

Peter H Janssen

List of Publications by Year in descending order

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133
papers

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146
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146
docs citations

146
times ranked

12454
citing authors

#	ARTICLE	IF	CITATIONS
1	Electron flow: key to mitigating ruminant methanogenesis. Trends in Microbiology, 2022, 30, 209-212.	3.5	21
2	Hydrogen and formate production and utilisation in the rumen and the human colon. Animal Microbiome, 2022, 4, 22.	1.5	23
3	Low-cost sample preservation methods for high-throughput processing of rumen microbiomes. Animal Microbiome, 2022, 4, .	1.5	2
4	Mapping immunogenic epitopes of an adhesin-like protein from Methanobrevibacter ruminantium M1 and comparison of empirical data with in silico prediction methods. Scientific Reports, 2022, 12, .	1.6	5
5	Individual-level correlations of rumen volatile fatty acids with enteric methane emissions for ranking methane yield in sheep fed fresh pasture. Animal Production Science, 2021, 61, 300.	0.6	7
6	Effects of long-acting, broad spectra anthelmintic treatments on the rumen microbial community compositions of grazing sheep. Scientific Reports, 2021, 11, 3836.	1.6	13
7	A protocol combining breath testing and ex vivo fermentations to study the human gut microbiome. STAR Protocols, 2021, 2, 100227.	0.5	0
8	Complete Genome Sequences of Three <i>Clostridiales</i> R-7 Group Strains Isolated from the Bovine Rumen in New Zealand. Microbiology Resource Announcements, 2021, 10, e0031021.	0.3	1
9	A restriction enzyme reduced representation sequencing approach for low-cost, high-throughput metagenome profiling. PLoS ONE, 2020, 15, e0219882.	1.1	23
10	Genetic parameters of plasma and ruminal volatile fatty acids in sheep fed alfalfa pellets and genetic correlations with enteric methane emissions ¹ . Journal of Animal Science, 2019, 97, 2711-2724.	0.2	16
11	Modelling thermodynamic feedback on the metabolism of hydrogenotrophic methanogens. Journal of Theoretical Biology, 2019, 477, 14-23.	0.8	12
12	Improved taxonomic assignment of rumen bacterial 16S rRNA sequences using a revised SILVA taxonomic framework. PeerJ, 2019, 7, e6496.	0.9	82
13	Sharpea and Kandleria are lactic acid producing rumen bacteria that do not change their fermentation products when co-cultured with a methanogen. Anaerobe, 2018, 54, 31-38.	1.0	37
14	Seasonal changes in the digesta-adherent rumen bacterial communities of dairy cattle grazing pasture. PLoS ONE, 2017, 12, e0173819.	1.1	35
15	Taxonomic Assessment of Rumen Microbiota Using Total RNA and Targeted Amplicon Sequencing Approaches. Frontiers in Microbiology, 2016, 7, 987.	1.5	61
16	Shifts in Rumen Fermentation and Microbiota Are Associated with Dissolved Ruminal Hydrogen Concentrations in Lactating Dairy Cows Fed Different Types of Carbohydrates. Journal of Nutrition, 2016, 146, 1714-1721.	1.3	60
17	Rumen metagenome and metatranscriptome analyses of low methane yield sheep reveals a Sharpea-enriched microbiome characterised by lactic acid formation and utilisation. Microbiome, 2016, 4, 56.	4.9	268
18	The complete genome sequence of the methanogenic archaeon ISO4-H5 provides insights into the methylotrophic lifestyle of a ruminal representative of the Methanomassiliicoccales. Standards in Genomic Sciences, 2016, 11, 59.	1.5	41

