Rumen microbial genomics: from cells to genes (and back to cells)

Milka Popova, Ibrahim Fakih, Evelyne Forano, Anne Siegel, Rafael Muñoz-Tamayo, Diego Morgavi

To cite this version:

Milka Popova, Ibrahim Fakih, Evelyne Forano, Anne Siegel, Rafael Muñoz-Tamayo, et al.. Rumen microbial genomics: from cells to genes (and back to cells). CAB Reviews Perspectives in Agriculture Veterinary Science Nutrition and Natural Resources, 2022, 2022, 10.1079/cabireviews202217025 . hal-03929845

HAL Id: hal-03929845
https://hal.inrae.fr/hal-03929845

Rumen microbial genomics: from cells to genes (and back to cells)

Milka Popova[1*], Ibraim Fakih[2,3], Evelyne Forano[2], Anne Siegel[4], Rafael Muñoz-Tamayo[3], Diego P. Morgavi[1]

[1]Université Clermont Auvergne, INRAE, VetAgro Sup, UMR Herbivores, F-63122 Saint-Genès-Champanelle, France

[2]Université Clermont Auvergne, INRAE, UMR 454 MEDIS, Clermont-Ferrand, France

[3]Université Paris-Saclay, INRAE, AgroParisTech, UMR Modélisation Systémique Appliquée aux Ruminants, 75005, Paris, France

[4]Université Rennes, Inria, CNRS, IRISA, Dyliss team, Rennes, France

* Corresponding author milka.popova@inrae.fr

Abstract

The rumen harbours countless bacteria, archaea, ciliated protozoa, fungi, and viruses: various microorganisms that have established multiplicity of relationships to efficiently digest complex plant fibres and polysaccharides to produce volatile fatty acids (VFAs), microbial proteins, and vitamins, essentials for the host's health, growth and performances. Recent studies using omics-based techniques have revealed that changes in rumen microbiota are associated with changes in ruminants' production and health parameters such as feed efficiency, methane yield, milk composition and ruminal acidity. However, traditionally, rumen microbes were unveiled using anaerobic culture-based techniques, which are at the origin of most of the basic concepts and understanding of the rumen functioning. Isolating and culturing microbes is frequently more difficult, time-consuming and requires more training than molecular techniques, which explains why culture seems to be abandoned in favour of sequencing. Microbial cultures enable the study of substrate preferences and product output, essential growth requirements, biocide production, and susceptibilities; obtaining a pure culture also enables genome sequencing of these strains. We propose here, after a brief report of published rumen isolates, a comprehensive review of current advances in molecular methods to identify novel rumen microbes and discuss how culturing and mathematics could enhance our understanding of rumen microbiology.

Key words: ruminants, microbiota, pure cultures, modelling, genomics

Review methodology

This review is reported under the PRISMA 2020 guidelines for a systematic review. We conducted a comprehensive Web of Science search, using search terms "rumen" and "isolate" spanning the period 1945-2022 for an overview of culture-based studies exploring rumen microbiota. Further, we searched academic databases (PubMed, Scopus, Web of Science) to identify articles reporting enhanced genomic and mathematic evaluation of rumen microbiota.

Introduction

Ruminant livestock systems make both positive and negative contributions to the development of sustainable agriculture. Ruminants convert roughages into high-quality proteins for human consumption while adding value to poor or erodable lands. At the same time, ruminant production is criticised for its negative impact on the environment and feeds that can be used for human consumption. Under the menace of climate change, ruminants face the challenges of feed scarcity, reduced productivity and increased health burden.

Ruminants have adapted their digestive systems to eat only plants, and they are most efficient to retrieve energy from the plant cell walls than monogastric herbivores. Their stomach has four separate compartments with a distinctive function, allowing them to digest without thoroughly chewing. The partially chewed plant material is further processed by microbes in the rumen section of the stomach. Microbes break down organic matter and ferment it to produce volatile fatty acids, the ruminants' primary energy source. Rumen microorganisms have a critical role in ruminant nutrition and health, but, on the downside, they generate methane – a potent greenhouse gas and contribute to ammonia emissions. Research in rumen microbiota started with the pioneering work of Robert Edward Hungate more than 50 years ago [1, 2]; the growing evidence of the importance of rumen microbes for sustainable livestock brought researchers to consolidate efforts in 2011 by forming The Rumen Microbial Genomics Network. The network serves as a global collaborative platform for researchers, employing microbial genomics methodologies to understand the rumen microbiome better to address global agricultural concerns. Several international projects underpin the network: Hungate 1000 [3, 4], Global Rumen Census [5], RuminOmics [6, 7], RumenPredict [8], MASTER, and HoloRuminant. These projects contributed to our enhanced comprehension of the rumen microbial ecosystem.

The rumen contains representatives of all domains of life: Bacteria, Archaea, Eucarya. Bacteria are the most abundant and diverse; however, a diverse range of protozoa can also be found. Anaerobic fungi are also widely distributed, and bacteriophages are integral to the microbiota. Archaea are the only group producing methane. Numerous reviews address the composition of rumen microbiota in different ruminant species and at different physiological stages [4, 6-12], with the main focus being on Bacteria and Archaea as of their implication in feed digestion and methane production. But scientists agree that gaps of knowledge remain. This review stresses the limited understanding of individual microbes, as specific species could be the key to improving the sustainability of ruminant production systems. We also discuss research challenges to improve rumen microbial understanding, including opportunities for developing enhanced predictive models of rumen metabolism.

Cultured rumen microbes

In 1959 [13] and later in 1964 [14], it was suggested that most of the functionally important bacterial groups had already been described. Rumen bacteria (and archaea — classified at the time within bacteria) were initially classified according to specific wall staining tests into Gram-negative or Gram-positive species and their ability to grow on certain substrates or produce specific metabolites. Hungate [15] proposed to divide them into cellulolytic, amylolytic, hemicellulolytic, saccharolytic, proteolytic, methanogenic, lipolytic, and bacteria that use the products formed by other microbes. This classification was recently brought back in the spotlight by the proposal of the functional group concept [16], dividing microorganisms into groups based on metabolic inputs and outputs and irrespective of the taxonomy. However, this implies that an in-depth knowledge of microbial physiology is accumulated. The time and effort required to isolate and identify pure rumen microbes in cultures preclude this technique as a tool for cataloguing the complex rumen microbiota; still, the culture of isolates alone or in defined mixtures remain essential for the understanding of critical mechanistic factors governing microbial functionning. Through the growth of pure cultures under conditions similar to those of the rumen, it is possible to infer information on the role of these strains in their complex natural environment. This information derived from pure culture alone or simplified combinations can be used to formulate a hypothesis to be tested in the diverse community of the rumen.

In this context, we conducted a systematic literature survey for microbial isolates from the rumen (Table1). The survey was performed in Web of Science (WoS) (accessed January 2022) with the search terms "rumen" and "isolate", spanning 1945-2022. We examined the resultant titles, abstracts, and full-text for relevance to the topic and extracted the relevant information from each study. However, the WoS search missed some important documents. Therefore, we reviewed the cited references in all relevant publications and journal articles not listed in WoS and extra references known to the authors. In addition, we included all ruminant animal species but excluded isolates from faecal contents.

Following the development of anaerobic techniques for the culture of strictly anaerobic bacteria in the 1950s [17], a renewed interest can be observed in the isolation of representative rumen microbes from the beginning of the 90s (Figure 1). Most of the studies included in the survey employed the classical "most probable number" [18] or the "roll-tube method" developed by R.E. Hungate [19]. In our survey, we counted more than 14 000 isolates. More than 80% of the articles and the large majority of the isolates were Bacteria (Figure 2), anaerobic fungi of the Neocallimastigomycota phylum were the second most reported (348 isolates). In addition, we enumerated 25 Archaea strains, 18 bacteriophages isolated from rumen contents and 15 protozoa.

The most frequently studied bacterial strains belong to the Firmicutes phylum, 22% of all isolates (15% were lactic acid bacteria characterised only by phenotypic screening), Fibrobacter far behind, represented 0.3%. The large majority, 65%, of the bacterial strains remained unclassified compared to only 0.4% of isolated fungi. This can be easily explained by the research strategy adopted in papers reporting many initial bacterial isolates. These pure strains were further screened for relevant phenotypic properties, as enhanced fibre degradation activity, detoxification potential (mainly tannins metabolism), fatty acids metabolism (mainly CLA-related), lactic acid production or consumption or acetogenesis; from this initial screening, only the best performers were retained and further characterised morphologically and taxonomically. Regretfully, non-selected isolates have probably been lost, and the selected strains' fate is also uncertain. In addition, not all the isolated strains in "rumen" labs worldwide have been mentioned in publications, and many strains may still reside in freezers. Nevertheless, such a large panel of deeply characterised microbes constitutes an excellent point of departure for exploring fundamental microbial interactions.To improve our understanding of cultured rumen microbes, in 2011, the Hungate1000 project was launched. Coordinated and led by the RMG network, this initiative aimed at generating a reference set of 1000 microbial genomes cultivated from various ruminant host species [3, 4]. At that time, only 14 bacteria and one methanogen from the rumen had their genomes sequenced. The project so far has produced more than 500 sequenced genomes, constituting the Hungate genome catalogue [3] (480 are bacterial, 21 are Archaea and 7 Viruses). Additionally, 221 cultured genomes were produced within independent studies [12].

As for the identified isolates, the Hungate1000 database is dominated by bacteria from the Firmicutes phylum, while Bacteroidetes members are under-represented (Figure 3) [3]. Additionally, there is only one Fibrobacteres-related strain, *Fibrobacter succinogenes* HM2, while in our survey, we numbered more than 50 strains isolated from bovine or sheep rumen, 38 of them having already their genomes sequenced [20]. *F. succinogenes* is a remarkably proficient fibre degrading bacterium whose enzymatic system has been extensively studied [20-24]. *F. succinogenes* S85 has been shown as an excellent model for exploring the species' fibrolytic traits, as the strain has preserved its enzymatic characteristics compared to numerous phylogenetically close isolates [23]. In a comparative pure culture assay, *F. succinogenes* strains S85 and A3C digested more cellulose than the other two prominent rumen cellulolytic bacteria: *Ruminococcus albus* and *R. flavefaciens* [25]. Furthermore , a recent *in vivo* work showed that *F. succinogenes* S85 was outcompeted by *Ruminococcus* strains in gnotobiotic model lambs [26]. However, the authors noticed a significant decrease in *F.succinogenes* numbers and transcriptional activity using classical microbiological tools and high throughput sequencing techniques and highlighted different enzymatic strategies for cellulose degradation. This work was built on previously whole sequenced genomes and the characterisation, using pure cultures, of genes essential to fibre digestion. Therefore, it remains decidedly clear that the pure culture approach generates valuable data for precise phylogenetic and phenotypic characterisation of rumen microbes and for exploring microbial interaction in fully-controlled conditions.

The Hungate collection is far from complete [3]. However, in a comparative study based on the 16S rRNA gene sequences, the authors estimated that the Hungate dataset covered 75% of the microbial genera retrieved in the rumen [3]. This is a pretty good achievement regarding that the estimated percentage of rumen prokaryotes that can be cultured is only 40% [27]. Despite that, Zehavi *et al.* noticed that less than 4% of their isolates were represented in the Hungate collection in their considerable isolation effort. In this regard, pursuing the isolation of rumen microbes for enriching culture collections is a challenge in the domain. Culture collections are critical for the conservation and long term utilisation of biological resources; they also support research by supplying biological material. High throughput culturomics approaches could help isolate new bacteria belonging to the rare biosphere or poorly represented taxa [27].

Metataxonomics of rumen microbes

Amplicon sequencing of the 16S rRNA gene is the most widely used approach to study rumen microbiota. However, scientists employed various primers (targeting variable regions V1, V3, V4, V5) and assigned taxonomy using various databases (GreenGenes, Ribosomal Database Project (RDP), SILVA), and various pipelines (mothur, QIIME, DADA2 …). In 2018, Denman *et al.* reviewed the limitations of these techniques, from the primer selection through the sequencing error removal and the OTU-clustering step to the accuracy of the databases for taxonomic affiliation. They argued that some of the weaknesses could be explained by the incorrect use of bioinformatics tools. Redoubling our efforts with a more precise application of these technologies will result in a complete and deep understanding of rumen microbes' compositional and functional capability [28]. The response was not long in coming, as since several research groups undertook the assessment of protocols for sample processing [29] and data analysis [30, 31]. Establishing standard operating procedures for analysing rumen microbiota is also embedded in collaborative projects such as RumenPredict, MASTER, HoloRuminant. A guide for database choice in rumen amplicon studies [31] employed a rumen-specific reference standard to compare 16S rRNA database classifications. This rumen reference standard comprised 16 bacterial and archaeal full-length 16S rRNA and 9 protozoal 18S rRNA, and libraries were prepared following a previously described sample preparation guide [29] with primers targeting the V4 region [32]. Taxonomic classification was performed against RDP (version 11.5), the Genome Taxonomy Database (GTDB; release date 20/11/2018), SILVA (version 132) and RefSeq + RDP (release date 14/05/2018); the latter two giving the more accurate classification at the genus level.

Meanwhile, amplicon sequencing enriched our knowledge of rumen microbial diversity. A meta-analysis of curated 16S rRNA gene sequences showed that Firmicutes, Bacteroidetes and Proteobacteria are the dominant phyla (93% of all sequences) out of 19 detected [33]. For Archaea, the Methanobacteria were the most abundant. The Rumen Microbial Census network conducted an extensive investigation of the rumen microbial community (742 samples from 32 ruminant species from 35 countries) to identify the core microbiota and elucidate variations in the rumen microbiome linked to ruminant species, diet, and geographical location [5]. This large scale survey confirmed the crucial role of the diet in shaping rumen microbial profile, undoubtedly explained by the amount, physical and chemical nature of feeds supplied.

On the other hand, the diet did not affect the methanogens population, with *Methanobrevibacter gottschalkii* and *Methanobrevibacter ruminantium* nearly ubiquitous and representing 74% of the archaeal sequences [5]. This complies with the ecological niche that methanogens occupy in the rumen as they use fermentation end products from other microbial species as an energy source. Reports on fungal and protozoal metataxonomy are more occasional. Neocallimastigomycota actively take part in the plant biomass degradation ingested by the host animal and their divergence time concorded with the shift of ancestral mammals from primarily insectivory to herbivory [34].Morphological features and complex life cycle have entangle taxonomic classification of anaerobic fungi, but the use of marker genes made this task easier [35]. Kittelmann *et al.* [36, 37] used the internal transcribed spacer (ITS1) as a taxonomic marker for describing the fungal community in New Zealand ruminants. Neocallimastix, Piromyces and Orpinomyces accounted for 60% of the detected genera, 24% belonging to novel clades. However, they highlighted that inter-animal variations are as high as 88%, pointing to the strong effect of the host and the diet. The high variations in ITS1 size and sequence questioned its accuracy [38, 39]; the potential of the large 28S rRNA subunit as a phylogenetic marker has also been explored [40].

