

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	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , 2018, 36, 359-367.	17.5	414
2	Opportunities to improve fiber degradation in the rumen: microbiology, ecology, and genomics. <i>FEMS Microbiology Reviews</i> , 2003, 27, 663-693.	8.6	409
3	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
4	Methane yield phenotypes linked to differential gene expression in the sheep rumen microbiome. <i>Genome Research</i> , 2014, 24, 1517-1525.	5.5	332
5	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.	11.1	268
6	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
7	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
8	Diverse hydrogen production and consumption pathways influence methane production in ruminants. <i>ISME Journal</i> , 2019, 13, 2617-2632.	9.8	132
9	Strategies to reduce methane emissions from farmed ruminants grazing on pasture. <i>Veterinary Journal</i> , 2011, 188, 11-17.	1.7	130
10	Ammonia-Hyperproducing Bacteria from New Zealand Ruminants. <i>Applied and Environmental Microbiology</i> , 1998, 64, 1796-1804.	3.1	123
11	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
12	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
13	Comparative Genomics of Rumen <i>Butyrivibrio</i> spp. Uncovers a Continuum of Polysaccharide-Degrading Capabilities. <i>Applied and Environmental Microbiology</i> , 2019, 86, .	3.1	65
14	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
15	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
16	Production of indolic compounds by rumen bacteria isolated from grazing ruminants. <i>Journal of Applied Microbiology</i> , 2006, 100, 1261-1271.	3.1	50
17	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
18	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

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19	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
20	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.	2.1	37
21	The complete genome sequence of Eubacterium limosum SA11, a metabolically versatile rumen acetogen. Standards in Genomic Sciences, 2016, 11, 26.	1.5	36
22	A1Ao-ATP Synthase of Methanobrevibacter ruminantium Couples Sodium Ions for ATP Synthesis under Physiological Conditions. Journal of Biological Chemistry, 2011, 286, 39882-39892.	3.4	35
23	Applications of the Soil, Plant and Rumen Microbiomes in Pastoral Agriculture. Frontiers in Nutrition, 2019, 6, 107.	3.7	30
24	The complete genome sequence of the rumen bacterium Butyrivibrio hungatei MB2003. Standards in Genomic Sciences, 2017, 12, 72.	1.5	29
25	<i>Butyrivibrio hungatei</i> MB2003 Competes Effectively for Soluble Sugars Released by <i>Butyrivibrio proteoclasticus</i> B316 ^T during Growth on Xylan or Pectin. Applied and Environmental Microbiology, 2019, 85, .	3.1	28
26	The complete genome sequence of the rumen methanogen Methanobacterium formicicum BRM9. Standards in Genomic Sciences, 2014, 9, 15.	1.5	27
27	Occurrence and expression of genes encoding methyl-compound production in rumen bacteria. Animal Microbiome, 2019, 1, 15.	3.8	27
28	Genetic diversity in ruminal isolates of Selenomonas ruminantium. Current Microbiology, 1991, 22, 279-284.	2.2	25
29	Isolation, Characterization, and Epidemiological Assessment of Shiga Toxin-Producing Escherichia coli O84 Isolates from New Zealand. Journal of Clinical Microbiology, 2006, 44, 1863-1866.	3.9	25
30	Characterization of the rumen microbial community composition of buffalo breeds consuming diets typical of dairy production systems in Southern China. Animal Feed Science and Technology, 2015, 207, 75-84.	2.2	24
31	Hydrogen and formate production and utilisation in the rumen and the human colon. Animal Microbiome, 2022, 4, 22.	3.8	23
32	Extracellular Polysaccharide-Degrading Proteome of <i>Butyrivibrio proteoclasticus</i> . Journal of Proteome Research, 2012, 11, 131-142.	3.7	21
33	Structure and function of an acetyl xylan esterase (Est2A) from the rumen bacterium <i>Butyrivibrio proteoclasticus</i> . Proteins: Structure, Function and Bioinformatics, 2013, 81, 911-917.	2.6	21
34	Phenotypic characterization of transposon-inserted mutants of Clostridium proteoclasticum B316T using extracellular metabolomics. Journal of Biotechnology, 2008, 134, 55-63.	3.8	18
35	Intimin subtyping of Escherichia coli: concomitant carriage of multiple intimin subtypes from forage-fed cattle and sheep. FEMS Microbiology Letters, 2007, 272, 163-171.	1.8	17
36	Complete Genome Sequence of the Polysaccharide-Degrading Rumen Bacterium Pseudobutyrovibrio xylanivorans MA3014 Reveals an Incomplete Glycolytic Pathway. Genome Biology and Evolution, 2020, 12, 1566-1572.	2.5	17

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37	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
38	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
39	Carbohydrate transporting membrane proteins of the rumen bacterium, <i>Butyrivibrio proteoclasticus</i> . <i>Journal of Proteomics</i> , 2012, 75, 3138-3144.	2.4	14
40	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
41	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
42	Improving the genetic representation of rare taxa within complex microbial communities using <sc>DNA</sc> normalization methods. <i>Molecular Ecology Resources</i> , 2015, 15, 464-476.	4.8	12
43	Draft Genome Sequence of the Rumen Methanogen <i>Methanobrevibacter olleyae</i> YLM1. <i>Genome Announcements</i> , 2016, 4, .	0.8	11
44	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
45	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
46	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
47	The Cytosolic Oligosaccharide-Degrading Proteome of <i>Butyrivibrio Proteoclasticus</i> . <i>Proteomes</i> , 2015, 3, 347-368.	3.5	7
48	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
49	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
50	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
51	Metagenomic analysis of the microbiomes in ruminants and other herbivores. , 2005, , 209-220.		3
52	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