

# Stuart E Denman

## List of Publications by Year in descending order

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Version: 2024-02-01

93  
papers

7,162  
citations

81900

39  
h-index

58581

82  
g-index

94  
all docs

94  
docs citations

94  
times ranked

7707  
citing authors

#	ARTICLE	IF	CITATIONS
1	Changes in rumen microbial community composition in yak in response to seasonal variations. <i>Journal of Applied Microbiology</i> , 2022, 132, 1652-1665.	3.1	19
2	Fleece rot in sheep: a review of pathogenesis, aetiology, resistance and vaccines. <i>Animal Production Science</i> , 2022, 62, 201-215.	1.3	4
3	Fleece rot and dermatophilosis (lumpy wool) in sheep: opportunities and challenges for new vaccines. <i>Animal Production Science</i> , 2022, 62, 301-320.	1.3	2
4	Dermatophilosis (lumpy wool) in sheep: a review of pathogenesis, aetiology, resistance and vaccines. <i>Animal Production Science</i> , 2022, 62, 101.	1.3	3
5	Potential GHG emission benefits of <i>Asparagopsis taxiformis</i> feed supplement in Australian beef cattle feedlots. <i>Journal of Cleaner Production</i> , 2022, 337, 130499.	9.3	25
6	Seasonal and Nutrient Supplement Responses in Rumen Microbiota Structure and Metabolites of Tropical Rangeland Cattle. <i>Microorganisms</i> , 2020, 8, 1550.	3.6	19
7	Genomic predictions for enteric methane production are improved by metabolome and microbiome data in sheep ( <i>Ovis aries</i> ). <i>Journal of Animal Science</i> , 2020, 98, .	0.5	4
8	Characterization and survey in cattle of a rumen <i>Pyrimadobacter</i> sp. which degrades the plant toxin fluoroacetate. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	14
9	Draft Genome Sequence and Annotation of <i>Sporanaerobacter acetigenes</i> Strain F-12, Isolated from a Cattle Rumen. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	0
10	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
11	Sample Processing Methods Impacts on Rumen Microbiome. <i>Frontiers in Microbiology</i> , 2019, 10, 861.	3.5	12
12	Draft Genome Sequence and Annotation of <i>Oribacterium</i> sp. Strain C9, Isolated from a Cattle Rumen. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	3
13	Detection of <i>Synergistes jonesii</i> and genetic variants in ruminants from different geographical locations. <i>Tropical Grasslands - Forrajes Tropicales</i> , 2019, 7, 154-163.	0.5	7
14	Greenhouse gas implications of leucaena-based pastures. Can we develop an emissions reduction methodology for the beef industry?. <i>Tropical Grasslands - Forrajes Tropicales</i> , 2019, 7, 267-272.	0.5	7
15	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , 2018, 36, 359-367.	17.5	414
16	Review: The application of omics to rumen microbiota function. <i>Animal</i> , 2018, 12, s233-s245.	3.3	31
17	Analysis of the Rumen Microbiome and Metabolome to Study the Effect of an Antimethanogenic Treatment Applied in Early Life of Kid Goats. <i>Frontiers in Microbiology</i> , 2018, 9, 2227.	3.5	31
18	Culture- and metagenomics-enabled analyses of the <i>Methanosphaera</i> genus reveals their monophyletic origin and differentiation according to genome size. <i>ISME Journal</i> , 2018, 12, 2942-2953.	9.8	24