Microbial profiling using the 16S rRNA amplicon approach provided valuable insights into the rumen ecosystem composition and its relationship with diet, feed efficiency, enteric methane emissions, milk quality, acidosis or its establishment in early life [6-8, 10, 28, 41-43]. A significant step forward in understanding the influence of microbial community structure on animal phenotype was achieved by identifying ruminotypes associated with methane emissions. Three independent studies, one in sheep [44] and two in dairy cattle [45, 46], established the link between high-methane production and species belonging to *Ruminococcaceae, Christensenellaceae* and *Lachnospiraceae*. At the same time, low methane emissions ruminotypes had higher relative abundances of succinate producing bacteria [44-46]. More specifically, Ramayo-Caldas *et al.* highlighted that an OTU classified as *Succinivibrionaceae_UCG-001* was only present in low emitting cows. In another study, the same OTU increased in abundance after calving, and authors linked it to the observed enhanced fermentations [47]. The abundance of *Succinivibrionaceae*-family was also positively associated with propionate concentrations, feed efficiency [48] and milk protein [49]. Furthermore, strong positive and negative interactions at the transcriptional level were reported between *Succinivibrionaceae* and other major bacterial and archaeal taxa from the rumen [50]. All of the above studies support the idea that *Succinivibrionaceae* members play an essential role in the rumen due to their ecological and metabolic functions. However, the Hungate genome catalogue has only two strains from the *Succinivibrionaceae family (Ruminobacter amylophilus* and *Ruminobacter* sp. RM87), and in our survey of cultured isolates, we found only one old article reporting the isolation of 7 *Succinivibrio* strains [51]. The need arises to isolate more representatives of this taxon. The road is almost paved, as using binned metagenomic data and metabolic predictions, Pope *et al.* in 2011 designed a defined medium for the for the culture of a *Succinivibrionaceae* sp. that until then could not be grown axenically in the laboratory [52].

Rumen Uncultured Genomes

The amplicon sequencing approach requires prior knowledge for the design of primers and taxonomic affiliation, but accumulated data in this field made it a highly discerning tool for the phylogenetic description of microbial environmental samples [53]. Nevertheless, functional diversity cannot be directly predicted from phylogenetic diversity in microbial communities. Arguably, the emergence and expansion of metagenomics have been one of the most impressive achievements in microbial ecology during the last decade. Metagenomics refers to the study of genomic material found in environmental samples and offers access to the functional gene content of microbial communities, providing a considerably more comprehensive description than metataxonomics. A significant breakthrough of metagenomics is building metagenomic assembled genomes (MAGs). In this approach, sequences are assembled into scaffolds, which are subsequently categorised into potential MAGs based on tetranucleotide frequencies, abundances, related marker genes, taxonomic alignments, and codon use [54]. In doing so, we can identify novel species and get an insight into their contribution to microbial ecosystem dynamics.

Since 2011 with the first report of 446 rumen genome bins (and 15 draft genomes) [55], thousands of novel MAGs were announced (251 by Parks *et al.* [56], 99 by Svartstrom *et al.* [57], 79 by Solden *et al.* [58], 5845 by Stewart *et al.* [59, 60], 324 by Li *et al.* [61], 1200 by Wilkinson *et al.* [62], 391 by Glendinning *et al.* [63], 2809 by Anderson & Fernando [64], 4960 in buffalos by Tong *et al.* [65], 719 by Peng *et al.* [66], 10373 by Xie *et al.* [12] around the whole gastrointestinal tract and the list is not exhaustive). Close to 34 000 rumen MAGs were retrieved from ten publicly available datasets [67]; 63% were seen in only one of the datasets, and no MAG was common in all datasets. In this work, the author stressed the need to have standardized procedures for MAGs and corresponding metadata description and a common repository for sharing data. This is a sensible comment which complies with the collaborative efforts of the Hungate1000 project and the SOP for metataxonomic analysis for standardized databases and tools for ruminants gut microbiota analysis.

In some of the studies mentioned above, authors mapped the retrieved MAGs to the Hungate1000 genome database. Li *et al.* [61] reported a mapping rate of 5.4% (similarity ≥ 95%); 3% of the MAGs from Stewart *et al.* [60] had ≥ 95% protein identity with Hungate genomes, and this figure increased to 5.4% for similarity rates ≥90%; 3.5% of the MAGs from Anderson & Fernando [64] had a similarity rate ≥95% with genomes from the Hungate1000 database. Only eighteen from the 719 high-quality MAGs in Peng *et al.* [66] were classified as eukaryotes and identified to belong to the fungal subphylum Neocallimastigomycota. Anyway, though this was the first report of rumen fungal MAGs, the authors underlined that these MAGs are only 73% complete. Indeed, it is particularly challenging to reconstruct eukaryotic genomes because of their size (>10 Mbp) and and the presence of frequent repeat region with high GC content. Zehavi *et al.* [27] accentuated that sequencing approaches (metataxonomics was used in their study) target mainly abundant microbes. In contrast, culture can recover abundant and rare microbes, as the ability to culture a microbe does on intrinsic characteristics and not on their abundance [68]. Though this could partially explain the low coverage of the Hungate database by MAGs, the question of whether these are real microbial species remains. In human faecal samples, MAGs recovered only 77% of the core genes (shared by more than 90% of the present microbial species) and 50 % of the variable genes (presents in more than 10%, but less than 90% of the population members) [69]. Moreover, human gut MAGs were shown to be systematically depleted for genes encoding essential functions supporting life [70]. MAGs produced from short-read metagenomic datasets do seldom contain 16S genes. The use of long reads sequencing platforms will bridge the gap between MAGs and cultured species, also with metataxonomics and function. Notwithstanding, to confirm the real biological existence of MAGs, returning to culturing seems necessary. This was already done with the *Succinovibrionaceae* isolate of the wallaby [52], where the genome reconstruction allowed designing appropriate culture media. Genomic analysis is particularly good at identifying genes and determining the functional relationships between microbes. For validating phenotypic predictions based on genetic data, detecting novel microbes, and investigating microbial interactions with precision, culture-based approaches are still required.

An alternative strategy to offset culture limitation is to isolate individual cells from fresh rumen contents as this was recently done for rumen ciliates [71]. Cells were selected based on morphological traits using electron microscope and subjected to whole genome sequencing using multiple displacement amplification or whole transcriptome amplification. The analysis yielded 52 high quality ciliate genomes and allowed the classification of 22 morphospecies in 13 genera and the of a new family Dasytrichidae [71].

Integrating culture-based approaches into the next generation models of the rumen microbiome

Rumen modelling started in the 70s with empirical and mechanistic developments [72]. Mechanistic rumen models have been consolidated in four modelling structures, namely Molly [73], CNCPS [74], COWPOLL [75] and Karoline [76], which have been incrementally improved over the years. However, the accuracy power to predict the rumen fermentation profile can still be ameliorated [77] by including improvements on physiological components (e.g., VFA absorption) [78], on rumen microbiota representation [79, 80], and the incorporation of thermodynamic, regulation and inhibition factors [81-85].

Kinetic modelling approaches are traditionally used for modelling microbial ecosystems. They are derived from mass-balance principles and have two sets of components: the first defining the mathematical functions representing the kinetic rates of substrate utilization and product formation, and the second containing the parameters that represent the stoichiometry of the reactions. Thus, incorporating data from pure-culture growth experiments in kinetic models detect key parameters, such as the maximal growth rate and the substrate affinity constants, and give insights on ecological properties such as microbial coexistence and exclusion. For example, in work with rumen methanogens, a kinetic modelling approach quantified the metabolic and energetic differences between three species, but the kinetic parameters alone did not explain microbial coexistence. Indeed, adhesion properties played a role in the ecology of methanogens in the rumen [86]. Current rumen fermentation models are in the category of kinetic models. In these models, the rumen microbiota is represented by macroscopic functional groups derived from the study of the main reactions documented in the rumen literature. This representation is then subjected to the modeller's choice and does not integrate data on microbial genomic knowledge.

Alternatively, genome-scale metabolic models (GEMs) allow the integration of microbial genomic information. The core of a GEM of a microorganism is a graph that links the metabolites and biochemical reactions that the organism can perform based on its genetic potential. This graph translates into a stoichiometry matrix of the metabolism. The stoichiometry matrix results from a metabolic reconstruction based on annotation, orthology, gap-filling, and manual curation [87] of the sequenced genome based on a large set of databases and toolboxes (KEGG [88], MetaCyc [89], BiGG [90], Pathway Tools [91], CarveMe [92], KBase [93] and AuReMe [94]). While models of the human gut microbiota already incorporate microbial genomic knowledge [95], genome-scale modelling of the rumen microbiota is at an infant stage [96, 97]. Recently, the GEM approach was used to investigate the interactions between dominant rumen microbial species and their associated phages. Individual GEMs of *Ruminococcus flavefaciens*, *Prevotella ruminicola*, and *M. gottschalkii* were constructed and integrated into a community model using multi-level mathematical frameworks [97]. The model predicted previously unknown interactions among the community members and the complementing role of viral genes in these interactions. In addition, the GEM of a rumen bacterium involved in lactate metabolism, *Megasphaera elsdenii*, highlighted the high number of metabolic pathways for the production of VFAs [98, 99]. GEMS are often large networks with thousand metabolites and reactions. For example, our preliminary reconstruction study on *F. succinogenes* S85 (Fakih *et al.* 2021) resulted in a network with 1567 metabolic reactions and 1588 metabolites.

The next generation of rumen models should build on straightened microbial knowledge, but the systemic understanding of microbial interactions and ruminal fermentation is still lacking. Therefore, *in vitro* culture systems (batch and continuous) are valuable tools to study rumen metabolism, despite their limitations to mimic the rumen ecosystem fully. These mini-consortia are suited for constructing tractable mathematical models with identifiable properties (see, e.g., [101] for a discussion on parameter identifiability). For studying the rumen ecosystem, mini-consortia can be built by selecting microbial species covering the major rumen metabolic cascades [3, 16]. Species selection can be performed from microbial expert knowledge or synthetic ecology approaches targeting specific metabolic functions or microbial interactions [102, 103].

Moreover, species selection can be performed using Metage2Metabo (M2M) [96]. M2M identifies mini-consortia by reconstructing draft GEMs of all members of a microbial community, followed by the identification of the individual and community metabolic potentials, the determination of the cooperation potential (set of metabolites whose production only occur via microbial cooperation), and finally, outputs minimal communities and identifies key species. The originality of M2M is its capability for handling hundreds of genomes and MAGs. M2M was applied to 913 rumen MAGs of the cow rumen [59] and highlighted 127 key species, consisting of 20 essential symbionts and 107 alternative ones [96].

The construction of metabolic networks of key rumen species is an excellent resource for studying the rumen microbial ecosystem via constraint-based reconstruction and analysis (COBRA) methods. COBRA approaches overcome the need to define kinetic rates and their parameters by assuming that internal metabolism operates at steady-state conditions. Genome information and COBRA methods provide analytical tools for (1) assisting the design of cultivation media allowing the study of uncultured gut bacteria [52], (2) designing strategies targeting the inhibition of methanogens in genome-sequenced rumen microbes such as *M. ruminantium* [104], (3) selecting probiotics to enhance rumen function and (4) enhancing our understanding on the robustness of the rumen ecosystem linked to its resilience and functional redundancy [105].

Modelling the rumen microbial ecosystem shares similar challenges to those discussed by [95] and [103] to model human gut microbiota. GEMS are often large networks with thousand metabolites and reactions. Model reductions are needed to construct dynamic parsimonious metabolic models of key rumen microbes within mini-consortia. Individual GEMs can be reduced using dedicated algorithms [106, 107] and exploit transcriptomic data to select active pathways. Reduced GEMs can be further decomposed into their elementary flux modes (EFMs) [108]to derive macroscopic reactions of the rumen fermentation, as it has been in studies on microalgae and yeast metabolism [109, 110]. Rumen modelling can then capitalize on the advances done in other ecosystems (e.g., human gut, engineering reactors). Finally, interdisciplinary research is paramount to get the most out of metabolic models and culture systems, implying rumen microbiologists, computational biologists, and mathematical modellers.

Conclusion

Advances in next-generation sequencing technologies coupled with sophisticated metagenomics and phylogenetic methodologies have radically altered our perceptions of microbial diversity. However, our inability to cultivate representatives for many newly identified lineages contrasts with the rapid expansion of genomic data, which has led to a better knowledge of archaeal and bacterial diversity and metabolic requirements. As a result, most of what we now know about rumen microbes comes from a small number of well-studied cultured lineages or reconstructed genomes from uncultured lineages. Even though this period of rapid genome-driven discovery has yielded numerous critical new insights into rumen microbial life, it is critical to isolate and culture species from these uncultured lineages to test genome-based predictions about their cell biology and physiology to comprehend their ecological roles fully.

Acknowledgements

Ibrahim Fakih was the recipient of an INRAE-Lallemand PhD fellowship. The INRAE part of the fellowship was supported by the INRAE metaprogramme Holoflux.

References

1. Hungate RE. The rumen bacteria. In: Hungate RE, editor. The Rumen and its Microbes: Academic Press; 1966. p. 8-90.
2. Hungate RE. The rumen protozoa. In: Hungate RE, editor. The Rumen and its Microbes: Academic Press; 1966. p. 91-147.
3. Seshadri R, Leahy SC, Attwood GT, Teh KH, Lambie SC, Cookson AL, et al. Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. Nature Biotechnology 2018;36(4):359-67.
4. Creevey CJ, Kelly WJ, Henderson G, Leahy SC. Determining the culturability of the rumen bacterial microbiome. Microbial Biotechnology 2014;7(5):467-79.
5. Henderson G, Cox F, Ganesh S, Jonker A, Young W, Global Rumen Census C, et al. Rumen microbial community composition varies with diet and host, but a core microbiome is found across a wide geographical range. Scientific Reports 2015;5:14567.
6. Wallace RJ, Snelling TJ, McCartney CA, Tapio I, Strozzi F. Application of meta-omics techniques to understand greenhouse gas emissions originating from ruminal metabolism. Genetics Selection Evolution 2017;49(1):9.
7. Tapio I, Snelling TJ, Strozzi F, Wallace RJ. The ruminal microbiome associated with methane emissions from ruminant livestock. Journal of Animal Science and Biotechnology 2017;8(1):7.
8. Huws SA, Creevey CJ, Oyama LB, Mizrahi I, Denman SE, Popova M, et al. Addressing global ruminant agricultural challenges through understanding the rumen microbiome: past, present, and future. Frontiers in microbiology 2018;9:2161.

9. Morgavi DP, Forano E, Martin C, Newbold CJ. Microbial ecosystem and methanogenesis in ruminants. animal 2010;4(7):1024-36.