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19	The complete genome sequence of <i>Eubacterium limosum</i> SA11, a metabolically versatile rumen acetogen. <i>Standards in Genomic Sciences</i> , 2016, 11, 26.	1.5	36
20	A mechanistic model of hydrogenâ€“methanogen dynamics in the rumen. <i>Journal of Theoretical Biology</i> , 2016, 393, 75-81.	0.8	6
21	An adhesin from hydrogenâ€“utilizing rumen methanogen <i>Methanobrevibacter ruminantium</i> binds a broad range of hydrogenâ€“producing microorganisms. <i>Environmental Microbiology</i> , 2016, 18, 3010-3021.	1.8	53
22	Natural variation in methane emission of sheep fed on a lucerne pellet diet is unrelated to rumen ciliate community type. <i>Microbiology (United Kingdom)</i> , 2016, 162, 459-465.	0.7	7
23	Vaccination of Sheep with a Methanogen Protein Provides Insight into Levels of Antibody in Saliva Needed to Target Ruminal Methanogens. <i>PLoS ONE</i> , 2016, 11, e0159861.	1.1	16
24	Rumen microbial community composition varies with diet and host, but a core microbiome is found across a wide geographical range. <i>Scientific Reports</i> , 2015, 5, 14567.	1.6	1,172
25	RUMINANT NUTRITION SYMPOSIUM: Use of genomics and transcriptomics to identify strategies to lower ruminal methanogenesis ^{1,2,3} . <i>Journal of Animal Science</i> , 2015, 93, 1431-1449.	0.2	52
26	Phylogeny of Intestinal Ciliates, Including <i>Charonina ventriculi</i> , and Comparison of Microscopy and 18S rRNA Gene Pyrosequencing for Rumen Ciliate Community Structure Analysis. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2433-2444.	1.4	65
27	A high-throughput screening assay for identification of inhibitors of the A1AO-ATP synthase of the rumen methanogen <i>Methanobrevibacter ruminantium</i> M1. <i>Journal of Microbiological Methods</i> , 2015, 110, 15-17.	0.7	3
28	Characterization of the rumen microbial community composition of buffalo breeds consuming diets typical of dairy production systems in Southern China. <i>Animal Feed Science and Technology</i> , 2015, 207, 75-84.	1.1	24
29	Vaccination of cattle with a methanogen protein produces specific antibodies in the saliva which are stable in the rumen. <i>Veterinary Immunology and Immunopathology</i> , 2015, 164, 201-207.	0.5	23
30	Considerations in the use of fluorescence in situ hybridization (FISH) and confocal laser scanning microscopy to characterize rumen methanogens and define their spatial distributions. <i>Canadian Journal of Microbiology</i> , 2015, 61, 417-428.	0.8	23
31	Buccal Swabbing as a Noninvasive Method To Determine Bacterial, Archaeal, and Eukaryotic Microbial Community Structures in the Rumen. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7470-7483.	1.4	52
32	Few Highly Abundant Operational Taxonomic Units Dominate within Rumen Methanogenic Archaeal Species in New Zealand Sheep and Cattle. <i>Applied and Environmental Microbiology</i> , 2015, 81, 986-995.	1.4	72
33	Lambs Fed Fresh Winter Forage Rape (<i>Brassica napus</i> L.) Emit Less Methane than Those Fed Perennial Ryegrass (<i>Lolium perenne</i> L.), and Possible Mechanisms behind the Difference. <i>PLoS ONE</i> , 2015, 10, e0119697.	1.1	50
34	Two Different Bacterial Community Types Are Linked with the Low-Methane Emission Trait in Sheep. <i>PLoS ONE</i> , 2014, 9, e103171.	1.1	246
35	Decreasing methane emissions from ruminants grazing forages: a fit with productive and financial realities?. <i>Animal Production Science</i> , 2014, 54, 1141.	0.6	50
36	Methane yield phenotypes linked to differential gene expression in the sheep rumen microbiome. <i>Genome Research</i> , 2014, 24, 1517-1525.	2.4	332

