

Peter H Janssen

List of Publications by Year in descending order

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133
papers

15,189
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34076

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146
docs citations

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times ranked

12454
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#	ARTICLE	IF	CITATIONS
1	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
2	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
3	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
4	Diversity and Structure of the Methanogenic Community in Anoxic Rice Paddy Soil Microcosms as Examined by Cultivation and Direct 16S rRNA Gene Sequence Retrieval. <i>Applied and Environmental Microbiology</i> , 1998, 64, 960-969.	1.4	679
5	Improved Culturability of Soil Bacteria and Isolation in Pure Culture of Novel Members of the Divisions <i>Acidobacteria</i> , <i>Actinobacteria</i> , <i>Proteobacteria</i> , and <i>Verrucomicrobia</i> . <i>Applied and Environmental Microbiology</i> , 2002, 68, 2391-2396.	1.4	631
6	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
7	Structure of the Archaeal Community of the Rumen. <i>Applied and Environmental Microbiology</i> , 2008, 74, 3619-3625.	1.4	519
8	Laboratory Cultivation of Widespread and Previously Uncultured Soil Bacteria. <i>Applied and Environmental Microbiology</i> , 2003, 69, 7210-7215.	1.4	439
9	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
10	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
11	Methane yield phenotypes linked to differential gene expression in the sheep rumen microbiome. <i>Genome Research</i> , 2014, 24, 1517-1525.	2.4	332
12	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
13	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
14	Rumen metagenome and metatranscriptome analyses of low methane yield sheep reveals a <i>Sharpea</i> -enriched microbiome characterised by lactic acid formation and utilisation. <i>Microbiome</i> , 2016, 4, 56.	4.9	268
15	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
16	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
17	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
18	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

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19	<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
20	<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
21	Energetics and kinetics of lactate fermentation to acetate and propionate via methylmalonyl-CoA or acrylyl-CoA. <i>FEMS Microbiology Letters</i> , 2002, 211, 65-70.	0.7	169
22	Disproportionation of inorganic sulfur compounds by the sulfate-reducing bacterium <i>Desulfocapsa thiozymogenes</i> gen. nov., sp. nov.. <i>Archives of Microbiology</i> , 1996, 166, 184-192.	1.0	165
23	<i>Chthoniobacter flavus</i> gen. nov., sp. nov., the First Pure-Culture Representative of Subdivision Two, <i>Spartobacteria classis</i> nov., of the Phylum Verrucomicrobia. <i>Applied and Environmental Microbiology</i> , 2004, 70, 5875-5881.	1.4	162
24	Rice roots and methanogenesis in a paddy soil: ferric iron as an alternative electron acceptor in the rooted soil. <i>Soil Biology and Biochemistry</i> , 1999, 31, 421-430.	4.2	154
25	Comparative Phylogenetic Assignment of Environmental Sequences of Genes Encoding 16S rRNA and Numerically Abundant Culturable Bacteria from an Anoxic Rice Paddy Soil. <i>Applied and Environmental Microbiology</i> , 1999, 65, 5050-5058.	1.4	145
26	Detection and Cultivation of Soil Verrucomicrobia. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8402-8410.	1.4	142
27	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
28	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
29	Characterization and Identification of Numerically Abundant Culturable Bacteria from the Anoxic Bulk Soil of Rice Paddy Microcosms. <i>Applied and Environmental Microbiology</i> , 1999, 65, 5042-5049.	1.4	131
30	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
31	Strategies to reduce methane emissions from farmed ruminants grazing on pasture. <i>Veterinary Journal</i> , 2011, 188, 11-17.	0.6	130
32	Phylum Verrucomicrobia representatives share a compartmentalized cell plan with members of bacterial phylum Planctomycetes. <i>BMC Microbiology</i> , 2009, 9, 5.	1.3	120
33	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
34	Cultivation of Walsby's square haloarchaeon. <i>FEMS Microbiology Letters</i> , 2004, 238, 469-473.	0.7	110
35	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
36	Cultivation of Walsby's square haloarchaeon. <i>FEMS Microbiology Letters</i> , 2004, 238, 469-473.	0.7	99