10. Morgavi DP, Popova M, Yáñez-Ruiz DR, Forano E. Colonization and establishment of the rumen microbiota opportunities to influence productivity and methane emissions. In: McSweeney CS, Mackie RI, editors. Improving rumen function: Burleigh Dodds Science Publishing Limited; 2020. p. 862.

11. Mizrahi I, Wallace RJ, Moraïs S. The rumen microbiome: balancing food security and environmental impacts. Nature Reviews Microbiology 2021;19(9):553-66.

12. Xie F, Jin W, Si H, Yuan Y, Tao Y, Liu J, et al. An integrated gene catalog and over 10,000 metagenome-assembled genomes from the gastrointestinal microbiome of ruminants. Microbiome 2021;9(1):137.

13. Bryant MP. Bacterial species of the rumen. Bacteriol Rev 1959;23(3):125-53.

14. Hungate RE, P BM, A MR. The rumen bacteria and protozoa. Annual Review of Microbiology 1964;18(1):131-66.

15. Hungate RE. Ruminant functions related to rumen microbial activity. In: Hungate RE, editor. The Rumen and its Microbes: Academic Press; 1966. p. 148-205.

16. Moraïs S, Mizrahi I. The road not taken: the rumen microbiome, functional groups, and community states. Trends in Microbiology 2019;27(6):538-49.

17. Hungate RE. The anaerobic mesophilic cellulolytic bacteria. Bacteriol Rev 1950;14(1):1-49.

18. Williams MG, Busta FF. Total viable counts | Most Probable Number (MPN). In: Robinson RK, editor. Encyclopedia of Food Microbiology. Oxford: Elsevier; 1999. p. 2166-8.

19. Hungate RE. A roll tube method for cultivation of strict anaerobes. In: Norris JR, Ribbons DW, editors. Methods in Microbiology. 3: Academic Press; 1969. p. 117-32.

20. Neumann AP, Suen G, Rodrigues JM. The phylogenomic diversity of herbivore-associated *Fibrobacter* spp. is correlated to lignocellulose-degrading potential. mSphere 2018;3(6):e00593-18.

21. Malburg Jr LM, Forsberg CW. Fibrobacter succinogenes S85 possesses at least nine distinct glucanase genes. Canadian journal of microbiology 1993;39(9):882-91.

22. Jun HS, Ha JK, Malburg J, Laercio M, Verrinder Gibbins AM, Forsberg CW. Characteristics of a cluster of xylanase genes in Fibrobacter succinogenes S85. Canadian journal of microbiology 2003;49(3):171-80.

23. Béra-Maillet C, Ribot Y, Forano E. Fiber-degrading systems of different strains of the genus Fibrobacter. Applied and Environmental Microbiology 2004;70(4):2172-9.

24. Neumann AP, McCormick CA, Suen G. Fibrobacter communities in the gastrointestinal tracts of diverse hindgut-fermenting herbivores are distinct from those of the rumen. Environmental Microbiology 2017;19(9):3768-83.

25. Dehority BA. Microbial ecology of cell wall fermentation. In: Jung HG, Buxton DR, Hatfield RD, Ralph J, editors. Forage Cell Wall Structure and Digestibility: American Society of Agronomy; 1993. p. 425-53.

26. Yeoman CJ, Fields CJ, Lepercq P, Ruiz P, Forano E, White BA, et al. *In vivo* competitions between Fibrobacter succinogenes, Ruminococcus flavefaciens, and Ruminoccus albus in a gnotobiotic sheep model revealed by multi-omic analyses. mBio 2021;12(2):e03533-20.

27. Zehavi T, Probst M, Mizrahi I. Insights into culturomics of the rumen microbiome. Frontiers in microbiology 2018;9(1999).

28. Denman SE, Morgavi DP, McSweeney CS. Review: The application of omics to rumen microbiota function. animal 2018;12:s233-s45.

29. McGovern E, Waters SM, Blackshields G, McCabe MS. Evaluating established methods for rumen 16S rRNA amplicon sequencing with mock microbial populations. Frontiers in microbiology 2018;9:1365-.

30. Henderson G, Yilmaz P, Kumar S, Forster RJ, Kelly WJ, Leahy SC, et al. Improved taxonomic assignment of rumen bacterial 16S rRNA sequences using a revised SILVA taxonomic framework. PeerJ 2019;7:e6496.

31. Smith PE, Waters SM, Gómez Expósito R, Smidt H, Carberry CA, McCabe MS. Synthetic sequencing standards: a guide to database choice for rumen microbiota amplicon sequencing analysis. Frontiers in microbiology 2020;11:606825-.

32. Caporaso JG, Lauber CL, Walters WA, Berg-Lyons D, Lozupone CA, Turnbaugh PJ, et al. Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. Proceedings of the national academy of sciences 2011;108(Supplement 1):4516-22.

33. Kim M, Morrison M, Yu Z. Status of the phylogenetic diversity census of ruminal microbiomes. FEMS Microbiology Ecology 2011;76(1):49-63.

34. Wang Y, Youssef NH, Couger MB, Hanafy RA, Elshahed MS, Stajich JE, et al. Molecular Dating of the Emergence of Anaerobic Rumen Fungi and the Impact of Laterally Acquired Genes. mSystems 2019;4(4):e00247-19.

35. Hess M, Paul SS, Puniya AK, van der Giezen M, Shaw C, Edwards JE, et al. Anaerobic Fungi: Past, Present, and Future. Frontiers in microbiology 2020;11.

36. Kittelmann S, Naylor GE, Koolaard JP, Janssen PH. A proposed taxonomy of anaerobic fungi (class neocallimastigomycetes) suitable for large-scale sequence-based community structure analysis. PLOS ONE 2012;7(5):e36866.

37. Kittelmann S, Seedorf H, Walters WA, Clemente JC, Knight R, Gordon JI, et al. Simultaneous amplicon sequencing to explore co-occurrence patterns of bacterial, archaeal and eukaryotic microorganisms in rumen microbial communities. PLOS ONE 2013;8(2):e47879.

38. Callaghan TM, Podmirseg SM, Hohlweck D, Edwards JE, Puniya AK, Dagar SS, et al. Buwchfawromyces eastonii gen. nov., sp. nov.: a new anaerobic fungus (Neocallimastigomycota) isolated from buffalo faeces. MycoKeys 2015;9:11-28.

39. Edwards JE, Hermes GDA, Kittelmann S, Nijsse B, Smidt H. Assessment of the accuracy of high-throughput sequencing of the ITS1 region of Neocallimastigomycota for community composition analysis. Frontiers in microbiology 2019;10:2370.

40. Hess M, Paul SS, Puniya AK, van der Giezen M, Shaw C, Edwards JE, et al. Anaerobic fungi: past, present, and future. Frontiers in microbiology 2020;11:584893-.

41. Wallace RJ, Sasson G, Garnsworthy PC, Tapio I, Gregson E, Bani P, et al. A heritable subset of the core rumen microbiome dictates dairy cow productivity and emissions. Science Advances 2019;5(7):eaav8391.

42. Buitenhuis B, Lassen J, Noel SJ, Plichta DR, Sørensen P, Difford GF, et al. Impact of the rumen microbiome on milk fatty acid composition of Holstein cattle. Genetics Selection Evolution 2019;51(1):23.

43. Jami E, White BA, Mizrahi I. Potential role of the bovine rumen microbiome in modulating milk composition and feed efficiency. PLOS ONE 2014;9(1):e85423.

44. Kittelmann S, Pinares-Patiño CS, Seedorf H, Kirk MR, Ganesh S, McEwan JC, et al. Two different bacterial community types are linked with the low-methane emission trait in sheep. PLOS ONE 2014;9(7):e103171.

45. Danielsson R, Dicksved J, Sun L, Gonda H, Müller B, Schnürer A, et al. Methane production in dairy cows correlates with rumen methanogenic and bacterial community structure. Frontiers in microbiology 2017;8.

46. Ramayo-Caldas Y, Zingaretti L, Popova M, Estelle J, Bernard A, Pons N, et al. Identification of rumen microbial biomarkers linked to methane emission in Holstein dairy cows. Journal of Animal Breeding and Genetics 2020;137(1):49-59.

47. Huang S, Ji S, Suen G, Wang F, Li S. The rumen bacterial community in dairy cows is correlated to production traits during freshening period. Frontiers in microbiology 2021;12:630605-.

48. Li F, Li C, Chen Y, Liu J, Zhang C, Irving B, et al. Host genetics influence the rumen microbiota and heritable rumen microbial features associate with feed efficiency in cattle. Microbiome 2019;7(1):92.

49. Xue MY, Sun HZ, Wu XH, Guan LL, Liu JX. Assessment of rumen bacteria in dairy cows with varied milk protein yield. Journal of Dairy Science 2019;102(6):5031-41.

50. Li F, Henderson G, Sun X, Cox F, Janssen PH, Guan LL. Taxonomic assessment of rumen microbiota using total RNA and targeted amplicon sequencing approaches. Frontiers in microbiology 2016;7:987.

51. Bryant MP, Small N. Characteristics of two new genera of anaerobic curved rods isolated from the rumen of cattle. Journal of bacteriology 1956;72(1):22-6.

52. Pope PB, Smith W, Denman SE, Tringe SG, Barry K, Hugenholtz P, et al. Isolation of Succinivibrionaceae implicated in low methane emissions from tammar wallabies. Science 2011;333(6042):646-8.

53. Tessler M, Neumann JS, Afshinnekoo E, Pineda M, Hersch R, Velho LFM, et al. Large-scale differences in microbial biodiversity discovery between 16S amplicon and shotgun sequencing. Scientific Reports 2017;7(1):6589.

54. Yang C, Chowdhury D, Zhang Z, Cheung WK, Lu A, Bian Z, et al. A review of computational tools for generating metagenome-assembled genomes from metagenomic sequencing data. Computational and Structural Biotechnology Journal 2021;19:6301-14.

55. Hess M, Sczyrba A, Egan R, Kim TW, Chokhawala H, Schroth G, et al. Metagenomic discovery of biomass-degrading genes and genomes from cow rumen. Science 2011;331(6016):463-7.

56. Parks DH, Rinke C, Chuvochina M, Chaumeil P-A, Woodcroft BJ, Evans PN, et al. Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life. Nature microbiology 2017;2(11):1533-42.

57. Svartström O, Alneberg J, Terrapon N, Lombard V, de Bruijn I, Malmsten J, et al. Ninety-nine de novo assembled genomes from the moose (Alces alces) rumen microbiome provide new insights into microbial plant biomass degradation. The ISME Journal 2017;11(11):2538-51.

58. Solden LM, Naas AE, Roux S, Daly RA, Collins WB, Nicora CD, et al. Interspecies cross-feeding orchestrates carbon degradation in the rumen ecosystem. Nature microbiology 2018;3(11):1274-84.

59. Stewart RD, Auffret MD, Warr A, Wiser AH, Press MO, Langford KW, et al. Assembly of 913 microbial genomes from metagenomic sequencing of the cow rumen. Nature Communications 2018;9(1):870.

60. Stewart RD, Auffret MD, Warr A, Walker AW, Roehe R, Watson M. Compendium of 4,941 rumen metagenome-assembled genomes for rumen microbiome biology and enzyme discovery. Nature Biotechnology 2019;37(8):953-61.

61. Li J, Zhong H, Ramayo-Caldas Y, Terrapon N, Lombard V, Potocki-Veronese G, et al. A catalog of microbial genes from the bovine rumen unveils a specialized and diverse biomass-degrading environment. GigaScience 2020;9(6).

62. Wilkinson T, Korir D, Ogugo M, Stewart RD, Watson M, Paxton E, et al. 1200 high-quality metagenome-assembled genomes from the rumen of African cattle and their relevance in the context of sub-optimal feeding. Genome biology 2020;21(1):1-25.

63. Glendinning L, Genç B, Wallace RJ, Watson M. Metagenomic analysis of the cow, sheep, reindeer and red deer rumen. Scientific Reports 2021;11(1):1-10.

64. Anderson CL, Fernando SC. Insights into rumen microbial biosynthetic gene cluster diversity through genome-resolved metagenomics. Communications Biology 2021;4(1):818.

65. Tong F, Wang T, Gao NL, Liu Z, Cui K, Duan Y, et al. The microbiome of the buffalo digestive tract. Nature Communications 2022;13(1):823.

66. Peng X, Wilken SE, Lankiewicz TS, Gilmore SP, Brown JL, Henske JK, et al. Genomic and functional analyses of fungal and bacterial consortia that enable lignocellulose breakdown in goat gut microbiomes. Nature microbiology 2021;6(4):499-511.

67. Watson M. New insights from 33,813 publicly available metagenome-assembled-genomes (MAGs) assembled from the rumen microbiome. bioRxiv 2021:2021.04.02.438222.

68. Pedros-Alio C. Marine microbial diversity: can it be determined? Trends in Microbiology 2006;14(6):257-63.

69. Meziti A, Rodriguez-R LM, Hatt JK, Peña-Gonzalez A, Levy K, Konstantinidis KT. The reliability of metagenome-assembled genomes (MAGs) in representing natural populations: insights from comparing MAGs against isolate genomes derived from the same fecal sample. Applied and Environmental Microbiology 2021;87(6):e02593-20.

70. Soverini M, Rampelli S, Turroni S, Brigidi P, Biagi E, Candela M. Do the human gut metagenomic species possess the minimal set of core functionalities necessary for life? BMC Genomics 2020;21(1):678.

71. Li Z, Wang X, Zhang Y, Yu Z, Zhang T, Dai X, et al. Genomic insights into the phylogeny and biomass-degrading enzymes of rumen ciliates. bioRxiv 2022:2022.01.05.474053.

72. Tedeschi LO, Ramirez-Restrepo CA, Muir JP. Developing a conceptual model of possible benefits of condensed tannins for ruminant production. animal 2014;8(7):1095-105.

73. Baldwin RL, Thornley JH, Beever DE. Metabolism of the lactating cow. II. Digestive elements of a mechanistic model. Journal of Dairy Research 1987;54(1):107-31.

74. Russell JB, O'Connor JD, Fox DG, Van Soest PJ, Sniffen CJ. A net carbohydrate and protein system for evaluating cattle diets: I. Ruminal fermentation. Journal of Animal Science 1992;70(11):3551-61.

75. Dijkstra J, Neal HD, Beever DE, France J. Simulation of nutrient digestion, absorption and outflow in the rumen: model description. The Journal of Nutrition 1992;122(11):2239-56.

76. Danfær AC, Huhtanen P, Udén P, Sveinbjörnsson J, Volden H, Kebreab E, et al. The Nordic dairy cow model, Karoline - description. In: Kebreab E, Dijkstra J, Bannink A, Gerrits WJJ, France J, editors. Nutrient digestion and utilization in farm animals: modelling approaches. : CAB eBooks; 2006.

77. Kass M, Ramin M, Hanigan MD, Huhtanen P. Comparison of Molly and Karoline models to predict methane production in growing and dairy cattle. Journal of Dairy Science 2022.