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37	Responses of methane production and fermentation pathways to the increased dissolved hydrogen concentration generated by eight substrates in in vitro ruminal cultures. <i>Animal Feed Science and Technology</i> , 2014, 194, 1-11.	1.1	92
38	Internal Transcribed Spacer 1 Secondary Structure Analysis Reveals a Common Core throughout the Anaerobic Fungi (Neocallimastigomycota). <i>PLoS ONE</i> , 2014, 9, e91928.	1.1	88
39	RIM-DB: a taxonomic framework for community structure analysis of methanogenic archaea from the rumen and other intestinal environments. <i>PeerJ</i> , 2014, 2, e494.	0.9	140
40	Simultaneous Amplicon Sequencing to Explore Co-Occurrence Patterns of Bacterial, Archaeal and Eukaryotic Microorganisms in Rumen Microbial Communities. <i>PLoS ONE</i> , 2013, 8, e47879.	1.1	304
41	Effect of DNA Extraction Methods and Sampling Techniques on the Apparent Structure of Cow and Sheep Rumen Microbial Communities. <i>PLoS ONE</i> , 2013, 8, e74787.	1.1	280
42	Nitrogen metabolism and rumen microbial enumeration in lactating cows with divergent residual feed intake fed high-digestibility pasture. <i>Journal of Dairy Science</i> , 2012, 95, 5024-5034.	1.4	117
43	A Proposed Taxonomy of Anaerobic Fungi (Class Neocallimastigomycetes) Suitable for Large-Scale Sequence-Based Community Structure Analysis. <i>PLoS ONE</i> , 2012, 7, e36866.	1.1	95
44	An exo- β -D-galactanase from <i>Streptomyces</i> sp. provides insights into type II arabinogalactan structure. <i>Carbohydrate Research</i> , 2012, 352, 70-81.	1.1	28
45	Isolation of previously uncultured rumen bacteria by dilution to extinction using a new liquid culture medium. <i>Journal of Microbiological Methods</i> , 2011, 84, 52-60.	0.7	84
46	<i>Acidobacteria</i> , <i>Rubrobacteridae</i> and <i>Chloroflexi</i> are abundant among very slow-growing and mini-colony-forming soil bacteria. <i>Environmental Microbiology</i> , 2011, 13, 798-805.	1.8	174
47	Characterization of rumen ciliate community composition in domestic sheep, deer, and cattle, feeding on varying diets, by means of PCR-DGGE and clone libraries. <i>FEMS Microbiology Ecology</i> , 2011, 75, 468-481.	1.3	95
48	Methanogen community structure in the rumens of farmed sheep, cattle and red deer fed different diets. <i>FEMS Microbiology Ecology</i> , 2011, 76, 311-326.	1.3	101
49	Strategies to reduce methane emissions from farmed ruminants grazing on pasture. <i>Veterinary Journal</i> , 2011, 188, 11-17.	0.6	130
50	Genome Sequence of the Verrucomicrobium <i>Opiritatus terrae</i> PB90-1, an Abundant Inhabitant of Rice Paddy Soil Ecosystems. <i>Journal of Bacteriology</i> , 2011, 193, 2367-2368.	1.0	44
51	Genome Sequence of <i>Chthoniobacter flavus</i> Ellin428, an Aerobic Heterotrophic Soil Bacterium. <i>Journal of Bacteriology</i> , 2011, 193, 2902-2903.	1.0	52
52	Genome Sequence of <i>Pedosphaera parvula</i> Ellin514, an Aerobic Verrucomicrobial Isolate from Pasture Soil. <i>Journal of Bacteriology</i> , 2011, 193, 2900-2901.	1.0	28
53	A1A α -ATP Synthase of <i>Methanobrevibacter ruminantium</i> Couples Sodium Ions for ATP Synthesis under Physiological Conditions. <i>Journal of Biological Chemistry</i> , 2011, 286, 39882-39892.	1.6	35
54	Presence of Novel, Potentially Homoacetogenic Bacteria in the Rumen as Determined by Analysis of Formyltetrahydrofolate Synthetase Sequences from Ruminants. <i>Applied and Environmental Microbiology</i> , 2010, 76, 2058-2066.	1.4	89

