

# Timothy J Snelling

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9642872/publications.pdf>

Version: 2024-02-01

17  
papers

1,718  
citations

516710

16  
h-index

839539

18  
g-index

18  
all docs

18  
docs citations

18  
times ranked

2177  
citing authors

#	ARTICLE	IF	CITATIONS
1	Dietary supplemental plant oils reduce methanogenesis from anaerobic microbial fermentation in the rumen. <i>Scientific Reports</i> , 2020, 10, 1613.	3.3	55
2	A heritable subset of the core rumen microbiome dictates dairy cow productivity and emissions. <i>Science Advances</i> , 2019, 5, eaav8391.	10.3	218
3	Identification of Rumen Microbial Genes Involved in Pathways Linked to Appetite, Growth, and Feed Conversion Efficiency in Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 701.	2.3	43
4	Temporal stability of the rumen microbiota in beef cattle, and response to diet and supplements. <i>Animal Microbiome</i> , 2019, 1, 16.	3.8	29
5	MAGpy: a reproducible pipeline for the downstream analysis of metagenome-assembled genomes (MAGs). <i>Bioinformatics</i> , 2019, 35, 2150-2152.	4.1	33
6	Assembly of 913 microbial genomes from metagenomic sequencing of the cow rumen. <i>Nature Communications</i> , 2018, 9, 870.	12.8	405
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	The ruminal microbiome associated with methane emissions from ruminant livestock. <i>Journal of Animal Science and Biotechnology</i> , 2017, 8, 7.	5.3	246
9	The rumen microbial metaproteome as revealed by SDS-PAGE. <i>BMC Microbiology</i> , 2017, 17, 9.	3.3	31
10	Application of meta-omics techniques to understand greenhouse gas emissions originating from ruminal metabolism. <i>Genetics Selection Evolution</i> , 2017, 49, 9.	3.0	59
11	Effect of Sunflower and Marine Oils on Ruminal Microbiota, In vitro Fermentation and Digesta Fatty Acid Profile. <i>Frontiers in Microbiology</i> , 2017, 8, 1124.	3.5	57
12	Identification, Comparison, and Validation of Robust Rumen Microbial Biomarkers for Methane Emissions Using Diverse Bos Taurus Breeds and Basal Diets. <i>Frontiers in Microbiology</i> , 2017, 8, 2642.	3.5	64
13	Oral Samples as Non-Invasive Proxies for Assessing the Composition of the Rumen Microbial Community. <i>PLoS ONE</i> , 2016, 11, e0151220.	2.5	70
14	Diversity and Community Composition of Methanogenic Archaea in the Rumen of Scottish Upland Sheep Assessed by Different Methods. <i>PLoS ONE</i> , 2014, 9, e106491.	2.5	32
15	Archaeal abundance in post-mortem ruminal digesta may help predict methane emissions from beef cattle. <i>Scientific Reports</i> , 2014, 4, 5892.	3.3	88
16	Differential recovery of bacterial and archaeal 16S rRNA genes from ruminal digesta in response to glycerol as cryoprotectant. <i>Journal of Microbiological Methods</i> , 2013, 95, 381-383.	1.6	21
17	Isolation of <i>Streptococcus thoralensis</i> from Rabbit Faeces. <i>Current Microbiology</i> , 2010, 61, 357-360.	2.2	10