78. Bannink A, van Lingen HJ, Ellis JL, France J, Dijkstra J. The contribution of mathematical modeling to understanding dynamic aspects of rumen metabolism. Frontiers in microbiology 2016;7:1820-.

79. Ellis JL, Dijkstra J, Kebreab E, Bannink A, Odongo NE, McBride BW, et al. Aspects of rumen microbiology central to mechanistic modelling of methane production in cattle. The Journal of Agricultural Science 2008;146(2):213-33.

80. Muñoz-Tamayo R, Giger-Reverdin S, Sauvant D. Mechanistic modelling of in vitro fermentation and methane production by rumen microbiota. Animal Feed Science and Technology 2016;220:1-21.

81. Janssen PH. Influence of hydrogen on rumen methane formation and fermentation balances through microbial growth kinetics and fermentation thermodynamics. Animal Feed Science and Technology 2010;160(1):1-22.

82. Muñoz-Tamayo R, Chagas JC, Ramin M, Krizsan SJ. Modelling the impact of the macroalgae *Asparagopsis taxiformis* on rumen microbial fermentation and methane production. Peer Community Journal 2021;1.

83. Ungerfeld EM. Metabolic hydrogen flows in rumen fermentation: principles and possibilities of interventions. Frontiers in microbiology 2020;11(589).

84. van Lingen HJ, Fadel JG, Moraes LE, Bannink A, Dijkstra J. Bayesian mechanistic modeling of thermodynamically controlled volatile fatty acid, hydrogen and methane production in the bovine rumen. Journal of Theoretical Biology 2019;480:150-65.

85. van Lingen HJ, Fadel JG, Yáñez-Ruiz DR, Kindermann M, Kebreab E. Inhibited methanogenesis in the rumen of cattle: microbial metabolism in response to supplemental 3-nitrooxypropanol and nitrate. Frontiers in microbiology 2021;12:705613.

86. Muñoz-Tamayo R, Popova M, Tillier M, Morgavi DP, Morel J-P, Fonty G, et al. Hydrogenotrophic methanogens of the mammalian gut: Functionally similar, thermodynamically different—A modelling approach. PLOS ONE 2019;14(12):e0226243.

87. Thiele I, Palsson BØ. A protocol for generating a high-quality genome-scale metabolic reconstruction. Nature Protocols 2010;5(1):93-121.

88. Ogata H, Goto S, Sato K, Fujibuchi W, Bono H, Kanehisa M. KEGG: Kyoto Encyclopedia of Genes and Genomes. Nucleic Acids Research 1999;27(1):29-34.

89. Caspi R, Billington R, Ferrer L, Foerster H, Fulcher CA, Keseler IM, et al. The MetaCyc database of metabolic pathways and enzymes and the BioCyc collection of pathway/genome databases. Nucleic Acids Research 2015;44(D1):D471-D80.

90. King ZA, Lu J, Dräger A, Miller P, Federowicz S, Lerman JA, et al. BiGG Models: A platform for integrating, standardizing and sharing genome-scale models. Nucleic Acids Research 2015;44(D1):D515-D22.

91. Karp PD, Paley S, Romero P. The Pathway Tools software. Bioinformatics (Oxford, England) 2002;18(suppl_1):S225-S32.

92. Machado D, Andrejev S, Tramontano M, Patil KR. Fast automated reconstruction of genome-scale metabolic models for microbial species and communities. Nucleic Acids Research 2018;46(15):7542-53.

93. Arkin AP, Cottingham RW, Henry CS, Harris NL, Stevens RL, Maslov S, et al. KBase: The United States department of energy systems biology knowledgebase. Nature Biotechnology 2018;36(7):566-9.

94. Aite M, Chevallier M, Frioux C, Trottier C, Got J, Cortés MP, et al. Traceability, reproducibility and wiki-exploration for “à-la-carte” reconstructions of genome-scale metabolic models. PLOS Computational Biology 2018;14(5):e1006146.

95. Kumar M, Ji B, Zengler K, Nielsen J. Modelling approaches for studying the microbiome. Nature microbiology 2019;4(8):1253-67.

96. Belcour A, Frioux C, Aite M, Bretaudeau A, Hildebrand F, Siegel A. Metage2Metabo, microbiota-scale metabolic complementarity for the identification of key species. eLife 2020;9:e61968.

97. Islam MM, Fernando SC, Saha R. Metabolic modeling elucidates the transactions in the rumen microbiome and the shifts upon virome interactions. Frontiers in microbiology 2019;10.

98. Lee N-R, Lee CH, Lee D-Y, Park J-B. Genome-scale metabolic network reconstruction and in silico analysis of hexanoic acid producing Megasphaera elsdenii. Microorganisms 2020;8(4):539.

99. Panikov NS. True and illusory benefits of modeling: comment on “Genome-scale metabolic network reconstruction and in silico analysis of hexanoic acid producing Megasphaera elsdenii. Microorganisms 2020, 8, 539”. Microorganisms 2020;8(11):1742.

100. Fakih I, Got J, Siegel A, Forano E, Munoz Tamayo R. Genome-scale network reconstruction of the predominant cellulolytic rumen bacterium Fibrobacter succinogenes S85. 2021 - 12th International Symposium on Gut Microbiology; 2021-10-13; Virtual, France2021.

101. Muñoz-Tamayo R, Puillet L, Daniel JB, Sauvant D, Martin O, Taghipoor M, et al. Review: To be or not to be an identifiable model. Is this a relevant question in animal science modelling? animal 2018;12(4):701-12.

102. Freilich S, Kreimer A, Meilijson I, Gophna U, Sharan R, Ruppin E. The large-scale organization of the bacterial network of ecological co-occurrence interactions. Nucleic Acids Research 2010;38(12):3857-68.

103. Vrancken G, Gregory AC, Huys GRB, Faust K, Raes J. Synthetic ecology of the human gut microbiota. Nature Reviews Microbiology 2019;17(12):754-63.

104. Leahy SC, Kelly WJ, Altermann E, Ronimus RS, Yeoman CJ, Pacheco DM, et al. The genome sequence of the rumen methanogen Methanobrevibacter ruminantium reveals new possibilities for controlling ruminant methane emissions. PLOS ONE 2010;5(1):e8926.

105. Weimer PJ. Redundancy, resilience, and host specificity of the ruminal microbiota: implications for engineering improved ruminal fermentations. Frontiers in microbiology 2015;6.

106. Erdrich P, Steuer R, Klamt S. An algorithm for the reduction of genome-scale metabolic network models to meaningful core models. BMC Systems Biology 2015;9(1):48.

107. Röhl A, Bockmayr A. A mixed-integer linear programming approach to the reduction of genome-scale metabolic networks. BMC Bioinformatics 2017;18(1):2.

108. Schuster S, Hilgetag C. On elementary flux modes in biochemical reaction systems at steady state. Journal of Biological Systems 1994;2(02):-.

109. Baroukh C, Muñoz-Tamayo R, Steyer J-P, Bernard O. DRUM: a new framework for metabolic modeling under non-balanced growth. Application to the carbon metabolism of unicellular microalgae. PLOS ONE 2014;9(8):e104499.

110. Robles-Rodriguez CE, Bideaux C, Guillouet SE, Gorret N, Cescut J, Uribelarrea J-L, et al. Dynamic metabolic modeling of lipid accumulation and citric acid production by Yarrowia lipolytica. Computers & Chemical Engineering 2017;100:139-52.

Table 1 Studies found in Web of Science with research terms “rumen” and isolates, spanning the period 1947-2022, reporting at least one new microbial isolate characterized phenotypically or phylogenetically

Authors	Article title	Source Title	ISSN	Publication Year	DOI	Date of Export
Bryant, MP; Doetsch, RN	A Study of Actively Cellulolytic Rod-Shaped Bacteria of the Bovine Rumen	J DAIRY SCI	0022-0302	1954		3/1/2022
Bauman, HE; Foster, EM	CHARACTERISTICS OF ORGANISMS ISOLATED FROM THE RUMEN OF COWS FED HIGH AND LOW ROUGHAGE RATIONS	J BACTERIOL	0021-9193	1956	10.1128/JB.71.3.333-338.1956	3/1/2022
Bryant, MP	The characteristics of strains of selenomonas isolated from bovine rumen contents	J BACTERIOL	0021-9193	1956	10.1128/JB.72.2.162-167.1956	3/1/2022
Bryant, MP; Small, N	Characteristics of 2 new genera of anaerobic curved rods isolated from the rumen of cattle	J BACTERIOL	0021-9193	1956	10.1128/JB.72.1.22-26.1956	3/1/2022
Ford, JE; Perry, KD; Briggs, CAE	Nutrition of lactic acid bacteria isolated from the rumen	J GEN MICROBIOL	0022-1287	1958	10.1099/00221287-18-1-273	3/1/2022
Hunt, WG; Moore, RO	The proteolytic system of a gram negative rod isolated from the bovine rumen	APPL MICROBIOL	0003-6919	1958	10.1128/AEM.6.1.36-39.1958	3/1/2022
Dehority, BA	Degradation and utilization of isolated hemicellulose BY pure cultures of cellulolytic rumen bacteria	J BACTERIOL	0021-9193	1965	10.1128/JB.89.6.1515-1520.1965	3/1/2022
Dehority, BA	Characterization of several bovine rumen bacteria isolated with a xylan medium	J BACTERIOL	0021-9193	1966	10.1128/JB.91.5.1724-1729.1966	3/1/2022
Paynter, MJB; Hungate, RE	Characterization of methanobacterium mobilis SP n isolated from bovine rumen	J BACTERIOL	0021-9193	1968	10.1128/JB.95.5.1943-1951.1968	3/1/2022
Brewer, D; Taylor, A	Aspergillus-fumigatus and sporormia-minima isolated from rumen of sheep	J GEN MICROBIOL	0022-1287	1969	10.1099/00221287-59-1-137	3/1/2022
Dehority, BA	Pectin-fermenting bacteria isolated from bovine rumen	J BACTERIOL	0021-9193	1969	10.1128/JB.99.1.189-196.1969	3/1/2022
Slyter, LL; Weaver, JM	Growth factor requirements of ruminococcus flavefaciens isolated from rumen of cattle fed purified diets	APPL MICROBIOL	0003-6919	1969	10.1128/AEM.17.5.737-741.1969	3/1/2022
Henderson, C	Improved method for enumerating and isolating lipolytic rumen bacteria	J APPL BACTERIOL	0021-8847	1973	10.1111/j.1365-2672.1973.tb04088.x	3/1/2022

Sharpe, ME; Latham, MJ; Garvie, EI; Zirngibl, J; Kandler, O	2 new species of lactobacillus isolated from bovine rumen, lactobacillus-ruminis SP-nov and lactobacillus-vitulinus SP-nov	J GEN MICROBIOL	0022-1287	1973	10.1099/00221287-77-1-37	3/1/2022
Coleman, GS; Laurie, JI	Metabolism of starch, glucose, amino-acids, purines, pyrimidines and bacteria BY 3 epidinium spp isolated from rumen	J GEN MICROBIOL	0022-1287	1974	10.1099/00221287-85-2-244	3/1/2022
Huisingh, J; Mcneill, JJ; Matrone, G	Sulfate reduction BY a desulfovibrio-species isolated from sheep rumen	APPL MICROBIOL	0003-6919	1974	10.1128/AEM.28.3.489-497.1974	3/1/2022
Kemp, P; White, RW; Lander, DJ	Hydrogenation of unsaturated fatty-acids BY 5 bacterial isolates from sheep rumen, including a new species	J GEN MICROBIOL	0022-1287	1975	10.1099/00221287-90-1-100	3/1/2022
Coleman, GS; Laurie, JI; Bailey, JE; Holdgate, SA	Cultivation of cellulolytic protozoa isolated from rumen	J GEN MICROBIOL	0022-1287	1976	10.1099/00221287-95-1-144	3/1/2022
Hayashi, T; Kitahara, K	Effect of carbon-dioxide and oxygen on growth of orange-colored streptococcus-bovis isolated from bovine rumen	J GEN APPL MICROBIOL	0022-1260	1976	10.2323/jgam.22.301	3/1/2022
Tarakanov, BV	Biological characteristics of streptococcus-bovis bacteriophages isolated from lysogenic cultures and sheep rumen	MICROBIOLOGY	0026-2617	1976		3/1/2022
Williams, AG; Harfoot, CG	Factors affecting uptake and metabolism of soluble carbohydrates BY rumen ciliate dasytricha-ruminantium isolated from ovine rumen contents BY filtration	J GEN MICROBIOL	0022-1287	1976	10.1099/00221287-96-1-125	3/1/2022
Minato, H; Suto, T	Technique for fractionation of bacteria in rumen microbial ecosystem .2. Attachment of bacteria isolated from bovine rumen to cellulose powder invitro and elution of bacteria attached therefrom	J GEN APPL MICROBIOL	0022-1260	1978	10.2323/jgam.24.1	3/1/2022
Hazlewood, G; Dawson, RMC	Characteristics of a lipolytic and fatty acid requiring butyrivibrio SP isolated from the ovine rumen	J GEN MICROBIOL	0022-1287	1979	10.1099/00221287-112-1-15	3/1/2022
Ledford, RA; Brown, JM	Characterization of group-n and group-d streptococci isolated from rumen fluids	J DAIRY SCI	0022-0302	1979	10.3168/jds.S0022-0302(79)83245-2	3/1/2022
Minato, H; Suto, T	Technique for fractionation of bacteria in rumen microbial ecosystem .3. Attachment of bacteria isolated from bovine rumen to starch granules invitro and elution of bacteria attached therefrom	J GEN APPL MICROBIOL	0022-1260	1979	10.2323/jgam.25.71	3/1/2022
Stevenson, IL	Effect of l-alpha-amino-normal-butyric acid on growth and production of extracellular isoleucine and valine BY eubacterium-ruminantium and a related rumen isolate	CAN J MICROBIOL	0008-4166	1979	10.1139/m79-218	3/1/2022