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55	The Genome Sequence of the Rumen Methanogen <i>Methanobrevibacter ruminantium</i> Reveals New Possibilities for Controlling Ruminant Methane Emissions. <i>PLoS ONE</i> , 2010, 5, e8926.	1.1	256
56	Development of a vaccine to mitigate greenhouse gas emissions in agriculture: Vaccination of sheep with methanogen fractions induces antibodies that block methane production <i>in vitro</i> . <i>New Zealand Veterinary Journal</i> , 2010, 58, 29-36.	0.4	49
57	Detection of a Reproducible, Single-Member Shift in Soil Bacterial Communities Exposed to Low Levels of Hydrogen. <i>Applied and Environmental Microbiology</i> , 2010, 76, 1471-1479.	1.4	50
58	<i>Halonotius pteroides</i> gen. nov., sp. nov., an extremely halophilic archaeon recovered from a saltern crystallizer. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010, 60, 1196-1199.	0.8	48
59	Influence of hydrogen on rumen methane formation and fermentation balances through microbial growth kinetics and fermentation thermodynamics. <i>Animal Feed Science and Technology</i> , 2010, 160, 1-22.	1.1	562
60	<i>Natronomonas moolapensis</i> sp. nov., non-alkaliphilic isolates recovered from a solar saltern crystallizer pond, and emended description of the genus <i>Natronomonas</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010, 60, 1173-1176.	0.8	33
61	Phylum <i>Verrucomicrobia</i> representatives share a compartmentalized cell plan with members of bacterial phylum <i>Planctomycetes</i> . <i>BMC Microbiology</i> , 2009, 9, 5.	1.3	120
62	Dormant microbes: scouting ahead or plodding along?. <i>Nature</i> , 2009, 458, 831-831.	13.7	11
63	Three Genomes from the Phylum <i>Acidobacteria</i> Provide Insight into the Lifestyles of These Microorganisms in Soils. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2046-2056.	1.4	804
64	Gut-Associated Denitrification and <i>In Vivo</i> Emission of Nitrous Oxide by the Earthworm Families <i>Megascolecidae</i> and <i>Lumbricidae</i> in New Zealand. <i>Applied and Environmental Microbiology</i> , 2009, 75, 3430-3436.	1.4	38
65	Structure of the Archaeal Community of the Rumen. <i>Applied and Environmental Microbiology</i> , 2008, 74, 3619-3625.	1.4	519
66	Chronic <i>Helicobacter pylori</i> Infection Does Not Significantly Alter the Microbiota of the Murine Stomach. <i>Applied and Environmental Microbiology</i> , 2007, 73, 1010-1013.	1.4	47
67	<i>Haloquadratum walsbyi</i> gen. nov., sp. nov., the square haloarchaeon of Walsby, isolated from saltern crystallizers in Australia and Spain. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 387-392.	0.8	173
68	Secretory antibodies reduce systemic antibody responses against the gastrointestinal commensal flora. <i>International Immunology</i> , 2007, 19, 257-265.	1.8	70
69	Identifying the Dominant Soil Bacterial Taxa in Libraries of 16S rRNA and 16S rRNA Genes. <i>Applied and Environmental Microbiology</i> , 2006, 72, 1719-1728.	1.4	1,462
70	Effect of pH on Isolation and Distribution of Members of Subdivision 1 of the Phylum <i>Acidobacteria</i> Occurring in Soil. <i>Applied and Environmental Microbiology</i> , 2006, 72, 1852-1857.	1.4	206
71	New Threshold and Confidence Estimates for Terminal Restriction Fragment Length Polymorphism Analysis of Complex Bacterial Communities. <i>Applied and Environmental Microbiology</i> , 2006, 72, 1270-1278.	1.4	130
72	PCR-generated artefact from 16S rRNA gene-specific primers. <i>FEMS Microbiology Letters</i> , 2005, 248, 183-187.	0.7	68