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19	Genetic Markers Are Associated with the Ruminal Microbiome and Metabolome in Grain and Sugar Challenged Dairy Heifers. <i>Frontiers in Genetics</i> , 2018, 9, 62.	2.3	24
20	3-NOP vs. Halogenated Compound: Methane Production, Ruminal Fermentation and Microbial Community Response in Forage Fed Cattle. <i>Frontiers in Microbiology</i> , 2018, 9, 1582.	3.5	62
21	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
22	Fluoroacetate in plants - a review of its distribution, toxicity to livestock and microbial detoxification. <i>Journal of Animal Science and Biotechnology</i> , 2017, 8, 55.	5.3	43
23	Differences in Ureolytic Bacterial Composition between the Rumen Digesta and Rumen Wall Based on ureC Gene Classification. <i>Frontiers in Microbiology</i> , 2017, 8, 385.	3.5	65
24	Phloroglucinol Degradation in the Rumen Promotes the Capture of Excess Hydrogen Generated from Methanogenesis Inhibition. <i>Frontiers in Microbiology</i> , 2017, 8, 1871.	3.5	41
25	Natural and artificial feeding management before weaning promote different rumen microbial colonization but not differences in gene expression levels at the rumen epithelium of newborn goats. <i>PLoS ONE</i> , 2017, 12, e0182235.	2.5	39
26	Methanogen Diversity in Indigenous and Introduced Ruminant Species on the Tibetan Plateau. <i>Archaea</i> , 2016, 2016, 1-10.	2.3	43
27	Methane Inhibition Alters the Microbial Community, Hydrogen Flow, and Fermentation Response in the Rumen of Cattle. <i>Frontiers in Microbiology</i> , 2016, 7, 1122.	3.5	97
28	Differences down-under: alcohol-fueled methanogenesis by archaea present in Australian macropodids. <i>ISME Journal</i> , 2016, 10, 2376-2388.	9.8	41
29	High Fat Diets Induce Colonic Epithelial Cell Stress and Inflammation that is Reversed by IL-22. <i>Scientific Reports</i> , 2016, 6, 28990.	3.3	243
30	Amino Acid and Peptide Utilization Profiles of the Fluoroacetate-Degrading Bacterium <i>Synergistetes</i> Strain MFA1 Under Varying Conditions. <i>Microbial Ecology</i> , 2016, 71, 494-504.	2.8	16
31	Metagenomic analysis of the rumen microbial community following inhibition of methane formation by a halogenated methane analog. <i>Frontiers in Microbiology</i> , 2015, 6, 1087.	3.5	97
32	Manipulating rumen fermentation and methanogenesis using an essential oil and monensin in beef cattle fed a tropical grass hay. <i>Animal Feed Science and Technology</i> , 2015, 200, 25-34.	2.2	49
33	Hydrogenotrophic culture enrichment reveals rumen <i>Lachnospiraceae</i> and <i>Ruminococcaceae</i> acetogens and hydrogen-responsive <i>Bacteroidetes</i> from pasture-fed cattle. <i>FEMS Microbiology Letters</i> , 2015, 362, fmv104.	1.8	79
34	Response of the rumen archaeal and bacterial populations to anti-methanogenic organosulphur compounds in continuous-culture fermenters. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv079.	2.7	23
35	The Early Impact of Genomics and Metagenomics on Ruminal Microbiology. <i>Annual Review of Animal Biosciences</i> , 2015, 3, 447-465.	7.4	13
36	Methane matters in animals and man: from beginning to end. <i>Microbiology Australia</i> , 2015, 36, 4.	0.4	0

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37	Investigation of a new acetogen isolated from an enrichment of the tammar wallaby forestomach. <i>BMC Microbiology</i> , 2014, 14, 314.	3.3	34
38	Effects of partial mixed rations and supplement amounts on milk production and composition, ruminal fermentation, bacterial communities, and ruminal acidosis. <i>Journal of Dairy Science</i> , 2014, 97, 5763-5785.	3.4	47
39	Ruminal bacterial community shifts in grain-, sugar-, and histidine-challenged dairy heifers. <i>Journal of Dairy Science</i> , 2014, 97, 5131-5150.	3.4	48
40	Effect of bromochloromethane and fumarate on phylogenetic diversity of the formyltetrahydrofolate synthetase gene in bovine rumen. <i>Animal Science Journal</i> , 2014, 85, 25-31.	1.4	11
41	Is there genetic diversity in the 'leucaena bug' <i>Synergistes jonesii</i> which may reflect ability to degrade leucaena toxins?. <i>Tropical Grasslands - Forrajes Tropicales</i> , 2014, 2, 113.	0.5	2
42	Identification of chicken intestinal microbiota correlated with the efficiency of energy extraction from feed. <i>Veterinary Microbiology</i> , 2013, 164, 85-92.	1.9	155
43	Highly Variable Microbiota Development in the Chicken Gastrointestinal Tract. <i>PLoS ONE</i> , 2013, 8, e84290.	2.5	231
44	Responses in digestion, rumen fermentation and microbial populations to inhibition of methane formation by a halogenated methane analogue. <i>British Journal of Nutrition</i> , 2012, 108, 482-491.	2.3	105
45	Draft Genome Sequence of <i>Treponema</i> sp. Strain JC4, a Novel Spirochete Isolated from the Bovine Rumen. <i>Journal of Bacteriology</i> , 2012, 194, 4130-4130.	2.2	33
46	Intestinal microbiota associated with differential feed conversion efficiency in chickens. <i>Applied Microbiology and Biotechnology</i> , 2012, 96, 1361-1369.	3.6	229
47	Changes in the caecal microflora of chickens following <i>Clostridium perfringens</i> challenge to induce necrotic enteritis. <i>Veterinary Microbiology</i> , 2012, 159, 155-162.	1.9	132
48	Methanogen Colonisation Does Not Significantly Alter Acetogen Diversity in Lambs Isolated 17h After Birth and Raised Aseptically. <i>Microbial Ecology</i> , 2012, 64, 628-640.	2.8	43
49	Isolation and survey of novel fluoroacetate-degrading bacteria belonging to the phylum Synergistetes. <i>FEMS Microbiology Ecology</i> , 2012, 80, 671-684.	2.7	45
50	Isolation of Succinivibrionaceae Implicated in Low Methane Emissions from Tammar Wallabies. <i>Science</i> , 2011, 333, 646-648.	12.6	179
51	Development of a colorimetric colony-screening assay for detection of defluorination by micro-organisms. <i>Letters in Applied Microbiology</i> , 2011, 53, 417-423.	2.2	9
52	High-Yield and Phylogenetically Robust Methods of DNA Recovery for Analysis of Microbial Biofilms Adherent to Plant Biomass in the Herbivore Gut. <i>Microbial Ecology</i> , 2011, 61, 448-454.	2.8	33
53	Strategy for Modular Tagged High-Throughput Amplicon Sequencing. <i>Applied and Environmental Microbiology</i> , 2011, 77, 6310-6312.	3.1	25
54	Evaluation of Subsampling-Based Normalization Strategies for Tagged High-Throughput Sequencing Data Sets from Gut Microbiomes. <i>Applied and Environmental Microbiology</i> , 2011, 77, 8795-8798.	3.1	125