Wojciechowicz, M; Heinrichova, K; Ziolecki, A	Polygalacturonate lyase produced BY lachnospira-multiparus isolated from the bovine rumen	J GEN MICROBIOL	0022-1287	1980	10.1099/00221287-117-1-193	3/1/2022
C S Stewart, C Paniagua, D Dinsdale, K J Cheng, And S H Garrow	Selective isolation and characteristics of Bacteriodes succinogenes from the rumen of a cow.	APPL ENVIRON MICROB	0099-2240	1981		3/1/2022
Williams, AG; Withers, SE	Bacillus spp in the rumen ecosystem - hemicellulose depolymerases and glycoside hydrolases of bacillus spp and rumen isolates grown under anaerobic conditions	J APPL BACTERIOL	0021-8847	1983	10.1111/j.1365-2672.1983.tb01325.x	3/1/2022
Miller, TL; Wolin, MJ; Hongxue, Z; Bryant, MP	Characteristics of methanogens isolated from bovine rumen	APPL ENVIRON MICROB	0099-2240	1986	10.1128/AEM.51.1.201-202.1986	3/1/2022
Fonty, G; Breton, A; Fevre, M; Citron, A; Hebraud, M; Gouet, P	Characterization of strictly anaerobic fungi isolated from the rumen of sheep - preliminary data	REPROD NUTR DEV	0926-5287	1987	10.1051/rnd:19870229	3/1/2022
Stewart, CS; Duncan, SH; Flint, HJ	Characteristics of isolates of lactobacillus-fermentum from the rumen of sheep	LETT APPL MICROBIOL	0266-8254	1988	10.1111/j.1472-765X.1988.tb01232.x	3/1/2022
Kostyukovskii, VA; Okunev, ON; Tarakanov, BV	Anaerobic cellulolytic fungi from cattle rumen	MICROBIOLOGY	0026-2617	1990		3/1/2022
Biavati, B; Mattarelli, P	Bifidobacterium-ruminantium SP-nov and bifidobacterium-merycicum SP-nov from the rumens of cattle	INT J SYST BACTERIOL	0020-7713	1991	10.1099/00207713-41-1-163	3/1/2022
Dominguezbello, MG; Stewart, CS	Characteristics of a rumen clostridium capable of degrading mimosine, 3(oh)-4-(1h)-pyridone and 2,3-dihydroxypyridine	SYST APPL MICROBIOL	0723-2020	1991	10.1016/S0723-2020(11)80363-2	3/1/2022
Galindo, J; Elias, A; Menchaca, MA; Piedra, R	Identification of isolated gram cellulolytic bacillus in the rumen of cows consuming silage	CUBAN J AGR SCI	0864-0408	1991		3/1/2022
Galindo, J; Elias, A; Piedra, R; Cordero, J; Menchaca, M; Riveri, Z; Boucourt, R; Elizarde, S	Identification of gram + cellulolytic coccus strains isolated from the rumen of cows consuming poor quality silage	CUBAN J AGR SCI	0864-0408	1991		3/1/2022
Ho, YW; Bauchop, T	Morphology of 3 polycentric rumen fungi and description of a procedure for the induction of zoosporogenesis and release of zoospores in cultures	J GEN MICROBIOL	0022-1287	1991	10.1099/00221287-137-1-213	3/1/2022
Klieve, AV; Bauchop, T	Phage resistance and altered growth habit in a strain of streptococcus-bovis	FEMS MICROBIOL LETT	0378-1097	1991		3/1/2022
Kostyukovsky, VA; Okunev, ON; Tarakanov, BV	Description of 2 anaerobic fungal strains from the bovine rumen and influence of diet on the fungal population invivo	J GEN MICROBIOL	0022-1287	1991	10.1099/00221287-137-7-1759	3/1/2022
Larsen, M; Wolstrup, J; Henriksen, SA; Dackman, C; Gronvold, J; Nansen, P	Invitro stress selection of nematophagous fungi for biocontrol of parasitic nematodes in ruminants	J HELMINTHOL	0022-149X	1991	10.1017/S0022149X00010701	3/1/2022

Mukhopadhyay, B; Purwantini, E; Demacario, EC; Daniels, L	Characterization of a methanosarcina strain isolated from goat feces, and that grows on h2-co2 only after adaptation	CURR MICROBIOL	0343-8651	1991	10.1007/BF02091977	3/1/2022
Ning, Z; Attwood, GT; Lockington, RA; Brooker, JD	Genetic diversity in ruminal isolates of selenomonas-ruminantium	CURR MICROBIOL	0343-8651	1991	10.1007/BF02091955	3/1/2022
Stevani, J; Grivet, JP; Hannequart, G; Durand, M	Glucose and lactate catabolism BY bacteria of the pig large-intestine and sheep rumen as assessed BY c-13 nuclear-magnetic-resonance	J APPL BACTERIOL	0021-8847	1991	10.1111/j.1365-2672.1991.tb03827.x	3/1/2022
Styriak, I; Galfi, P; Kmet, V	Preliminary-observations of interaction between bacteriophages and streptococcus-bovis bacteria on ruminal epithelium primoculture	VET MICROBIOL	0378-1135	1991	10.1016/0378-1135(91)90135-3	3/1/2022
Teunissen, MJ; Dencamp, Hjmo; Orpin, CG; Veld, Jhjhi; Vogels, GD	Comparison of growth-characteristics of anaerobic fungi isolated from ruminant and non-ruminant herbivores during cultivation in a defined medium	J GEN MICROBIOL	0022-1287	1991	10.1099/00221287-137-6-1401	3/1/2022
Webb, J; Theodorou, MK	Neocallimastix-hurleyensis SP-nov AN anaerobic fungus from the ovine rumen	CAN J BOT	0008-4026	1991	10.1139/b91-156	3/1/2022
Wubah, DA; Fuller, MS; Akin, DE	Isolation of monocentric and polycentric fungi from the rumen and feces of cows in georgia	CAN J BOT	0008-4026	1991	10.1139/b91-158	3/1/2022
A. Ziolecki, Wanda Guczyńska, Maria Wojciechowicz	Rumen bacteria degrading fructan	LETT APPL MICROBIOL	0266-8254	1992		3/1/2022
Allison, MJ; Mayberry, WR; Mcsweeney, CS; Stahl, DA	Synergistes-jonesii, gen-nov, SP-nov - a rumen bacterium that degrades toxic pyridinediols	SYST APPL MICROBIOL	0723-2020	1992	10.1016/S0723-2020(11)80111-6	3/1/2022
Javorsky, P; Vanat, I	Deoxyribonuclease activity in streptococcus-bovis	LETT APPL MICROBIOL	0266-8254	1992	10.1111/j.1472-765X.1992.tb00660.x	3/1/2022
Laukova, A	Biochemical and physiological-properties of enterococci isolated from the rumen of calves	ZIVOCISNA VYROBA	0044-4847	1992		3/1/2022
Laukova, A; Kmet, V	The biochemical and physiological traits of the coagulase negative rumen staphylococci and of those producing bacteriocin	ZIVOCISNA VYROBA	0044-4847	1992		3/1/2022
Laukova, A; Marounek, M	Physiological and biochemical characteristics of staphylococci isolated from the rumen of young calves and lambs	ZBL MIKROBIOL	0232-4393	1992	10.1016/S0232-4393(11)80322-7	3/1/2022
Mckain, N; Wallace, RJ; Watt, ND	Selective isolation of bacteria with dipeptidyl aminopeptidase type-i activity from the sheep rumen	FEMS MICROBIOL LETT	0378-1097	1992		3/1/2022
N Mckain, R J Wallace, N D Watt	Selective isolation of bacteria with dipeptidyl aminopeptidase type I activity from the sheep rumen	FEMS MICROBIOL LETT	0266-8254	1992		3/1/2022

Tabassum, R; Rajoka, MI; Malik, KA	Use of chemostat for enhanced production of beta-glucosidase BY newly isolated anaerobic cellulolytic clostridium strain rt9	APPL BIOCHEM BIOTECH	0273-2289	1992	10.1007/BF02920555	3/1/2022
Wachenheim, DE; Patterson, JA	Anaerobic production of extracellular polysaccharide BY butyrivibrio-fibrisolvens nyx	APPL ENVIRON MICROB	0099-2240	1992	10.1128/AEM.58.1.385-391.1992	3/1/2022
Ziolecki, A; Guczynska, W; Wojciechowicz, M	Some rumen bacteria degrading fructan	LETT APPL MICROBIOL	0266-8254	1992	10.1111/j.1472-765X.1992.tb00774.x	3/1/2022
Fujimoto, K; Kimoto, H; Shishikura, M; Endo, Y; Ogimoto, K	Biohydrogenation of linoleic-acid BY anaerobic-bacteria isolated from rumen	BIOSCI BIOTECH BIOCH	0916-8451	1993	10.1271/bbb.57.1026	3/1/2022
Laukova, A	Enterococci and staphylococci isolates from rumen of fallow deer and their antimicrobial activity	MICROBIOLOGICA	1121-7138	1993		3/1/2022
Laukova, A	The properties of adherent staphylococci isolated from the rumen wall of lambs	VET MED-CZECH	0375-8427	1993		3/1/2022
Laukova, A; Marekova, M; Javorsky, P	Detection and antimicrobial spectrum of a bacteriocin-like substance produced BY enterococcus-faecium ccm4231	LETT APPL MICROBIOL	0266-8254	1993	10.1111/j.1472-765X.1993.tb01413.x	3/1/2022
Brooker, JD; Odonovan, LA; Skene, I; Clarke, K; Blackall, L; Muslera, P	Streptococcus-caprinus SP-nov, a tannin-resistant ruminal bacterium from feral goats	LETT APPL MICROBIOL	0266-8254	1994	10.1111/j.1472-765X.1994.tb00877.x	3/1/2022
Laukova, A	Antimicrobial susceptibility of ruminal coagulase-negative staphylococci	MICROBIOLOGICA	1121-7138	1994		3/1/2022
Laukova, A	Identification of ruminal enterococcal and streptococcal flora of sheep	J APPL ANIM RES	0971-2119	1994	10.1080/09712119.1994.9705999	3/1/2022
Attwood, GT; Reilly, K	Identification of proteolytic rumen bacteria isolated from new-zealand cattle	J APPL BACTERIOL	0021-8847	1995	10.1111/j.1365-2672.1995.tb03119.x	3/1/2022
Cummings, BA; Caldwell, DR; Gould, DH; Hamar, DW	Identity and interactions of rumen microbes associated with dietary sulfate-induced polioencephalomalacia in cattle	AM J VET RES	0002-9645	1995		3/1/2022
Galindo, J; Geerken, CM; Elias, A; Aranda, N; Piedra, R; Chongo, B; Delgado, D	Bacteria degrading mimosine, the 2,3-dihydroxypiridine and 3-hydroxy-4 pyridone in the rumen	CUBAN J AGR SCI	0864-0408	1995		3/1/2022
Hudson, JA; Mackenzie, CAM; Joblin, KN	Conversion of oleic acid to 10-hydroxystearic acid BY two species of ruminal bacteria	APPL MICROBIOL BIOT	0175-7598	1995		3/1/2022
Jiang, WH; Patterson, JA; Steenson, LR	Isolation and characterization of a temperate bacteriophage from a ruminal acetogen	CURR MICROBIOL	0343-8651	1995	10.1007/BF00294695	3/1/2022

Nelson, KE; Pell, AN; Schofield, P; Zinder, S	Isolation and characterization of AN anaerobic ruminal bacterium capable of degrading hydrolyzable tannins	APPL ENVIRON MICROB	0099-2240	1995	10.1128/AEM.61.9.3293-3298.1995	3/1/2022
Rieulesme, F; Fonty, G; Dore, J	Isolation and characterization of a new hydrogen-utilizing bacterium from the rumen	FEMS MICROBIOL LETT	0378-1097	1995	10.1111/j.1574-6968.1995.tb07338.x	3/1/2022
Skene, IK; Brooker, JD	Characterization of tannin acylhydrolase activity in the ruminal bacterium Selenomonas ruminantium	ANAEROBE	1075-9964	1995	10.1006/anae.1995.1034	3/1/2022
Vangylswyk, NO	Succiniclasticum ruminis gen-nov, SP-nov, a ruminal bacterium converting succinate to propionate as the sole energy-yielding mechanism	INT J SYST BACTERIOL	0020-7713	1995	10.1099/00207713-45-2-297	3/1/2022
Wong, MVL; Ho, YW; Tan, SG; Abdullah, N; Jalaludin, S	Isozyme and morphological-characteristics of the anaerobic fungus piromyces mae isolated from the duodenum, rumen and feces of sheep	FEMS MICROBIOL LETT	0378-1097	1995	10.1016/0378-1097(95)00351-5	3/1/2022
Anderson, RC; Rasmussen, MA; Allison, MJ	Enrichment and isolation of a nitropropanol-metabolizing bacterium from the rumen	APPL ENVIRON MICROB	0099-2240	1996	10.1128/AEM.62.10.3885-3886.1996	3/1/2022
Attwood, GT; Reilly, K; Patel, BKC	Clostridium proteoclasticum SP nov, a novel proteolytic bacterium from the bovine rumen	INT J SYST BACTERIOL	0020-7713	1996	10.1099/00207713-46-3-753	3/1/2022
Calsamiglia, S; Stern, MD; Firkins, JL	Comparison of nitrogen-15 and purines as microbial markers in continuous culture	J ANIM SCI	0021-8812	1996		3/1/2022
Forster, RJ; Teather, RM; Gong, J	16S rdna analysis of Butyrivibrio fibrisolvens: Phylogenetic position and relation to butyrate-producing anaerobic bacteria from the rumen of white-tailed deer	LETT APPL MICROBIOL	0266-8254	1996	10.1111/j.1472-765X.1996.tb00069.x	3/1/2022
Krause, DO; Russell, JB	How many ruminal bacteria are there?	J DAIRY SCI	0022-0302	1996	10.3168/jds.S0022-0302(96)76506-2	3/1/2022
Rieulesme, F; Dauga, C; Morvan, B; Bouvet, OMM; Grimont, PAD; Dore, J	Acetogenic coccoid spore-forming bacteria isolated from the rumen	RES MICROBIOL	0923-2508	1996	10.1016/S0923-2508(97)85122-4	3/1/2022
Rieulesme, F; Morvan, B; Collins, MD; Fonty, G; Willems, A	A new H-2/CO2-using acetogenic bacterium from the rumen: Description of Ruminococcus schinkii SP nov	FEMS MICROBIOL LETT	0378-1097	1996		3/1/2022
Vangylswyk, NO; Hippe, H; Rainey, FA	Pseudobutyrivibrio ruminis gen nov, SP nov, a butyrate-producing bacterium from the rumen that closely resembles Butyrivibrio fibrisolvens in phenotype	INT J SYST BACTERIOL	0020-7713	1996	10.1099/00207713-46-2-559	3/1/2022
Anderson, RC; Rasmussen, MA; Dispirito, AA; Allison, MJ	Characteristics of a nitropropanol-metabolizing bacterium isolated from the rumen	CAN J MICROBIOL	0008-4166	1997	10.1139/m97-088	3/1/2022