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73	Effects of Growth Medium, Inoculum Size, and Incubation Time on Culturability and Isolation of Soil Bacteria. <i>Applied and Environmental Microbiology</i> , 2005, 71, 826-834.	1.4	438
74	Variations in the abundance and identity of class II aromatic ring-hydroxylating dioxygenase genes in groundwater at an aromatic hydrocarbon-contaminated site. <i>Environmental Microbiology</i> , 2005, 7, 140-146.	1.8	16
75	Detection and Cultivation of Soil Verrucomicrobia. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8402-8410.	1.4	142
76	Haloviruses and Their Hosts. , 2005, , 553-563.		4
77	Liquid Serial Dilution Is Inferior to Solid Media for Isolation of Cultures Representative of the Phylum-Level Diversity of Soil Bacteria. <i>Applied and Environmental Microbiology</i> , 2004, 70, 4363-4366.	1.4	136
78	Variability of the <i>Chlamydia trachomatis</i> omp1 Gene Detected in Samples from Men Tested in Male-Only Saunas in Melbourne, Australia. <i>Journal of Clinical Microbiology</i> , 2004, 42, 2596-2601.	1.8	30
79	<i>Chthoniobacter flavus</i> gen. nov., sp. nov., the First Pure-Culture Representative of Subdivision Two, Spartobacteria classis nov., of the Phylum Verrucomicrobia. <i>Applied and Environmental Microbiology</i> , 2004, 70, 5875-5881.	1.4	162
80	Cultivation of Walsby's square haloarchaeon. <i>FEMS Microbiology Letters</i> , 2004, 238, 469-473.	0.7	99
81	Combined Use of Cultivation-Dependent and Cultivation-Independent Methods Indicates that Members of Most Haloarchaeal Groups in an Australian Crystallizer Pond Are Cultivable. <i>Applied and Environmental Microbiology</i> , 2004, 70, 5258-5265.	1.4	180
82	Propanol as an end product of threonine fermentation. <i>Archives of Microbiology</i> , 2004, 182, 482-486.	1.0	26
83	Cultivation of Walsby's square haloarchaeon. <i>FEMS Microbiology Letters</i> , 2004, 238, 469-473.	0.7	110
84	Laboratory Cultivation of Widespread and Previously Uncultured Soil Bacteria. <i>Applied and Environmental Microbiology</i> , 2003, 69, 7210-7215.	1.4	439
85	Fermentation of glycolate by a pure culture of a strictly anaerobic gram-positive bacterium belonging to the family Lachnospiraceae. <i>Archives of Microbiology</i> , 2003, 179, 321-328.	1.0	14
86	Selective enrichment and purification of cultures of <i>Methanosaeta</i> spp.. <i>Journal of Microbiological Methods</i> , 2003, 52, 239-244.	0.7	33
87	Secretory Antibodies Do Not Affect the Composition of the Bacterial Microbiota in the Terminal Ileum of 10-Week-Old Mice. <i>Applied and Environmental Microbiology</i> , 2003, 69, 2100-2109.	1.4	86
88	Propionate Formation by <i>Opiritatus terrae</i> in Pure Culture and in Mixed Culture with a Hydrogenotrophic Methanogen and Implications for Carbon Fluxes in Anoxic Rice Paddy Soil. <i>Applied and Environmental Microbiology</i> , 2002, 68, 2089-2092.	1.4	57
89	Improved Culturability of Soil Bacteria and Isolation in Pure Culture of Novel Members of the Divisions Acidobacteria , Actinobacteria , Proteobacteria , and Verrucomicrobia. <i>Applied and Environmental Microbiology</i> , 2002, 68, 2391-2396.	1.4	631
90	Cultivation of globally distributed soil bacteria from phylogenetic lineages previously only detected in cultivation-independent surveys. <i>Environmental Microbiology</i> , 2002, 4, 654-666.	1.8	408

