

# 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	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
2	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , 2018, 36, 359-367.	17.5	414
3	Methane yield phenotypes linked to differential gene expression in the sheep rumen microbiome. <i>Genome Research</i> , 2014, 24, 1517-1525.	5.5	332
4	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
5	Getting better with bifidobacteria. <i>Journal of Applied Microbiology</i> , 2005, 98, 1303-1315.	3.1	274
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	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
8	Determining the culturability of the rumen bacterial microbiome. <i>Microbial Biotechnology</i> , 2014, 7, 467-479.	4.2	159
9	Diverse hydrogen production and consumption pathways influence methane production in ruminants. <i>ISME Journal</i> , 2019, 13, 2617-2632.	9.8	132
10	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
11	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
12	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
13	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
14	Improved taxonomic assignment of rumen bacterial 16S rRNA sequences using a revised SILVA taxonomic framework. <i>PeerJ</i> , 2019, 7, e6496.	2.0	82
15	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
16	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
17	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
18	From bacterial genome to functionality; case bifidobacteria. <i>International Journal of Food Microbiology</i> , 2007, 120, 2-12.	4.7	67

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19	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
20	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
21	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
22	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
23	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
24	The Complete Genome Sequence of <i>Methanobrevibacter</i> sp. AbM4. <i>Standards in Genomic Sciences</i> , 2013, 8, 215-227.	1.5	42
25	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
26	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
27	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
28	Applications of the Soil, Plant and Rumen Microbiomes in Pastoral Agriculture. <i>Frontiers in Nutrition</i> , 2019, 6, 107.	3.7	30
29	The complete genome sequence of the rumen bacterium <i>Butyrivibrio hungatei</i> MB2003. <i>Standards in Genomic Sciences</i> , 2017, 12, 72.	1.5	29
30	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
31	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
32	Occurrence and expression of genes encoding methyl-compound production in rumen bacteria. <i>Animal Microbiome</i> , 2019, 1, 15.	3.8	27
33	Hydrogen and formate production and utilisation in the rumen and the human colon. <i>Animal Microbiome</i> , 2022, 4, 22.	3.8	23
34	Extracellular Polysaccharide-Degrading Proteome of <i>Butyrivibrio proteoclasticus</i> . <i>Journal of Proteome Research</i> , 2012, 11, 131-142.	3.7	21
35	Electron flow: key to mitigating ruminant methanogenesis. <i>Trends in Microbiology</i> , 2022, 30, 209-212.	7.7	21
36	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

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37	Genomic analysis of three Bifidobacterium species isolated from the calf gastrointestinal tract. Scientific Reports, 2016, 6, 30768.	3.3	20
38	Complete Genome Sequence of the Polysaccharide-Degrading Rumen Bacterium Pseudobutyribrio xylanivorans MA3014 Reveals an Incomplete Glycolytic Pathway. Genome Biology and Evolution, 2020, 12, 1566-1572.	2.5	17
39	The complete genome sequence of the rumen methanogen Methanobrevibacter millerae SM9. Standards in Genomic Sciences, 2016, 11, 49.	1.5	15
40	Carbohydrate transporting membrane proteins of the rumen bacterium, Butyrivibrio proteoclasticus. Journal of Proteomics, 2012, 75, 3138-3144.	2.4	14
41	Dynamics and genetic diversification of <i>Escherichia coli</i> during experimental adaptation to an anaerobic environment. PeerJ, 2017, 5, e3244.	2.0	14
42	Metasecretome-selective phage display approach for mining the functional potential of a rumen microbial community. BMC Genomics, 2014, 15, 356.	2.8	13
43	Application of rumen microbial genome information to livestock systems in the postgenomic era. Australian Journal of Experimental Agriculture, 2008, 48, 695.	1.0	11
44	Transposition of Tn916 in the four replicons of the Butyrivibrio proteoclasticus B316T genome. FEMS Microbiology Letters, 2011, 316, 144-151.	1.8	10
45	Mitigating greenhouse gas emissions from New Zealand pasture-based livestock farm systems. Journal of New Zealand Grasslands, 0, , 101-110.	0.0	10
46	Draft Genome Sequence of Lactococcus lactis subsp. cremoris HP T , the First Defined-Strain Dairy Starter Culture Bacterium. Genome Announcements, 2014, 2, .	0.8	8
47	Gene and transcript abundances of bacterial type III secretion systems from the rumen microbiome are correlated with methane yield in sheep. BMC Research Notes, 2017, 10, 367.	1.4	8
48	The Cytosolic Oligosaccharide-Degrading Proteome of Butyrivibrio Proteoclasticus. Proteomes, 2015, 3, 347-368.	3.5	7
49	The large episomes of Butyrivibrio proteoclasticus B316T have arisen through intragenomic gene shuttling from the chromosome to smaller Butyrivibrio-specific plasmids. Plasmid, 2011, 66, 67-78.	1.4	6
50	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 Butyrivibrio and Pseudobutyribrio strains. Annals of Microbiology, 2014, 64, 1623-1631.	2.6	4
51	Manipulating the rumen microbiome to address challenges facing Australasian dairy farming. Animal Production Science, 2020, 60, 36.	1.3	4