Binder, J; Horvath, EM; Schatzmayr, G; Ellend, N; Danner, H; Krska, R; Braun, R	Screening for deoxynivalenol-detoxifying anaerobic rumen microorganisms	CEREAL RES COMMUN	0133-3720	1997		3/1/2022
Forster, RJ; Gong, JH; Teather, RM	Group-specific 16S rrna hybridization probes for determinative and community structure studies of Butyrivibrio fibrisolvens in the rumen	APPL ENVIRON MICROB	0099-2240	1997	10.1128/AEM.63.4.1256-1260.1997	3/1/2022
Jarvis, GN; Moore, ERB; Thiele, JH	Formate and ethanol are the major products of glycerol fermentation produced BY a Klebsiella planticola strain isolated from red deer	J APPL MICROBIOL	1364-5072	1997	10.1046/j.1365-2672.1997.00217.x	3/1/2022
Jarvis, GN; Strompl, C; Moore, ERB; Thiele, JH	Isolation and characterization of glycerol-fermenting bacteria from the rumen of red deer	CAN J MICROBIOL	0008-4166	1997	10.1139/m97-158	3/1/2022
Vangylswyk, NO; Hippe, H; Rainey, FA	Schwartzia succinivorans gen nov, SP nov, another ruminal bacterium utilizing succinate as the sole energy source	INT J SYST BACTERIOL	0020-7713	1997	10.1099/00207713-47-1-155	3/1/2022
Wells, JE; Krause, DO; Callaway, TR; Russell, JB	A bacteriocin-mediated antagonism BY ruminal lactobacilli against Streptococcus bovis	FEMS MICROBIOL ECOL	0168-6496	1997	10.1016/S0168-6496(96)00095-5	3/1/2022
Attwood, GT; Klieve, AV; Ouwerkerk, D; Patel, BKC	Ammonia-hyperproducing bacteria from New Zealand ruminants	APPL ENVIRON MICROB	0099-2240	1998		3/1/2022
Chhabra, A; Kaur, J; Malik, RK; Kaur, H	Isolation and characterization of ruminal bacteria degrading DHP, the toxic metabolite of mimosine	INDIAN J ANIM SCIS	0367-8318	1998		3/1/2022
Hudson, JA; Morvan, B; Joblin, KN	Hydration of linoleic acid BY bacteria isolated from ruminants	FEMS MICROBIOL LETT	0378-1097	1998	10.1111/j.1574-6968.1998.tb13329.x	3/1/2022
Jarvis, GN; Strompl, C; Moore, ERB; Thiele, JH	Isolation and characterisation of obligately anaerobic, lipolytic bacteria from the rumen of red deer	SYST APPL MICROBIOL	0723-2020	1998	10.1016/S0723-2020(98)80017-9	3/1/2022
Julliand, V; Riondet, C; DE Vaux, A; Alcaraz, G; Fonty, G	Comparison of metabolic activities between Piromyces citronii, and equine fungal species, and Piromyces communis, a ruminal species	ANIM FEED SCI TECH	0377-8401	1998	10.1016/S0377-8401(97)00043-6	3/1/2022
Odenyo, AA; Osuji, PO	Tannin-tolerant ruminal bacteria from East African ruminants	CAN J MICROBIOL	0008-4166	1998	10.1139/cjm-44-9-905	3/1/2022
Rieu-Lesme, F; Dauga, C; Fonty, G; Dore, J	Isolation from the rumen of a new acetogenic bacterium phylogenetically closely related to Clostridium difficile	ANAEROBE	1075-9964	1998	10.1006/anae.1998.0153	3/1/2022
Tarakanov, BV; Lavlinskii, DY	Cellulolytic bacteria of the genus Ruminococcus from bovine rumen	MICROBIOLOGY	0026-2617	1998		3/1/2022
Yanke, LJ; Cheng, KJ	A method for the selective enumeration and isolation of ruminal Lactobacillus and Streptococcus	LETT APPL MICROBIOL	0266-8254	1998		3/1/2022

Duncan, SH; Doherty, CJ; Govan, JRW; Neogrady, S; Galfi, P; Stewart, CS	Characteristics of sheep-rumen isolates of Pseudomonas aeruginosa inhibitory to the growth of Escherichia coli O157	FEMS MICROBIOL LETT	0378-1097	1999	10.1016/S0378-1097(99)00493-0	3/1/2022
Guettler, MV; Rumler, D; Jain, MK	Actinobacillus succinogenes SP. Nov., a novel succinic-acid-producing strain from the bovine rumen	INT J SYST BACTERIOL	0020-7713	1999	10.1099/00207713-49-1-207	3/1/2022
Klieve, AV; Heck, GL; Prance, MA; Shu, Q	Genetic homogeneity and phage susceptibility of ruminal strains of Streptococcus bovis isolated in Australia	LETT APPL MICROBIOL	0266-8254	1999	10.1046/j.1365-2672.1999.00596.x	3/1/2022
Laukova, A	Vancomycin-resistant enterococci isolates from the rumen content of deer	MICROBIOS	0026-2633	1999		3/1/2022
Mcsweeney, CS; Palmer, B; Bunch, R; Krause, DO	Isolation and characterization of proteolytic ruminal bacteria from sheep and goats fed the tannin-containing shrub legume Calliandra calothyrsus	APPL ENVIRON MICROB	0099-2240	1999		3/1/2022
Morvan, B; Joblin, KN	Hydration of oleic acid BY Enterococcus gallinarum, Pediococcus acidilactici and Lactobacillus SP isolated from the rumen	ANAEROBE	1075-9964	1999	10.1006/anae.1999.0306	3/1/2022
Anderson, RC; Rasmussen, MA; Jensen, NS; Allison, MJ	Denitrobacterium detoxificans gen. Nov., SP nov., a ruminal bacterium that respires on nitrocompounds	INT J SYST EVOL MICR	1466-5026	2000	10.1099/00207713-50-2-633	3/1/2022
Brookman, JL; Ozkose, E; Rogers, S; Trinci, APJ; Theodorou, MK	Identification of spores in the polycentric anaerobic gut fungi which enhance their ability to survive	FEMS MICROBIOL ECOL	0168-6496	2000	10.1111/j.1574-6941.2000.tb00692.x	3/1/2022
Cheong, JPE; Brooker, JD	Isolation of a virulent bacteriophage from a Propionibacterium species in the sheep rumen	AUST J AGR RES	0004-9409	2000	10.1071/AR99069	3/1/2022
Jarvis, GN; Strompl, C; Burgess, DM; Skillman, LC; Moore, ERB; Joblin, KN	Isolation and identification of ruminal methanogens from grazing cattle	CURR MICROBIOL	0343-8651	2000	10.1007/s002849910065	3/1/2022
Kopecny, J; Hodrova, B	Chitinolytic enzymes produced BY ovine rumen bacteria	FOLIA MICROBIOL	0015-5632	2000	10.1007/BF02817622	3/1/2022
Ambrozic, J; Ferme, D; Grabnar, M; Ravnikar, M; Avgustin, G	The bacteriophages of ruminal prevotellas	FOLIA MICROBIOL	0015-5632	2001	10.1007/BF02825881	3/1/2022
Ha, JK; Lee, SS; Gao, Z; Kim, CH; Kim, SW; Ko, JY; Cheng, KJ	The effect of saturated fatty acids on cellulose digestion BY the rumen anaerobic fungus, Neocallimatix frontalis C5-1	ASIAN AUSTRAL J ANIM	1011-2367	2001	10.5713/ajas.2001.941	3/1/2022
Kopecny, J; Logar, RM; Kobayashi, Y	Phenotypic and genetic data supporting reclassification of Butyrivibrio fibrisolvens isolates	FOLIA MICROBIOL	0015-5632	2001	10.1007/BF02825883	3/1/2022
Mantovani, HC; Kam, DK; Ha, JK; Russell, JB	The antibacterial activity and sensitivity of Streptococcus bovis strains isolated from the rumen of cattle	FEMS MICROBIOL ECOL	0168-6496	2001	10.1016/S0168-6496(01)00166-0	3/1/2022

Michalowski, T; Rybicka, K; Wereszka, K; Kasperowicz, A	Ability of the rumen ciliate Epidinium ecaudatum to digest and use crystalline cellulose and xylan for in vitro growth	ACTA PROTOZOOL	0065-1583	2001		3/1/2022
Odenyo, AA; Bishop, R; Asefa, G; Jamnadass, R; Odongo, D; Osuji, P	Characterization of tannin-tolerant bacterial isolates from East African ruminants	ANAEROBE	1075-9964	2001	10.1006/anae.2000.0367	3/1/2022
Ozkose, E; Thomas, BJ; Davies, DR; Griffith, GW; Theodorou, MK	Cyllamyces aberensis gen.nov SP.nov., a new anaerobic gut fungus with branched sporangiophores isolated from cattle	CAN J BOT	0008-4026	2001	10.1139/b01-047	3/1/2022
Pattnaik, P; Kaushik, JK; Grover, S; Batish, VK	Purification and characterization of a bacteriocin-like compound (Lichenin) produced anaerobically BY Bacillus licheniformis isolated from water buffalo	J APPL MICROBIOL	1364-5072	2001	10.1046/j.1365-2672.2001.01429.x	3/1/2022
Rinta-Koski, M; Beasley, S; Montonen, L; Mantere-Alhonen, S	Propionibacteria isolated from rumen used as possible probiotics together with bifidobacteria	MILCHWISSENSCHAFT	0026-3788	2001		3/1/2022
Whitford, MF; Yanke, LJ; Forster, RJ; Teather, RM	Lachnobacterium bovis gen. Nov., SP nov., a novel bacterium isolated from the rumen and faeces of cattle	INT J SYST EVOL MICR	1466-5026	2001	10.1099/00207713-51-6-1977	3/1/2022
Chen, YC; Hseu, RS	Piromyces polycephalus (Neocallimastigaceae), a new rumen fungus	NOVA HEDWIGIA	0029-5035	2002	10.1127/0029-5035/2002/0075-0409	3/1/2022
Eschenlauer, SCP; Mckain, N; Walker, ND; Mcewan, NR; Newbold, CJ; Wallace, RJ	Ammonia production BY ruminal microorganisms and enumeration, isolation, and characterization of bacteria capable of growth on peptides and amino acids from the sheep rumen	APPL ENVIRON MICROB	0099-2240	2002	10.1128/AEM.68.10.4925-4931.2002	3/1/2022
Kim, YJ; Liu, RH; Rychlik, JL; Russell, JB	The enrichment of a ruminal bacterium (Megasphaera elsdenii YJ-4) that produces the trans-10, cis-12 isomer of conjugated linoleic acid	J APPL MICROBIOL	1365-2672	2002	10.1046/j.1365-2672.2002.01610.x	3/1/2022
Lan, GQ; Ho, YW; Abdullah, N	Mitsuokella jalaludinii SP nov., from the rumens of cattle in Malaysia	INT J SYST EVOL MICR	1466-5026	2002	10.1099/00207713-52-3-713	3/1/2022
Lee, PC; Lee, SY; Hong, SH; Chang, HN	Isolation and characterization of a new succinic acid-producing bacterium, Mannheimia succiniciproducens MBEL55E, from bovine rumen	APPL MICROBIOL BIOT	1432-0614	2002	10.1007/s00253-002-0935-6	3/1/2022
Ouwerkerk, D; Klieve, AV; Forster, RJ	Enumeration of Megasphaera elsdenii in rumen contents BY real-time Taq nuclease assay	J APPL MICROBIOL	1364-5072	2002	10.1046/j.1365-2672.2002.01580.x	3/1/2022
Rychlik, JL; Lavera, R; Russell, JB	Amino acid deamination BY ruminal Megasphaera elsdenii strains	CURR MICROBIOL	0343-8651	2002	10.1007/s00284-002-3743-4	3/1/2022
Rychlik, JL; Russell, JB	Bacteriocin-like activity of Butyrivibrio fibrisolvens JL5 and its effect on other ruminal bacteria and ammonia production	APPL ENVIRON MICROB	0099-2240	2002	10.1128/AEM.68.3.1040-1046.2002	3/1/2022

Kopecny, J; Zorec, M; Mrazek, J; Kobayashi, Y; Marinsek-Logar, R	Butyrivibrio hungatei SP nov and Pseudobutyrivibrio xylanivorans SP nov., butyrate-producing bacteria from the rumen	INT J SYST EVOL MICR	1466-5026	2003	10.1099/ijs.0.02345-0	3/1/2022
Krause, DO; Smith, WJM; Conlan, LL; Gough, JM; Williamson, MA; Mcsweeney, CS	Diet influences the ecology of lactic acid bacteria and Escherichia coli along the digestive tract of cattle: neural networks and 16S rdna	MICROBIOLOGY-SGM	1350-0872	2003	10.1099/mic.0.25685-0	3/1/2022
Sankar, M; Delgado, O; Mattiasson, B	Isolation and characterization of solventogenic, cellulase-free xylanolytic Clostridia from cow rumen	WATER SCI TECHNOL	0273-1223	2003	10.2166/wst.2003.0251	3/1/2022
Van DE Vossenberg, JLCM; Joblin, KN	Biohydrogenation of C18 unsaturated fatty acids to stearic acid BY a strain of Butyrivibrio hungatei from the bovine rumen	LETT APPL MICROBIOL	0266-8254	2003	10.1046/j.1472-765X.2003.01421.x	3/1/2022
Wallace, RJ; Mckain, N; Mcewan, NR; Miyagawa, E; Chaudhary, LC; King, TP; Walker, ND; Apajalahti, JHA; Newbold, CJ	Eubacterium pyruvativorans SP nov., a novel non-saccharolytic anaerobe from the rumen that ferments pyruvate and amino acids, forms caproate and utilizes acetate and propionate	INT J SYST EVOL MICR	1466-5026	2003	10.1099/ijs.0.02110-0	3/1/2022
Bera-Maillet, C; Ribot, Y; Forano, E	Fiber-degrading systems of different strains of the genus Fibrobacter	APPL ENVIRON MICROB	0099-2240	2004	10.1128/AEM.70.4.2172-2179.2004	3/1/2022
Cookson, AL; Noel, SJ; Kelly, WJ; Attwood, GT	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	FEMS MICROBIOL ECOL	0168-6496	2004	10.1016/j.femsec.2004.01.003	3/1/2022
Fliegerova, K; Hodrova, B; Voigt, K	Classical and molecular approaches as a powerful tool for the characterization of rumen polycentric fungi	FOLIA MICROBIOL	0015-5632	2004	10.1007/BF02931392	3/1/2022
Klieve, AV; Bain, PA; Yokoyama, MT; Ouwerkerk, D; Forster, RJ; Turner, AF	Bacteriophages that infect the cellulolytic ruminal bacterium Ruminococcus albus AR67	LETT APPL MICROBIOL	0266-8254	2004	10.1111/j.1472-765X.2004.01493.x	3/1/2022
Paul, SS; Kamra, DN; Sastry, VRB; Sahu, NP; Agarwal, N	Effect of anaerobic fungi on in vitro feed digestion BY mixed rumen microflora of buffalo	REPROD NUTR DEV	0926-5287	2004	10.1051/rnd:2004036	3/1/2022
Piknova, M; Filova, M; Javorsky, P; Pristas, P	Different restriction and modification phenotypes in ruminal lactate-utilizing bacteria	FEMS MICROBIOL LETT	0378-1097	2004	10.1111/j.1574-6968.2004.tb09632.x	3/1/2022
Sahu, NP; Kamra, DN; Paul, SS	Effect of cellulose degrading bacteria isolated from wild and domestic ruminants on in vitro dry matter digestibility of feed and enzyme production	ASIAN AUSTRAL J ANIM	1011-2367	2004	10.5713/ajas.2004.199	3/1/2022
Shin, HT; Lee, SW; Park, KM; Kim, LT; Son, AH; Lee, JH	Nutritional requirements of Prevotella SP isolated from the rumen of the goat	BIOTECHNOL BIOPROC E	1226-8372	2004	10.1007/BF02942350	3/1/2022
Goel, G; Puniya, AK; Singh, K	Tannic acid resistance in ruminal streptococcal isolates	J BASIC MICROB	0233-111X	2005	10.1002/jobm.200410517	3/1/2022