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55	Dysbiosis of fecal microbiota in Crohn's disease patients as revealed by a custom phylogenetic microarray. <i>Inflammatory Bowel Diseases</i> , 2010, 16, 2034-2042.	1.9	314
56	Adaptation to herbivory by the Tammar wallaby includes bacterial and glycoside hydrolase profiles different from other herbivores. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14793-14798.	7.1	234
57	Functional Gene Analysis Suggests Different Acetogen Populations in the Bovine Rumen and Tammar Wallaby Forestomach. <i>Applied and Environmental Microbiology</i> , 2010, 76, 7785-7795.	3.1	127
58	Recent developments in nucleic acid based techniques for use in rumen manipulation. <i>Revista Brasileira De Zootecnia</i> , 2009, 38, 341-351.	0.8	8
59	An Efficient RNA Extraction Method for Estimating Gut Microbial Diversity by Polymerase Chain Reaction. <i>Current Microbiology</i> , 2009, 58, 464-471.	2.2	47
60	Colon, Rectum. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2009, 24, A239-A247.	2.8	0
61	Plant biomass degradation by gut microbiomes: more of the same or something new?. <i>Current Opinion in Biotechnology</i> , 2009, 20, 358-363.	6.6	102
62	The stimulatory effect of the organic sulfur supplement, mercaptopropane sulfonic acid on cellulolytic rumen microorganisms and microbial protein synthesis in cattle fed low sulfur roughages. <i>Animal</i> , 2009, 3, 802-809.	3.3	7
63	Detection and monitoring of anaerobic rumen fungi using an ARISA method. <i>Letters in Applied Microbiology</i> , 2008, 47, 492-499.	2.2	32
64	Effect of tea saponin on methanogenesis, microbial community structure and expression of <i>mcrA</i> gene, in cultures of rumen micro-organisms. <i>Letters in Applied Microbiology</i> , 2008, 47, 421-426.	2.2	163
65	An improved method for RNA extraction from carcass samples for detection of viable <i>Escherichia coli</i> O157:H7 by reverse-transcriptase polymerase chain reaction. <i>Letters in Applied Microbiology</i> , 2008, 47, 399-404.	2.2	14
66	Effect of diet on the concentration of complex Shiga toxin-producing <i>Escherichia coli</i> and EHEC virulence genes in bovine faeces, hide and carcass. <i>International Journal of Food Microbiology</i> , 2008, 121, 208-216.	4.7	9
67	Effect of sulfur supplements on cellulolytic rumen micro-organisms and microbial protein synthesis in cattle fed a high fibre diet. <i>Journal of Applied Microbiology</i> , 2007, 103, 1757-1765.	3.1	36
68	Quantitation and diversity analysis of ruminal methanogenic populations in response to the antimethanogenic compound bromochloromethane. <i>FEMS Microbiology Ecology</i> , 2007, 62, 313-322.	2.7	429
69	Molecular cloning and expression analysis of two distinct $\beta$ -glucosidase genes, <i>bg1</i> and <i>aven1</i> , with very different biological roles from the thermophilic, saprophytic fungus <i>Talaromyces emersonii</i> . <i>Mycological Research</i> , 2007, 111, 840-849.	2.5	34
70	Application of Recent DNA/RNA-based Techniques in Rumen Ecology. <i>Asian-Australasian Journal of Animal Sciences</i> , 2007, 20, 283-294.	2.4	36
71	Screening of Bacteria from the Cattle Gastrointestinal Tract for Inhibitory Activity against Enterohemorrhagic <i>Escherichia coli</i> O157:H7, O111:H $\alpha$ , and O26:H11. <i>Journal of Food Protection</i> , 2006, 69, 2843-2850.	1.7	3
72	Evaluation of a PCR detection method for <i>Escherichia coli</i> O157:H7/H- bovine faecal samples. <i>Letters in Applied Microbiology</i> , 2006, 42, 386-391.	2.2	16