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37	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
38	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
39	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
40	<i>Ilyobacter delafieldii</i> sp. nov., a metabolically restricted anaerobic bacterium fermenting PHB. <i>Archives of Microbiology</i> , 1990, 154, 253-259.	1.0	90
41	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
42	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
43	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
44	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
45	Improved taxonomic assignment of rumen bacterial 16S rRNA sequences using a revised SILVA taxonomic framework. <i>PeerJ</i> , 2019, 7, e6496.	0.9	82
46	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
47	Secretory antibodies reduce systemic antibody responses against the gastrointestinal commensal flora. <i>International Immunology</i> , 2007, 19, 257-265.	1.8	70
48	PCR-generated artefact from 16S rRNA gene-specific primers. <i>FEMS Microbiology Letters</i> , 2005, 248, 183-187.	0.7	68
49	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
50	Taxonomic Assessment of Rumen Microbiota Using Total RNA and Targeted Amplicon Sequencing Approaches. <i>Frontiers in Microbiology</i> , 2016, 7, 987.	1.5	61
51	Shifts in Rumen Fermentation and Microbiota Are Associated with Dissolved Ruminal Hydrogen Concentrations in Lactating Dairy Cows Fed Different Types of Carbohydrates. <i>Journal of Nutrition</i> , 2016, 146, 1714-1721.	1.3	60
52	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
53	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
54	An adhesin from hydrogen-utilizing rumen methanogen <i>Methanobrevibacter ruminantium</i> binds a broad range of hydrogen-producing microorganisms. <i>Environmental Microbiology</i> , 2016, 18, 3010-3021.	1.8	53

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55	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
56	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
57	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
58	Methanogenic Degradation of Polysaccharides and the Characterization of Polysaccharolytic Clostridia from Anoxic Rice Field Soil. <i>Systematic and Applied Microbiology</i> , 1998, 21, 185-200.	1.2	51
59	Bacteremia due to <i>Leptotrichia trevisanii</i> sp. nov.. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2001, 20, 765-769.	1.3	50
60	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
61	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
62	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
63	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
64	<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
65	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
66	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
67	Genome Sequence of the <i>Verrucomicrobium Opitutus terrae</i> PB90-1, an Abundant Inhabitant of Rice Paddy Soil Ecosystems. <i>Journal of Bacteriology</i> , 2011, 193, 2367-2368.	1.0	44
68	Pathway of anaerobic poly- γ -hydroxybutyrate degradation by <i>lyllobacter delafieldii</i> . <i>Biodegradation</i> , 1993, 4, 179-185.	1.5	43
69	Culturable Populations of <i>Sporomusa</i> spp. and <i>Desulfovibrio</i> spp. in the Anoxic Bulk Soil of Flooded Rice Microcosms. <i>Applied and Environmental Microbiology</i> , 1999, 65, 3526-3533.	1.4	43
70	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
71	The complete genome sequence of the methanogenic archaeon ISO4-H5 provides insights into the methylophilic lifestyle of a ruminal representative of the <i>Methanomassiliicoccales</i> . <i>Standards in Genomic Sciences</i> , 2016, 11, 59.	1.5	41
72	Detection of <i>Verrucomicrobia</i> in a Pasture Soil by PCR-Mediated Amplification of 16S rRNA Genes. <i>Applied and Environmental Microbiology</i> , 1999, 65, 4280-4284.	1.4	39