Keating, AF; Stanton, C; Murphy, JJ; Smith, TJ; Ross, RP; Cairns, MT	Isolation and characterization of the bovine Stearoyi-coa desaturase promoter and analysis of polymorphisms in the promoter region in dairy cows	MAMM GENOME	0938-8990	2005	10.1007/s00335-004-2325-0	3/1/2022
Marichamy, S; Yigzaw, Y; Gorton, L; Mattiasson, B	Isolation of obligate anaerobic rumen bacteria capable of degrading the neurotoxin beta-ODAP (beta-N-oxalyl-L-alpha,beta-diaminopropionic acid) as evaluated BY a liquid chromatography/biosensor analysis system	J SCI FOOD AGR	0022-5142	2005	10.1002/jsfa.2211	3/1/2022
Marrero, Y; Galindo, J; Alvarez, E; Torres, V; Aldama, AI; Boucourt, R; Elias, A; Delgado, DC	Methodology for the isolation and characterization of yeasts from the ruminal ecosystem	CUBAN J AGR SCI	0864-0408	2005		3/1/2022
Mcsweeney, CS; Blackall, LL; Collins, E; Conlan, LL; Webb, RI; Denman, SE; Krause, DO	Enrichment, isolation and characterisation of ruminal bacteria that degrade non-protein amino acids from the tropical legume Acacia angustissima	ANIM FEED SCI TECH	0377-8401	2005	10.1016/j.anifeedsci.2005.02.018	3/1/2022
Ohmiya, K; Sakka, K; Kimura, T	Anaerobic bacterial degradation for the effective utilization of biomass	BIOTECHNOL BIOPROC E	1226-8372	2005	10.1007/BF02932282	3/1/2022
Russell, JB	Enrichment of fusobacteria from the rumen that can utilize lysine as AN energy source for growth	ANAEROBE	1075-9964	2005	10.1016/j.anaerobe.2005.01.001	3/1/2022
Singh, R; Singh, M; Nayyar, S	Characterization of rumen bacteria isolated from the buffalo calves	THE INDIAN J ANIM SCIS	0367-8318	2005		3/1/2022
Sprincova, A; Stovcik, V; Javorsky, P; Pristas, P	Occurrence of ps86/pef47-related plasmids in Gram-positive cocci	CURR MICROBIOL	0343-8651	2005	10.1007/s00284-005-4564-z	3/1/2022
Styriak, I; Spanova, A; Zitnan, R	Partial characterization of two ruminal bacteriophages with similar restriction patterns and different capsids morphology	ARCH TIERZUCHT	0003-9438	2005	10.5194/aab-48-572-2005	3/1/2022
Belzecki, G; Michalowski, T	The ability of the rumen ciliate, Diploplastron affine, to digest polysaccharides from fungal and bacterial cell walls	J ANIM FEED SCI	1230-1388	2006		3/1/2022
Piknova, M; Javorsky, P; Guczynska, W; Kasperowicz, A; Michalowski, T; Pristas, P	New species of rumen treponemes	FOLIA MICROBIOL	0015-5632	2006	10.1007/BF02931819	3/1/2022
Wang, AJ; Gao, LF; Ren, NQ; Xu, JF; Liu, C	Bio-hydrogen production from cellulose BY sequential CO-culture of cellulosic hydrogen bacteria of Enterococcus gallinarum G1 and Ethanoigenens harbinense B49	BIOTECHNOL LETT	0141-5492	2009	10.1007/s10529-009-0028-z	3/1/2022
Yang, HJ; Yue, Q; Cao, YC; Zhang, DF; Wang, JQ	Effects of crude feruloyl and acetyl esterase solutions of Neocallimastix SP YQ1 and Anaeromyces SP YQ3 isolated from Holstein steers on hydrolysis of Chinese wildrye grass hay, wheat bran, maize bran, wheat straw and corn stalks	ANIM FEED SCI TECH	0377-8401	2009	10.1016/j.anifeedsci.2009.09.006	3/1/2022

Zhang, KG; Dong, XZ	Selenomonas bovis SP nov., isolated from yak rumen contents	INT J SYST EVOL MICR	1466-5026	2009	10.1099/ijs.0.007641-0	3/1/2022
Belzecki, G; Miltko, R; Kwiatkowska, E; Michalowski, T	Mureinolytic Ability of the Rumen Ciliate Diploplastron affine	FOLIA MICROBIOL	0015-5632	2010		3/1/2022
Cai, SC; Dong, XZ	Cellulosilyticum ruminicola gen. Nov., SP nov., isolated from the rumen of yak, and reclassification of Clostridium lentocellum as Cellulosilyticum lentocellum comb. Nov.	INT J SYST EVOL MICR	1466-5026	2010	10.1099/ijs.0.014712-0	3/1/2022
Cai, SC; Li, JB; Hu, FZ; Zhang, KG; Luo, YM; Janto, B; Boissy, R; Ehrlich, G; Dong, XZ	Cellulosilyticum ruminicola, a Newly Described Rumen Bacterium That Possesses Redundant Fibrolytic-Protein-Encoding Genes and Degrades Lignocellulose with Multiple Carbohydrate-Borne Fibrolytic Enzymes	APPL ENVIRON MICROB	0099-2240	2010	10.1128/AEM.03124-09	3/1/2022
Henning, PH; Horn, CH; Steyn, DG; Meissner, HH; Hagg, FM	The potential of Megasphaera elsdenii isolates to control ruminal acidosis	ANIM FEED SCI TECH	0377-8401	2010	10.1016/j.anifeedsci.2009.12.011	3/1/2022
Kasperowicz, A; Stan-Glasek, K; Guczynska, W; Piknova, M; Pristas, P; Nigutova, K; Javorsky, P; Michalowski, T	Fructanolytic and Saccharolytic Enzymes of the Rumen Bacterium Pseudobutyrivibrio ruminis strain 3-preliminary study	FOLIA MICROBIOL	0015-5632	2010	10.1007/s12223-010-0051-4	3/1/2022
Kuhnert, P; Scholten, E; Haefner, S; Mayor, D; Frey, J	Basfia succiniciproducens gen. Nov., SP nov., a new member of the family Pasteurellaceae isolated from bovine rumen	INT J SYST EVOL MICR	1466-5026	2010	10.1099/ijs.0.011809-0	3/1/2022
Mamen, D; Vadivel, V; Pugalenthi, M; Parimelazhagan, T	Evaluation of Fibrolytic Activity of Two Different Anaerobic Rumen Fungal Isolates for their Utilization as Microbial Feed Additive	ANIM NUTR FEED TECHN	0972-2963	2010		3/1/2022
Paul, SS; Deb, SM; Punia, BS; Singh, D; Kumar, R	Fibrolytic potential of anaerobic fungi (Piromyces SP.) Isolated from wild cattle and blue bulls in pure culture and effect of their addition on in vitro fermentation of wheat straw and methane emission BY rumen fluid of buffaloes	J SCI FOOD AGR	0022-5142	2010	10.1002/jsfa.3952	3/1/2022
Paul, SS; Kamra, DN; Sastry, VRB	Fermentative characteristics and fibrolytic activities of anaerobic gut fungi isolated from wild and domestic ruminants	ARCH ANIM NUTR	1745-039X	2010	10.1080/17450391003625037	3/1/2022
Zhang, KG; Song, L; Dong, XZ	Proteiniclasticum ruminis gen. Nov., SP. Nov., a strictly anaerobic proteolytic bacterium isolated from yak rumen	INT J SYST EVOL MICR	1466-5026	2010	10.1099/ijs.0.011759-0	3/1/2022
Chen, YX; Wang, J; Xing, Y; Zhou, HQ; Tong, J	Isolation and Characterization of a lignolytic rumen microorganism	ISBE 2011: 2011 INT C BIOMED E, VOL 3		2011		3/1/2022
Cobos, MA; DE Coss, AL; Ramirez, ND; Gonzalez, SS; Cerrato, RF	Pediococcus acidilactici isolated from the rumen of lambs with rumen acidosis, 16S rrna identification and sensibility to monensin and lasalocid	RES VET SCI	0034-5288	2011	10.1016/j.rvsc.2010.05.006	3/1/2022

Kenters, N; Henderson, G; Jeyanathan, J; Kittelmann, S; Janssen, PH	Isolation of previously uncultured rumen bacteria BY dilution to extinction using a new liquid culture medium	J MICROBIOL METH	0167-7012	2011	10.1016/j.mimet.2010.10.011	3/1/2022
Ko, KC; Han, Y; Choi, JH; Kim, GJ; Lee, SG; Song, JJ	A novel bifunctional endo-/exo-type cellulase from AN anaerobic ruminal bacterium	APPL MICROBIOL BIOT	0175-7598	2011	10.1007/s00253-010-2949-9	3/1/2022
Kraatz, M; Wallace, RJ; Svensson, L	Olsenella umbonata SP. Nov., a microaerotolerant anaerobic lactic acid bacterium from the sheep rumen and pig jejunum, and emended descriptions of Olsenella, Olsenella uli and Olsenella profusa	INT J SYST EVOL MICR	1466-5026	2011	10.1099/ijs.0.022954-0	3/1/2022
Nagpal, R; Puniya, AK; Sehgal, JP; Singh, K	In vitro fibrolytic potential of anaerobic rumen fungi from ruminants and non-ruminant herbivores	MYCOSCIENCE	1340-3540	2011	10.1007/s10267-010-0071-6	3/1/2022
Paul, SS; Deb, SM; Singh, D	Isolation and characterization of novel sulphate-reducing Fusobacterium SP and their effects on in vitro methane emission and digestion of wheat straw BY rumen fluid from Indian riverine buffaloes	ANIM FEED SCI TECH	0377-8401	2011	10.1016/j.anifeedsci.2011.04.062	3/1/2022
Salem, AZM; Ammar, H; Lopez, S; Gohar, YM; Gonzalez, JS	Sensitivity of ruminal bacteria isolates of sheep, cattle and buffalo to some heavy metals	ANIM FEED SCI TECH	0377-8401	2011	10.1016/j.anifeedsci.2010.10.017	3/1/2022
Weimer, PJ; Stevenson, DM	Isolation, characterization, and quantification of Clostridium kluyveri from the bovine rumen	APPL MICROBIOL BIOT	0175-7598	2012	10.1007/s00253-011-3751-z	3/1/2022
Cao, YC; Yang, HJ; Zhang, DF	Enzymatic characteristics of crude feruloyl and acetyl esterases of rumen fungus Neocallimastix SP YAK11 isolated from yak (Bos grunniens)	J ANIM PHYSIOL AN N	0931-2439	2013	10.1111/j.1439-0396.2012.01281.x	3/1/2022
Grilli, DJ; Ceron, ME; Paez, S; Egea, V; Schnittger, L; Cravero, S; Escudero, MS; Allegretti, L; Arenas, GN	Isolation of Pseudobutyrivibrio ruminis and Pseudobutyrivibrio xylanivorans from rumen of Creole goats fed native forage diet	FOLIA MICROBIOL	0015-5632	2013	10.1007/s12223-012-0219-1	3/1/2022
Kumar, A; Kamra, DN; Agarwal, N; Rikhari, K; Chaudhary, LC	Phenotypic and Phylogenetic Characterization of Cellulose Degrading Bacteria Isolated from Rumen of Buffalo	ANIM NUTR FEED TECHN	0972-2963	2013		3/1/2022
Lawley, B; Sims, IM; Tannock, GW	Whole-Transcriptome Shotgun Sequencing (RNA-seq) Screen Reveals Upregulation of Cellobiose and Motility Operons of Lactobacillus ruminis L5 during Growth on Tetrasaccharides Derived from Barley beta-Glucan	APPL ENVIRON MICROB	0099-2240	2013	10.1128/AEM.01887-13	3/1/2022
Lee, GH; Rhee, MS; Chang, DH; Lee, J; Kim, S; Yoon, MH; Kim, BC	Oscillibacter ruminantium SP nov., isolated from the rumen of Korean native cattle	INT J SYST EVOL MICR	1466-5026	2013	10.1099/ijs.0.041749-0	3/1/2022
Lee, JH; Kumar, S; Lee, GH; Chang, DH; Rhee, MS; Yoon, MH; Kim, BC	Methanobrevibacter boviskoreani SP nov., isolated from the rumen of Korean native cattle	INT J SYST EVOL MICR	1466-5026	2013	10.1099/ijs.0.054056-0	3/1/2022