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91	Energetics and kinetics of lactate fermentation to acetate and propionate via methylmalonyl-CoA or acrylyl-CoA. FEMS Microbiology Letters, 2002, 211, 65-70.	0.7	169
92	Detection of known and novel genes encoding aromatic ring-hydroxylating dioxygenases in soils and in aromatic hydrocarbon-degrading bacteria. FEMS Microbiology Letters, 2002, 216, 61-66.	0.7	32
93	Bacteremia due to <i>Leptotrichia trevisanii</i> sp. nov.. European Journal of Clinical Microbiology and Infectious Diseases, 2001, 20, 765-769.	1.3	50
94	A Member of the Delta Subgroup of Proteobacteria from a Pyogenic Liver Abscess Is a Typical Sulfate Reducer of the Genus <i>Desulfovibrio</i> . Journal of Clinical Microbiology, 2001, 39, 787-790.	1.8	16
95	Severe <i>Bordetella holmesii</i> infection in a Previously Healthy Adolescent Confirmed by Gene Sequence Analysis. Clinical Infectious Diseases, 2001, 33, 129-130.	2.9	37
96	<i>Succinispira mobilis</i> gen. nov., sp. nov., a succinate-decarboxylating anaerobic bacterium. International Journal of Systematic and Evolutionary Microbiology, 1999, 49, 1009-1013.	0.8	29
97	Transient Production of Formate During Chemolithotrophic Growth of Anaerobic Microorganisms on Hydrogen. Current Microbiology, 1999, 38, 285-289.	1.0	35
98	Rice roots and methanogenesis in a paddy soil: ferric iron as an alternative electron acceptor in the rooted soil. Soil Biology and Biochemistry, 1999, 31, 421-430.	4.2	154
99	Characterization and Identification of Numerically Abundant Culturable Bacteria from the Anoxic Bulk Soil of Rice Paddy Microcosms. Applied and Environmental Microbiology, 1999, 65, 5042-5049.	1.4	131
100	Comparative Phylogenetic Assignment of Environmental Sequences of Genes Encoding 16S rRNA and Numerically Abundant Culturable Bacteria from an Anoxic Rice Paddy Soil. Applied and Environmental Microbiology, 1999, 65, 5050-5058.	1.4	145
101	Culturable Populations of <i>Sporomusa</i> spp. and <i>Desulfovibrio</i> spp. in the Anoxic Bulk Soil of Flooded Rice Microcosms. Applied and Environmental Microbiology, 1999, 65, 3526-3533.	1.4	43
102	Detection of <i>Verrucomicrobia</i> in a Pasture Soil by PCR-Mediated Amplification of 16S rRNA Genes. Applied and Environmental Microbiology, 1999, 65, 4280-4284.	1.4	39
103	Methanogenic Degradation of Polysaccharides and the Characterization of Polysaccharolytic <i>Clostridia</i> from Anoxic Rice Field Soil. Systematic and Applied Microbiology, 1998, 21, 185-200.	1.2	51
104	Diversity and Structure of the Methanogenic Community in Anoxic Rice Paddy Soil Microcosms as Examined by Cultivation and Direct 16S rRNA Gene Sequence Retrieval. Applied and Environmental Microbiology, 1998, 64, 960-969.	1.4	679
105	Pathway of Glucose Catabolism by Strain VeGlc2, an Anaerobe Belonging to the <i>Verrucomicrobiales</i> Lineage of Bacterial Descent. Applied and Environmental Microbiology, 1998, 64, 4830-4833.	1.4	20
106	Effects of alternative methyl group acceptors on the growth energetics of the O-demethylating anaerobe <i>Holophaga foetida</i> . Microbiology (United Kingdom), 1997, 143, 1105-1114.	0.7	26
107	Disproportionation of inorganic sulfur compounds by the sulfate-reducing bacterium <i>Desulfocapsa thiozymogenes</i> gen. nov., sp. nov.. Archives of Microbiology, 1996, 166, 184-192.	1.0	165
108	Sodium-dependent succinate decarboxylation by a new anaerobic bacterium belonging to the genus <i>Peptostreptococcus</i> . Antonie Van Leeuwenhoek, 1996, 70, 11-20.	0.7	23

