogenic granular sludge in UASB reactors. <i>Water Research</i> , 1991, 25, 21-27.	5.3	91