

Sinead C Leahy

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

4,850
citations

186265

28
h-index

189892

50
g-index

53
all docs

53
docs citations

53
times ranked

4684
citing authors

#	ARTICLE	IF	CITATIONS
1	Electron flow: key to mitigating ruminant methanogenesis. <i>Trends in Microbiology</i> , 2022, 30, 209-212.	7.7	21
2	Hydrogen and formate production and utilisation in the rumen and the human colon. <i>Animal Microbiome</i> , 2022, 4, 22.	3.8	23
3	How necessary and feasible are reductions of methane emissions from livestock to support stringent temperature goals?. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2021, 379, 20200452.	3.4	49
4	Manipulating the rumen microbiome to address challenges facing Australasian dairy farming. <i>Animal Production Science</i> , 2020, 60, 36.	1.3	4
5	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
6	Challenges and Prospects for Agricultural Greenhouse Gas Mitigation Pathways Consistent With the Paris Agreement. <i>Frontiers in Sustainable Food Systems</i> , 2020, 4, .	3.9	54
7	Applications of the Soil, Plant and Rumen Microbiomes in Pastoral Agriculture. <i>Frontiers in Nutrition</i> , 2019, 6, 107.	3.7	30
8	Diverse hydrogen production and consumption pathways influence methane production in ruminants. <i>ISME Journal</i> , 2019, 13, 2617-2632.	9.8	132
9	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
10	Use of Lactic Acid Bacteria to Reduce Methane Production in Ruminants, a Critical Review. <i>Frontiers in Microbiology</i> , 2019, 10, 2207.	3.5	53
11	Occurrence and expression of genes encoding methyl-compound production in rumen bacteria. <i>Animal Microbiome</i> , 2019, 1, 15.	3.8	27
12	Improved taxonomic assignment of rumen bacterial 16S rRNA sequences using a revised SILVA taxonomic framework. <i>PeerJ</i> , 2019, 7, e6496.	2.0	82
13	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , 2018, 36, 359-367.	17.5	414
14	Toward Understanding Phage:Host Interactions in the Rumen; Complete Genome Sequences of Lytic Phages Infecting Rumen Bacteria. <i>Frontiers in Microbiology</i> , 2017, 8, 2340.	3.5	28
15	Anaerobically Grown <i>Escherichia coli</i> Has an Enhanced Mutation Rate and Distinct Mutational Spectra. <i>PLoS Genetics</i> , 2017, 13, e1006570.	3.5	60
16	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
17	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
18	Dynamics and genetic diversification of <i>Escherichia coli</i> during experimental adaptation to an anaerobic environment. <i>PeerJ</i> , 2017, 5, e3244.	2.0	14

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19	Genome Analysis and Characterisation of the Exopolysaccharide Produced by <i>Bifidobacterium longum</i> subsp. <i>longum</i> 35624, <i>PLoS ONE</i> , 2016, 11, e0162983.	2.5	76
20	Genomic analysis of three <i>Bifidobacterium</i> species isolated from the calf gastrointestinal tract. <i>Scientific Reports</i> , 2016, 6, 30768.	3.3	20
21	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
22	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
23	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
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.	3.3	1,172
25	The Cytosolic Oligosaccharide-Degrading Proteome of <i>Butyrivibrio proteoclasticus</i> . <i>Proteomes</i> , 2015, 3, 347-368.	3.5	7
26	Determining the culturability of the rumen bacterial microbiome. <i>Microbial Biotechnology</i> , 2014, 7, 467-479.	4.2	159
27	Atypical bacterial rRNA operon structure is prevalent within the Lachnospiraceae, and use of the 16S-23S rRNA internal transcribed spacer region for the rapid identification of ruminal <i>Butyrivibrio</i> and <i>Pseudobutyrvibrio</i> strains. <i>Annals of Microbiology</i> , 2014, 64, 1623-1631.	2.6	4
28	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
29	Methane yield phenotypes linked to differential gene expression in the sheep rumen microbiome. <i>Genome Research</i> , 2014, 24, 1517-1525.	5.5	332
30	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
31	Draft Genome Sequence of <i>Lactococcus lactis</i> subsp. <i>cremoris</i> HP T, the First Defined-Strain Dairy Starter Culture Bacterium. <i>Genome Announcements</i> , 2014, 2, .	0.8	8
32	The Complete Genome Sequence of <i>Methanobrevibacter</i> sp. AbM4. <i>Standards in Genomic Sciences</i> , 2013, 8, 215-227.	1.5	42
33	Interaction between the genomes of <i>Lactococcus lactis</i> and phages of the P335 species. <i>Frontiers in Microbiology</i> , 2013, 4, 257.	3.5	36
34	Extracellular Polysaccharide-Degrading Proteome of <i>Butyrivibrio proteoclasticus</i> . <i>Journal of Proteome Research</i> , 2012, 11, 131-142.	3.7	21
35	Carbohydrate transporting membrane proteins of the rumen bacterium, <i>Butyrivibrio proteoclasticus</i> . <i>Journal of Proteomics</i> , 2012, 75, 3138-3144.	2.4	14
36	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

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37	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
38	Functional genome analysis of <i>Bifidobacterium breve</i> UCC2003 reveals type IVb tight adherence (Tad) pili as an essential and conserved host-colonization factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11217-11222.	7.1	328
39	Chromosomal diversity in <i>Lactococcus lactis</i> and the origin of dairy starter cultures. <i>Genome Biology and Evolution</i> , 2010, 2, 729-44.	2.5	90
40	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
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.	3.1	89
42	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
43	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
44	Analysis of the <i>Methanobrevibacter ruminantium</i> draft genome: understanding methanogen biology to inhibit their action in the rumen. <i>Australian Journal of Experimental Agriculture</i> , 2008, 48, 83.	1.0	20
45	Application of rumen microbial genome information to livestock systems in the postgenomic era. <i>Australian Journal of Experimental Agriculture</i> , 2008, 48, 695.	1.0	11
46	From bacterial genome to functionality; case bifidobacteria. <i>International Journal of Food Microbiology</i> , 2007, 120, 2-12.	4.7	67
47	Multireplicon genome architecture of <i>Lactobacillus salivarius</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6718-6723.	7.1	216
48	Comparative Genomics and Transcriptional Analysis of Prophages Identified in the Genomes of <i>Lactobacillus gasseri</i> , <i>Lactobacillus salivarius</i> , and <i>Lactobacillus casei</i> . <i>Applied and Environmental Microbiology</i> , 2006, 72, 3130-3146.	3.1	75
49	Getting better with bifidobacteria. <i>Journal of Applied Microbiology</i> , 2005, 98, 1303-1315.	3.1	274
50	Prophage-Like Elements in Bifidobacteria: Insights from Genomics, Transcription, Integration, Distribution, and Phylogenetic Analysis. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8692-8705.	3.1	70
51	Mitigating greenhouse gas emissions from New Zealand pasture-based livestock farm systems. <i>Journal of New Zealand Grasslands</i> , 0, , 101-110.	0.0	10