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73	Gut-Associated Denitrification and In Vivo Emission of Nitrous Oxide by the Earthworm Families Megascolecidae and Lumbricidae in New Zealand. <i>Applied and Environmental Microbiology</i> , 2009, 75, 3430-3436.	1.4	38
74	Metabolic pathways and energetics of the acetone-oxidizing, sulfate-reducing bacterium, <i>Desulfobacterium cetonicum</i> . <i>Archives of Microbiology</i> , 1995, 163, 188-194.	1.0	37
75	Severe <i>Bordetella holmesii</i> infection in a Previously Healthy Adolescent Confirmed by Gene Sequence Analysis. <i>Clinical Infectious Diseases</i> , 2001, 33, 129-130.	2.9	37
76	<i>Sharpea</i> and <i>Kandleria</i> are lactic acid producing rumen bacteria that do not change their fermentation products when co-cultured with a methanogen. <i>Anaerobe</i> , 2018, 54, 31-38.	1.0	37
77	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
78	Microbial degradation of natural and of new synthetic polymers. <i>FEMS Microbiology Letters</i> , 1992, 103, 311-316.	0.7	35
79	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
80	Transient Production of Formate During Chemolithotrophic Growth of Anaerobic Microorganisms on Hydrogen. <i>Current Microbiology</i> , 1999, 38, 285-289.	1.0	35
81	A1 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
82	Seasonal changes in the digesta-adherent rumen bacterial communities of dairy cattle grazing pasture. <i>PLoS ONE</i> , 2017, 12, e0173819.	1.1	35
83	Heterotrophic sulfur reduction by <i>Thermotogasp.</i> strain FjSS3.B1. <i>FEMS Microbiology Letters</i> , 1992, 96, 213-217.	0.7	33
84	Selective enrichment and purification of cultures of <i>Methanosaeta</i> spp.. <i>Journal of Microbiological Methods</i> , 2003, 52, 239-244.	0.7	33
85	<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
86	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
87	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
88	Detection of known and novel genes encoding aromatic ring-hydroxylating dioxygenases in soils and in aromatic hydrocarbon-degrading bacteria. <i>FEMS Microbiology Letters</i> , 2002, 216, 61-66.	0.7	32
89	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
90	<i>Succinispira mobilis</i> gen. nov., sp. nov., a succinate-decarboxylating anaerobic bacterium. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 1999, 49, 1009-1013.	0.8	29

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91	Genome Sequence of <i>Pedospira parvula</i> Ellin514, an Aerobic Verrucomicrobial Isolate from Pasture Soil. <i>Journal of Bacteriology</i> , 2011, 193, 2900-2901.	1.0	28
92	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
93	Energetics and kinetics of lactate fermentation to acetate and propionate via methylmalonyl-CoA or acrylyl-CoA. <i>FEMS Microbiology Letters</i> , 2002, 211, 65-70.	0.7	27
94	Effects of alternative methyl group acceptors on the growth energetics of the O-demethylating anaerobe <i>Holophaga foetida</i> . <i>Microbiology (United Kingdom)</i> , 1997, 143, 1105-1114.	0.7	26
95	Propanol as an end product of threonine fermentation. <i>Archives of Microbiology</i> , 2004, 182, 482-486.	1.0	26
96	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
97	Endospore Formation by <i>Thermoanaerobium brockii</i> HTD4. <i>Systematic and Applied Microbiology</i> , 1991, 14, 240-244.	1.2	23
98	Sodium-dependent succinate decarboxylation by a new anaerobic bacterium belonging to the genus <i>Peptostreptococcus</i> . <i>Antonie Van Leeuwenhoek</i> , 1996, 70, 11-20.	0.7	23
99	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
100	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
101	A restriction enzyme reduced representation sequencing approach for low-cost, high-throughput metagenome profiling. <i>PLoS ONE</i> , 2020, 15, e0219882.	1.1	23
102	Hydrogen and formate production and utilisation in the rumen and the human colon. <i>Animal Microbiome</i> , 2022, 4, 22.	1.5	23
103	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
104	<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
105	Electron flow: key to mitigating ruminant methanogenesis. <i>Trends in Microbiology</i> , 2022, 30, 209-212.	3.5	21
106	Pathway of Glucose Catabolism by Strain VeGlc2, an Anaerobe Belonging to the Verrucomicrobiales Lineage of Bacterial Descent. <i>Applied and Environmental Microbiology</i> , 1998, 64, 4830-4833.	1.4	20
107	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
108	A Member of the Delta Subgroup of Proteobacteria from a Pyogenic Liver Abscess Is a Typical Sulfate Reducer of the Genus <i>Desulfovibrio</i> . <i>Journal of Clinical Microbiology</i> , 2001, 39, 787-790.	1.8	16