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109	14CO ₂ Exchange with Acetoacetate Catalyzed by Dialyzed Cell-Free Extracts of the Bacterial Strain Bunn Grown with Acetone and Nitrate. <i>FEBS Journal</i> , 1995, 228, 677-682.	0.2	15
110	Succinate decarboxylation by <i>Propionigenium maris</i> sp. nov., a new anaerobic bacterium from an estuarine sediment. <i>Archives of Microbiology</i> , 1995, 164, 29-35.	1.0	35
111	Phylogenetic analysis by 16S ribosomal DNA sequence comparison reveals two unrelated groups of species within the genus <i>Ruminococcus</i> . <i>FEMS Microbiology Letters</i> , 1995, 129, 69-73.	0.7	41
112	Metabolic pathways and energetics of the acetone-oxidizing, sulfate-reducing bacterium, <i>Desulfohalobium acetoxidans</i> . <i>Archives of Microbiology</i> , 1995, 163, 188-194.	1.0	37
113	Phylogenetic analysis by 16S ribosomal DNA sequence comparison reveals two unrelated groups of species within the genus. <i>FEMS Microbiology Letters</i> , 1995, 129, 69-73.	0.7	54
114	A biphasic approach to the determination of the phenotypic and genotypic diversity of some anaerobic, cellulolytic, thermophilic, rod-shaped bacteria. <i>Antonie Van Leeuwenhoek</i> , 1994, 64, 341-355.	0.7	17
115	A thermophilic, lipolytic <i>Bacillus</i> sp., and continuous assay of its p-nitrophenyl-palmitate esterase activity. <i>FEMS Microbiology Letters</i> , 1994, 120, 195-200.	0.7	46
116	Fermentative degradation of acetone by an enrichment culture in membrane-separated culture devices and in cell suspensions. <i>FEMS Microbiology Letters</i> , 1994, 122, 27-32.	0.7	32
117	<i>Clostridium viride</i> sp. nov., a strictly anaerobic bacterium using 5-aminovalerate as growth substrate, previously assigned to <i>Clostridium aminovalericum</i> . <i>Archives of Microbiology</i> , 1994, 162, 387-394.	1.0	21
118	<i>Clostridium viride</i> sp. nov., a strictly anaerobic bacterium using 5-aminovalerate as growth substrate, previously assigned to <i>Clostridium aminovalericum</i> . <i>Archives of Microbiology</i> , 1994, 162, 387-394.	1.0	3
119	Pathway of anaerobic poly- β -hydroxybutyrate degradation by <i>lyobacter delafieldii</i> . <i>Biodegradation</i> , 1993, 4, 179-185.	1.5	43
120	Growth yield increase and ATP formation linked to succinate decarboxylation in <i>Veillonella parvula</i> . <i>Archives of Microbiology</i> , 1992, 157, 442-445.	1.0	22
121	Anaerobic malonate decarboxylation by <i>Citrobacter diversus</i> . <i>Archives of Microbiology</i> , 1992, 157, 471-474.	1.0	11
122	Heterotrophic sulfur reduction by <i>Thermotoga</i> sp. strain FjSS3.B1. <i>FEMS Microbiology Letters</i> , 1992, 96, 213-217.	0.7	33
123	Microbial degradation of natural and of new synthetic polymers. <i>FEMS Microbiology Letters</i> , 1992, 103, 311-316.	0.7	35
124	Endospore Formation by <i>Thermoanaerobium brockii</i> HTD4. <i>Systematic and Applied Microbiology</i> , 1991, 14, 240-244.	1.2	23
125	Growth of Enterobacteria on Malonate Under Strictly Anaerobic Conditions. <i>Systematic and Applied Microbiology</i> , 1991, 14, 93-97.	1.2	3
126	Isolation of <i>Clostridium propionicum</i> strain 19acry3 and further characteristics of the species. <i>Archives of Microbiology</i> , 1991, 155, 566-571.	1.0	32

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127	Characterization of a succinate-fermenting anaerobic bacterium isolated from a glycolate-degrading mixed culture. Archives of Microbiology, 1991, 155, 288-293.	1.0	8
128	Effects of medium composition on extracellular proteinase stability and yield in batch cultures of a Thermus sp.. Applied Microbiology and Biotechnology, 1991, 34, 789.	1.7	13
129	Ilyobacter delafieldii sp. nov., a metabolically restricted anaerobic bacterium fermenting PHB. Archives of Microbiology, 1990, 154, 253-259.	1.0	90
130	Fermentation of Glycollate by a Mixed Culture of Anaerobic Bacteria. Systematic and Applied Microbiology, 1990, 13, 327-332.	1.2	10
131	Rapid determination of amino acid concentrations in microbiological media: Evaluation of Borchers' cuprizon method. Journal of Microbiological Methods, 1989, 10, 311-316.	0.7	8
132	Energetics and kinetics of lactate fermentation to acetate and propionate via methylmalonyl-CoA or acrylyl-CoA. , 0, .		27
133	New Cultivation Strategies for Terrestrial Microorganisms. , 0, , 171-192.		8