

Graeme T Attwood

List of Publications by Year in descending order

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52
papers

3,819
citations

257450

24
h-index

182427

51
g-index

55
all docs

55
docs citations

55
times ranked

3580
citing authors

#	ARTICLE	IF	CITATIONS
1	Hydrogen and formate production and utilisation in the rumen and the human colon. <i>Animal Microbiome</i> , 2022, 4, 22.	3.8	23
2	Complete Genome Sequence of the Polysaccharide-Degrading Rumen Bacterium <i>Pseudobutyribrio xylanivorans</i> MA3014 Reveals an Incomplete Glycolytic Pathway. <i>Genome Biology and Evolution</i> , 2020, 12, 1566-1572.	2.5	17
3	Applications of the Soil, Plant and Rumen Microbiomes in Pastoral Agriculture. <i>Frontiers in Nutrition</i> , 2019, 6, 107.	3.7	30
4	Diverse hydrogen production and consumption pathways influence methane production in ruminants. <i>ISME Journal</i> , 2019, 13, 2617-2632.	9.8	132
5	Comparative Genomics of Rumen <i>Butyribrio</i> spp. Uncovers a Continuum of Polysaccharide-Degrading Capabilities. <i>Applied and Environmental Microbiology</i> , 2019, 86, .	3.1	65
6	Occurrence and expression of genes encoding methyl-compound production in rumen bacteria. <i>Animal Microbiome</i> , 2019, 1, 15.	3.8	27
7	<i>Butyribrio hungatei</i> MB2003 Competes Effectively for Soluble Sugars Released by <i>Butyribrio proteoclasticus</i> B316 ^T during Growth on Xylan or Pectin. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	28
8	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , 2018, 36, 359-367.	17.5	414
9	Sharpea and Kandleria 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.	2.1	37
10	Addressing Global Ruminant Agricultural Challenges Through Understanding the Rumen Microbiome: Past, Present, and Future. <i>Frontiers in Microbiology</i> , 2018, 9, 2161.	3.5	255
11	Gene and transcript abundances of bacterial type III secretion systems from the rumen microbiome are correlated with methane yield in sheep. <i>BMC Research Notes</i> , 2017, 10, 367.	1.4	8
12	The complete genome sequence of the rumen bacterium <i>Butyribrio hungatei</i> MB2003. <i>Standards in Genomic Sciences</i> , 2017, 12, 72.	1.5	29
13	Draft Genome Sequence of the Rumen Methanogen <i>Methanobrevibacter olleyae</i> YLM1. <i>Genome Announcements</i> , 2016, 4, .	0.8	11
14	Complete Genome Sequence of Methanogenic Archaeon ISO4-G1, a Member of the <i>Methanomassiliicoccales</i> , Isolated from a Sheep Rumen. <i>Genome Announcements</i> , 2016, 4, .	0.8	9
15	Rumen metagenome and metatranscriptome analyses of low methane yield sheep reveals a Sharpea-enriched microbiome characterised by lactic acid formation and utilisation. <i>Microbiome</i> , 2016, 4, 56.	11.1	268
16	The complete genome sequence of the methanogenic archaeon ISO4-H5 provides insights into the methylotrophic lifestyle of a ruminal representative of the <i>Methanomassiliicoccales</i> . <i>Standards in Genomic Sciences</i> , 2016, 11, 59.	1.5	41
17	The complete genome sequence of the rumen methanogen <i>Methanobrevibacter millerae</i> SM9. <i>Standards in Genomic Sciences</i> , 2016, 11, 49.	1.5	15
18	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