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73	Development of a real-time PCR assay for monitoring anaerobic fungal and cellulolytic bacterial populations within the rumen. <i>FEMS Microbiology Ecology</i> , 2006, 58, 572-582.	2.7	643
74	Enzymatic properties of native and deglycosylated hybrid aspen ( <i>Populus tremula</i> – <i>tremuloides</i> ) xyloglucan endotransglycosylase 16A expressed in <i>Pichia pastoris</i> . <i>Biochemical Journal</i> , 2005, 390, 105-113.	3.7	72
75	Rumen bacteria. , 2005, , 23-37.		29
76	Carbohydrate-Active Enzymes Involved in the Secondary Cell Wall Biogenesis in Hybrid Aspen. <i>Plant Physiology</i> , 2005, 137, 983-997.	4.8	173
77	Enrichment, isolation and characterisation of ruminal bacteria that degrade non-protein amino acids from the tropical legume <i>Acacia angustissima</i> . <i>Animal Feed Science and Technology</i> , 2005, 121, 191-204.	2.2	11
78	Application of Molecular Microbial Ecology Tools to Facilitate the Development of Feeding Systems for Ruminant Livestock that Reduce Greenhouse Gas Emissions. , 2005, , 387-395.		1
79	RAPD, RFLP, T-RFLP, AFLP, RISA. , 2005, , 151-159.		2
80	Quantitative (real-time) PCR. , 2005, , 105-115.		29
81	Crystal Structures of a Poplar Xyloglucan Endotransglycosylase Reveal Details of Transglycosylation Acceptor Binding. <i>Plant Cell</i> , 2004, 16, 874-886.	6.6	155
82	Recombinant Expression and Enzymatic Characterization of PttCel9A, a KOR Homologue from <i>Populus tremula</i> x <i>tremuloides</i> . <i>Biochemistry</i> , 2004, 43, 10080-10089.	2.5	54
83	Opportunities to improve fiber degradation in the rumen: microbiology, ecology, and genomics. <i>FEMS Microbiology Reviews</i> , 2003, 27, 663-693.	8.6	409
84	Crystallization and preliminary X-ray analysis of a xyloglucan endotransglycosylase from <i>Populus tremula</i> – <i>tremuloides</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 535-537.	2.5	14
85	N-linked glycosylation of native and recombinant cauliflower xyloglucan endotransglycosylase 16A. <i>Biochemical Journal</i> , 2003, 375, 61-73.	3.7	51
86	Molecular Features of Family GH9 Cellulases in Hybrid Aspen and the Filamentous Fungus <i>Phanerochaete chrysosporium</i> . <i>Journal of Applied Glycoscience</i> (1999), 2003, 50, 253-256.	0.7	11
87	Functional Genomics of Wood Formation in Hybrid Aspen. , 2003, , 453-454.		0
88	Transcript Analysis of Genes Encoding a Family 61 Endoglucanase and a Putative Membrane-Anchored Family 9 Glycosyl Hydrolase from <i>Phanerochaete chrysosporium</i> . <i>Applied and Environmental Microbiology</i> , 2002, 68, 5765-5768.	3.1	37
89	Xyloglucan Endotransglycosylases Have a Function during the Formation of Secondary Cell Walls of Vascular Tissues. <i>Plant Cell</i> , 2002, 14, 3073-3088.	6.6	208
90	Improved Enantioselectivity of a Lipase by Rational Protein Engineering. <i>ChemBioChem</i> , 2001, 2, 766.	2.6	108

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91	Stable linker peptides for a cellulose-binding domainâ€“lipase fusion protein expressed in <i>Pichia pastoris</i> . <i>Protein Engineering, Design and Selection</i> , 2001, 14, 711-715.	2.1	79
92	<i>Caloramator indicus</i> sp. nov., a New Thermophilic Anaerobic Bacterium Isolated from the Deep-Seated Nonvolcanically Heated Waters of an Indian Artesian Aquifer. <i>International Journal of Systematic Bacteriology</i> , 1996, 46, 497-501.	2.8	36
93	Modification of a xylanase cDNA isolated from an anaerobic fungus <i>Neocallimastix patriciarum</i> for high-level expression in <i>Escherichia coli</i> . <i>Journal of Biotechnology</i> , 1995, 38, 269-277.	3.8	27