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109	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
110	Genetic parameters of plasma and ruminal volatile fatty acids in sheep fed alfalfa pellets and genetic correlations with enteric methane emissions ¹ . <i>Journal of Animal Science</i> , 2019, 97, 2711-2724.	0.2	16
111	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
112	¹⁴ CO 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
113	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
114	Effects of medium composition on extracellular proteinase stability and yield in batch cultures of a <i>Thermus</i> sp.. <i>Applied Microbiology and Biotechnology</i> , 1991, 34, 789.	1.7	13
115	Effects of long-acting, broad spectra anthelmintic treatments on the rumen microbial community compositions of grazing sheep. <i>Scientific Reports</i> , 2021, 11, 3836.	1.6	13
116	Modelling thermodynamic feedback on the metabolism of hydrogenotrophic methanogens. <i>Journal of Theoretical Biology</i> , 2019, 477, 14-23.	0.8	12
117	Anaerobic malonate decarboxylation by <i>Citrobacter diversus</i> . <i>Archives of Microbiology</i> , 1992, 157, 471-474.	1.0	11
118	Dormant microbes: scouting ahead or plodding along?. <i>Nature</i> , 2009, 458, 831-831.	13.7	11
119	Fermentation of Glycollate by a Mixed Culture of Anaerobic Bacteria. <i>Systematic and Applied Microbiology</i> , 1990, 13, 327-332.	1.2	10
120	Rapid determination of amino acid concentrations in microbiological media: Evaluation of Borchers' cuprizone method. <i>Journal of Microbiological Methods</i> , 1989, 10, 311-316.	0.7	8
121	Characterization of a succinate-fermenting anaerobic bacterium isolated from a glycolate-degrading mixed culture. <i>Archives of Microbiology</i> , 1991, 155, 288-293.	1.0	8
122	New Cultivation Strategies for Terrestrial Microorganisms. , 0, , 171-192.		8
123	Individual-level correlations of rumen volatile fatty acids with enteric methane emissions for ranking methane yield in sheep fed fresh pasture. <i>Animal Production Science</i> , 2021, 61, 300.	0.6	7
124	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
125	A mechanistic model of hydrogenâ€™methanogen dynamics in the rumen. <i>Journal of Theoretical Biology</i> , 2016, 393, 75-81.	0.8	6
126	Mapping immunogenic epitopes of an adhesin-like protein from <i>Methanobrevibacter ruminantium</i> M1 and comparison of empirical data with in silico prediction methods. <i>Scientific Reports</i> , 2022, 12, .	1.6	5

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127	Haloviruses and Their Hosts. , 2005, , 553-563.		4
128	Growth of Enterobacteria on Malonate Under Strictly Anaerobic Conditions. Systematic and Applied Microbiology, 1991, 14, 93-97.	1.2	3
129	A high-throughput screening assay for identification of inhibitors of the A1AO-ATP synthase of the rumen methanogen Methanobrevibacter ruminantium M1. Journal of Microbiological Methods, 2015, 110, 15-17.	0.7	3
130	Clostridium viride sp. nov., a strictly anaerobic bacterium using 5-aminovalerate as growth substrate, previously assigned to Clostridium aminovalericum. Archives of Microbiology, 1994, 162, 387-394.	1.0	3
131	Low-cost sample preservation methods for high-throughput processing of rumen microbiomes. Animal Microbiome, 2022, 4, .	1.5	2
132	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
133	A protocol combining breath testing and ex vivo fermentations to study the human gut microbiome. STAR Protocols, 2021, 2, 100227.	0.5	0