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19	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.	3.8	53
20	The complete genome sequence of the rumen methanogen <i>Methanosarcina barkeri</i> CM1. <i>Standards in Genomic Sciences</i> , 2015, 10, 57.	1.5	42
21	The Cytosolic Oligosaccharide-Degrading Proteome of <i>Butyrivibrio proteoclasticus</i> . <i>Proteomes</i> , 2015, 3, 347-368.	3.5	7
22	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.	2.2	24
23	Improving the genetic representation of rare taxa within complex microbial communities using DNA normalization methods. <i>Molecular Ecology Resources</i> , 2015, 15, 464-476.	4.8	12
24	A 3-D Model of a Perennial Ryegrass Primary Cell Wall and Its Enzymatic Degradation. <i>Computation</i> , 2014, 2, 23-46.	2.0	6
25	Metasecretome-selective phage display approach for mining the functional potential of a rumen microbial community. <i>BMC Genomics</i> , 2014, 15, 356.	2.8	13
26	Methane yield phenotypes linked to differential gene expression in the sheep rumen microbiome. <i>Genome Research</i> , 2014, 24, 1517-1525.	5.5	332
27	The complete genome sequence of the rumen methanogen <i>Methanobacterium formicicum</i> BRM9. <i>Standards in Genomic Sciences</i> , 2014, 9, 15.	1.5	27
28	Structure and function of an acetyl xylan esterase (Est2A) from the rumen bacterium <i>Butyrivibrio proteoclasticus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 911-917.	2.6	21
29	Extracellular Polysaccharide-Degrading Proteome of <i>Butyrivibrio proteoclasticus</i> . <i>Journal of Proteome Research</i> , 2012, 11, 131-142.	3.7	21
30	Carbohydrate transporting membrane proteins of the rumen bacterium, <i>Butyrivibrio proteoclasticus</i> . <i>Journal of Proteomics</i> , 2012, 75, 3138-3144.	2.4	14
31	Transposition of Tn916 in the four replicons of the <i>Butyrivibrio proteoclasticus</i> B316T genome. <i>FEMS Microbiology Letters</i> , 2011, 316, 144-151.	1.8	10
32	Strategies to reduce methane emissions from farmed ruminants grazing on pasture. <i>Veterinary Journal</i> , 2011, 188, 11-17.	1.7	130
33	The large episomes of <i>Butyrivibrio proteoclasticus</i> B316T have arisen through intragenomic gene shuttling from the chromosome to smaller <i>Butyrivibrio</i> -specific plasmids. <i>Plasmid</i> , 2011, 66, 67-78.	1.4	6
34	A1Ao-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.	3.4	35
35	Structural and functional characterization of a promiscuous feruloyl esterase (Est1E) from the rumen bacterium <i>Butyrivibrio proteoclasticus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1457-1469.	2.6	62
36	The Glycobiome of the Rumen Bacterium <i>Butyrivibrio proteoclasticus</i> B316T Highlights Adaptation to a Polysaccharide-Rich Environment. <i>PLoS ONE</i> , 2010, 5, e11942.	2.5	102

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37	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.	2.5	256
38	Relationship between Virulence Gene Profiles of Atypical Enteropathogenic <i>Escherichia coli</i> and Shiga Toxin-Producing <i>E. coli</i> Isolates from Cattle and Sheep in New Zealand. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3744-3747.	3.1	12
39	Molecular Subtyping and Distribution of the Serine Protease from Shiga Toxin-Producing <i>Escherichia coli</i> among Atypical Enteropathogenic <i>E. coli</i> Strains. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2246-2249.	3.1	5
40	A new growth medium for rapid selection and purification of <i>Clostridium proteoclasticum</i> transposon mutants. <i>Journal of Microbiological Methods</i> , 2008, 73, 203-207.	1.6	2
41	Phenotypic characterization of transposon-inserted mutants of <i>Clostridium proteoclasticum</i> B316T using extracellular metabolomics. <i>Journal of Biotechnology</i> , 2008, 134, 55-63.	3.8	18
42	Reclassification of <i>Clostridium proteoclasticum</i> as <i>Butyrivibrio proteoclasticus</i> comb. nov., a butyrate-producing ruminal bacterium. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 2041-2045.	1.7	90
43	Molecular Subtyping and Genetic Analysis of the Enterohemolysin Gene (<i>ehxA</i>) from Shiga Toxin-Producing <i>Escherichia coli</i> and Atypical Enteropathogenic <i>E. coli</i> . <i>Applied and Environmental Microbiology</i> , 2007, 73, 6360-6369.	3.1	42
44	Intimin subtyping of <i>Escherichia coli</i> : concomitant carriage of multiple intimin subtypes from forage-fed cattle and sheep. <i>FEMS Microbiology Letters</i> , 2007, 272, 163-171.	1.8	17
45	Production of indolic compounds by rumen bacteria isolated from grazing ruminants. <i>Journal of Applied Microbiology</i> , 2006, 100, 1261-1271.	3.1	50
46	Isolation, Characterization, and Epidemiological Assessment of Shiga Toxin-Producing <i>Escherichia coli</i> O84 Isolates from New Zealand. <i>Journal of Clinical Microbiology</i> , 2006, 44, 1863-1866.	3.9	25
47	Methane production from in vitro rumen incubations with <i>Lotus pedunculatus</i> and <i>Medicago sativa</i> , and effects of extractable condensed tannin fractions on methanogenesis. <i>Animal Feed Science and Technology</i> , 2005, 123-124, 403-419.	2.2	361
48	Metagenomic analysis of the microbiomes in ruminants and other herbivores. , 2005, , 209-220.		3
49	The use of PCR for the identification and characterisation of bacteriocin genes from bacterial strains isolated from rumen or caecal contents of cattle and sheep. <i>FEMS Microbiology Ecology</i> , 2004, 48, 199-207.	2.7	14
50	Opportunities to improve fiber degradation in the rumen: microbiology, ecology, and genomics. <i>FEMS Microbiology Reviews</i> , 2003, 27, 663-693.	8.6	409
51	Ammonia-Hyperproducing Bacteria from New Zealand Ruminants. <i>Applied and Environmental Microbiology</i> , 1998, 64, 1796-1804.	3.1	123
52	Genetic diversity in ruminal isolates of <i>Selenomonas ruminantium</i> . <i>Current Microbiology</i> , 1991, 22, 279-284.	2.2	25