Priji, P; Unni, KN; Sajith, S; Benjamin, S	Candida tropicalis BPU1, a novel isolate from the rumen of the Malabari goat, is a dual producer of biosurfactant and polyhydroxybutyrate	YEAST	0749-503X	2013	10.1002/yea.2944	3/1/2022
Seo, JK; Park, TS; Kwon, IH; Piao, MY; Lee, CH; Ha, JK	Characterization of Cellulolytic and Xylanolytic Enzymes of Bacillus licheniformis JK7 Isolated from the Rumen of a Native Korean Goat	ASIAN AUSTRAL J ANIM	1011-2367	2013	10.5713/ajas.2012.12506	3/1/2022
Sirisan, V; Pattarajinda, V; Vichitphan, K; Leesing, R	Isolation, identification and growth determination of lactic acid-utilizing yeasts from the ruminal fluid of dairy cattle	LETT APPL MICROBIOL	0266-8254	2013	10.1111/lam.12078	3/1/2022
Sirohi, SK; Choudhury, PK; Dagar, SS; Puniya, AK; Singh, D	Isolation, characterization and fibre degradation potential of anaerobic rumen fungi from cattle	ANN MICROBIOL	1590-4261	2013	10.1007/s13213-012-0577-6	3/1/2022
Williams, AG; Withers, S; Sutherland, AD	The potential of bacteria isolated from ruminal contents of seaweed-eating North Ronaldsay sheep to hydrolyse seaweed components and produce methane BY anaerobic digestion in vitro	MICROB BIOTECHNOL	1751-7907	2013	10.1111/1751-7915.12000	3/1/2022
AL-Dilaimi, A; Albersmeier, A; Kalinowski, J; Ruckert, C	Complete genome sequence of Corynebacterium vitaeruminis DSM 20294(T), isolated from the cow rumen as a vitamin B producer	J BIOTECHNOL	0168-1656	2014	10.1016/j.jbiotec.2014.08.036	3/1/2022
Almeida, PNM; Freitas, CES; Abrao, FO; Ribeiro, ICO; Vieira, EA; Geraseev, LC; Duarte, ER	Cellulolytic activity of aerobic fungi isolated from dairy cattle fed with forage tropical	REV CAATINGA	0100-316X	2014		3/1/2022
Arokiyaraj, S; Islam, VIH; Bharanidharan, R; Raveendar, S; Lee, J; Kim, DH; Oh, YK; Kim, EK; Kim, KH	Antibacterial, anti-inflammatory and probiotic potential of Enterococcus hirae isolated from the rumen of Bos primigenius	WORLD J MICROB BIOT	0959-3993	2014	10.1007/s11274-014-1625-0	3/1/2022
Chen, J; Xu, LX; Wu, Y; Tong, J; Chen, YX	Production, characterization of acetyl esterase from a rumen bacteria strain RB3, and application potential of the strain in biodegradation of crop residues	RENEW ENERG	0960-1481	2014	10.1016/j.renene.2014.01.033	3/1/2022
Chen, YC; Chen, WT; Liu, Jc; Tsai, LC; Cheng, Hl	A highly active beta-glucanase from a new strain of rumen fungus Orpinomyces SP.Y102 exhibits cellobiohydrolase and cellotriohydrolase activities	BIORESOURCE TECHNOL	0960-8524	2014	10.1016/j.biortech.2014.08.016	3/1/2022
DE Aguiar, SC; Zeoula, LM; DO Prado, OPP; Arcuri, PB; Forano, E	Characterization of rumen bacterial strains isolated from enrichments of rumen content in the presence of propolis	WORLD J MICROB BIOT	0959-3993	2014	10.1007/s11274-014-1719-8	3/1/2022
Fraga, M; Perelmuter, K; Valencia, MJ; Martinez, M; Abin-Carriquiry, A; Cajarville, C; Zunino, P	Evaluation of native potential probiotic bacteria using AN in vitro ruminal fermentation system	ANN MICROBIOL	1590-4261	2014	10.1007/s13213-013-0753-3	3/1/2022
Gagen, EJ; Wang, JK; Padmanabha, J; Liu, J; DE Carvalho, IPC; Liu, JX; Webb, RI; AL Jassim, R; Morrison, M; Denman, SE; Mcsweeney, CS	Investigation of a new acetogen isolated from AN enrichment of the tammar wallaby forestomach	BMC MICROBIOL	1471-2180	2014	10.1186/s12866-014-0314-3	3/1/2022

Kelly, WJ; Leahy, SC; Li, D; Perry, R; Lambie, SC; Attwood, GT; Altermann, E	The complete genome sequence of the rumen methanogen Methanobacterium formicicum BRM9	STAND GENOMIC SCI	1944-3277	2014	10.1186/1944-3277-9-15	3/1/2022
Leis, S; Dresch, P; Peintner, U; Fliegerova, K; Sandbichler, AM; Insam, H; Podmirseg, SM	Finding a robust strain for biomethanation: Anaerobic fungi (Neocallimastigomycota) from the Alpine ibex (Capra ibex) and their associated methanogens	ANAEROBE	1075-9964	2014	10.1016/j.anaerobe.2013.12.002	3/1/2022
Nyonyo, T; Shinkai, T; Mitsumori, M	Improved culturability of cellulolytic rumen bacteria and phylogenetic diversity of culturable cellulolytic and xylanolytic bacteria newly isolated from the bovine rumen	FEMS MICROBIOL ECOL	0168-6496	2014	10.1111/1574-6941.12318	3/1/2022
Babaei, Y; Rouzbehan, Y; Alipour, D	Effect of rumen bacteria from sheep adapted to a tanninferous diet on in vitro fermentation parameters of pistachio hulls using bovine inoculum	IRAN J VET RES	1728-1997	2015		3/1/2022
Callaghan, TM; Podmirseg, SM; Hohlweck, D; Edwards, JE; Puniya, AK; Dagar, SS; Griffith, GW	Buwchfawromyces eastonii gen. Nov., SP nov.: a new anaerobic fungus (Neocallimastigomycota) isolated from buffalo faeces	MYCOKEYS	1314-4057	2015	10.3897/mycokeys.9.9032	3/1/2022
Hamann, PRV; Serpa, DL; Da Cunha, ASB; DE Camargo, BR; Osiro, KO; DE Sousa, MV; Felix, CR; Miller, RNG; Noronha, EF	Evaluation of plant cell wall degrading enzyme production BY Clostridium thermocellum B8 in the presence of raw agricultural wastes	INT BIODETER BIODEGR	0964-8305	2015	10.1016/j.ibiod.2015.08.013	3/1/2022
Ishaq, SL; Kim, CJ; Reis, D; Wright, ADG	Fibrolytic Bacteria Isolated from the Rumen of North American Moose (Alces alces) and Their Use as a Probiotic in Neonatal Lambs	PLOS ONE	1932-6203	2015	10.1371/journal.pone.0144804	3/1/2022
Lambie, SC; Kelly, WJ; Leahy, SC; Li, D; Reilly, K; Mcallister, TA; Valle, ER; Attwood, GT; Altermann, E	The complete genome sequence of the rumen methanogen Methanosarcina barkeri CM1	STAND GENOMIC SCI	1944-3277	2015	10.1186/s40793-015-0038-5	3/1/2022
Miltko, R; Pietrzak, M; Belzecki, G; Wereszka, K; Michalowski, T; Hackstein, JHP	Isolation and in vitro cultivation of the fibrolytic rumen ciliate Eremoplastron (Eudiplodinium) dilobum	EUR J PROTISTOL	0932-4739	2015	10.1016/j.ejop.2014.11.002	3/1/2022
Sun, WT; Liu, JJ; Xu, H; Li, WJ; Zhang, J	L-Lactic acid fermentation BY Enterococcus faecium: a new isolate from bovine rumen	BIOTECHNOL LETT	0141-5492	2015	10.1007/s10529-015-1821-5	3/1/2022
Tan, H; Zhang, ZM; Hu, YC; Wu, L; Liao, F; He, J; Luo, B; He, YJ; Zuo, ZC; Ren, ZH; Peng, GN; Deng, JL	Isolation and characterization of Pseudomonas otitidis TH-N1 capable of degrading Zearalenone	FOOD CONTROL	0956-7135	2015	10.1016/j.foodcont.2014.07.013	3/1/2022
Baltaci, MO; Adiguzel, A	Isolation, Identification and Molecular Characterization of Cellulolytic Bacteria from Rumen Samples collected from Erzurum Slaughter House, Turkey	RES J BIOTECHNOL	2278-4535	2016		3/1/2022
Chen, LM; Luo, Y; Wang, HR; Liu, SM; Shen, YZ; Wang, MZ	Effects of Glucose and Starch on Lactate Production BY Newly Isolated Streptococcus bovis S1 from Saanen Goats	APPL ENVIRON MICROB	0099-2240	2016	10.1128/AEM.01994-16	3/1/2022
Fohler, S; Klein, G; Hoedemaker, M; Scheu, T; Seyboldt, C; Campe, A; Jensen, KC; Abdulmawjood, A	Diversity of Clostridium perfringens toxin-genotypes from dairy farms	BMC MICROBIOL	1471-2180	2016	10.1186/s12866-016-0812-6	3/1/2022

Hussain, SKA; Srivastava, A; Tyagi, A; Shandilya, UK; Kumar, A; Kumar, S; Panwar, S; Tyagi, AK	Characterization of CLA-producing Butyrivibrio spp. Reveals strain-specific variations	3 BIOTECH	2190-572X	2016	10.1007/s13205-016-0401-2	3/1/2022
Jeon, BS; Choi, O; Um, Y; Sang, BI	Production of medium-chain carboxylic acids BY Megasphaera SP MH with supplemental electron acceptors	BIOTECHNOL BIOFUELS	1754-6834	2016	10.1186/s13068-016-0549-3	3/1/2022
Kelly, WJ; Henderson, G; Pacheco, DM; Li, D; Reilly, K; Naylor, GE; Janssen, PH; Attwood, GT; Altermann, E; Leahy, SC	The complete genome sequence of Eubacterium limosum SA11, a metabolically versatile rumen acetogen	STAND GENOMIC SCI	1944-3277	2016	10.1186/s40793-016-0147-9	3/1/2022
Kelly, WJ; Pacheco, DM; Li, D; Attwood, GT; Altermann, E; Leahy, SC	The complete genome sequence of the rumen methanogen Methanobrevibacter millerae SM9	STAND GENOMIC SCI	1944-3277	2016	10.1186/s40793-016-0171-9	3/1/2022
Kim, SH; Mamuad, LL; Kim, Dw; Kim, SK; Lee, SS	Fumarate Reductase-Producing Enterococci Reduce Methane Production in Rumen Fermentation In Vitro	J MICROBIOL BIOTECHN	1017-7825	2016	10.4014/jmb.1512.12008	3/1/2022
Nathani, NM; Duggirala, SM; Bhatt, VD; Patel, AK; Kothari, RK; Joshi, CG	Correlation between genomic analyses with metatranscriptomic study reveals various functional pathways of Clostridium sartagoforme AAU1, a buffalo rumen isolate	J APPL ANIM RES	0971-2119	2016	10.1080/09712119.2015.1091346	3/1/2022
Neethu, KB; Priji, P; Unni, KN; Sajith, S; Sreedevi, S; Ramani, N; Anitha, K; Rosana, B; Girish, MB; Benjamin, S	New Bacillus thuringiensis strain isolated from the gut of Malabari goat is effective against Tetranychus macfarlanei	J APPL ENTOMOL	0931-2048	2016	10.1111/jen.12235	3/1/2022
Palakawong, NAS; Pristas, P; Hrehova, L; Javorsky, P; Stams, AJM; Plugge, CM	Actinomyces succiniciruminis SP nov and Actinomyces glycerinitolerans SP nov., two novel organic acid-producing bacteria isolated from rumen	SYST APPL MICROBIOL	0723-2020	2016	10.1016/j.syapm.2016.08.001	3/1/2022
Rosero, JA; Killer, J; Sechovcova, H; Mrazek, J; Benada, O; Fliegerova, K; Havlik, J; Kopecny, J	Reclassification of Eubacterium rectale (Hauduroy ET AL. 1937) Prevot 1938 in a new genus Agathobacter gen. Nov as Agathobacter rectalis comb. Nov., and description of Agathobacter ruminis SP nov., isolated from the rumen contents of sheep and cows	INT J SYST EVOL MICR	1466-5026	2016	10.1099/ijsem.0.000788	3/1/2022
Unni, KN; Priji, P; Sajith, S; Faisal, PA; Benjamin, S	Pseudomonas aeruginosa strain BUP2, a novel bacterium inhabiting the rumen of Malabari goat, produces AN efficient lipase	BIOLOGIA	0006-3088	2016	10.1515/biolog-2016-0057	3/1/2022
Wei, YQ; Long, RJ; Yang, H; Yang, HJ; Shen, XH; Shi, RF; Wang, ZY; Du, JG; QI, XJ; Ye, QH	Fiber degradation potential of natural CO-cultures of Neocallimastix frontalis and Methanobrevibacter ruminantium isolated from yaks (Bos grunniens) grazing on the Qinghai Tibetan Plateau	ANAEROBE	1075-9964	2016	10.1016/j.anaerobe.2016.03.005	3/1/2022
Abrao, FO; Duarte, ER; Pessoa, MS; Dos Santos, VL; De Freitas, LF; Barros, KD; Hughes, AFD; Silva, TD; Rodriguez, NM	Notable fibrolytic enzyme production BY Aspergillus spp. Isolates from the gastrointestinal tract of beef cattle fed in lignified pastures	PLOS ONE	1932-6203	2017	10.1371/journal.pone.0183628	3/1/2022
Asem, D; Leo, VV; Passari, AK; Tonsing, MV; Joshi, JB; Uthandi, S; Hashem, A; Abd Allah, EF; Singh, BP	Evaluation of gastrointestinal bacterial population for the production of holocellulose enzymes for biomass deconstruction	PLOS ONE	1932-6203	2017	10.1371/journal.pone.0186355	3/1/2022

Ayudthaya, SPN; Hornung, B; Varadarajan, AR; Plugge, W; Plugge, CM	Draft Genome Sequence of Actinomyces succiniciruminis Strain Am4(T), Isolated from Cow Rumen Fluid	MICROBIOLOGY RESOURCE ANNOUNCEMENTS	2576-098X	2017	10.1128/genomea.01587-16	3/1/2022
Chun, BH; Lee, HJ; Jeong, SE; Schumann, P; Jeon, CO	Leucobacter ruminantium SP nov., isolated from the bovine rumen	INT J SYST EVOL MICR	1466-5026	2017	10.1099/ijsem.0.002003	3/1/2022
Colombo, M; Castilho, NPA; Todorov, SD; Nero, LA	Beneficial and Safety Properties of a Corynebacterium vitaeruminis Strain Isolated from the Cow Rumen	PROBIOTICS ANTIMICRO	1867-1306	2017	10.1007/s12602-017-9263-0	3/1/2022
Gilbert, RA; Kelly, WJ; Altermann, E; Leahy, SC; Minchin, C; Ouwerkerk, D; Klieve, AV	Toward Understanding Phage: Host Interactions in the Rumen; Complete Genome Sequences of Lytic Phages Infecting Rumen Bacteria	FRONT MICROBIOL	1664-302X	2017	10.3389/fmicb.2017.02340	3/1/2022
Harlow, BE; Goodman, JP; Lynn, BC; Flythe, MD; Ji, H; Aiken, GE	Ruminal tryptophan-utilizing bacteria degrade ergovaline from tall fescue seed extract	J ANIM SCI	0021-8812	2017	10.2527/jas.2016.1128	3/1/2022
Henske, JK; Gilmore, SP; Knop, D; Cunningham, FJ; Sexton, JA; Smallwood, CR; Shutthanandan, V; Evans, JE; Theodorou, MK; O'malley, MA	Transcriptomic characterization of Caecomyces churrovis: a novel, non-rhizoid-forming lignocellulolytic anaerobic fungus	BIOTECHNOL BIOFUELS	1754-6834	2017	10.1186/s13068-017-0997-4	3/1/2022
Jeon, BS; Kim, S; Sang, BI	Megasphaera hexanoica SP nov., a medium-chain carboxylic acid-producing bacterium isolated from a cow rumen	INT J SYST EVOL MICR	1466-5026	2017	10.1099/ijsem.0.001888	3/1/2022
Neumann, AP; Mccormick, CA; Suen, G	Fibrobacter communities in the gastrointestinal tracts of diverse hindgut-fermenting herbivores are distinct from those of the rumen	ENVIRON MICROBIOL	1462-2912	2017	10.1111/1462-2920.13878	3/1/2022
Newbrook, K; Staton, GJ; Clegg, SR; Birtles, RJ; Carter, SD; Evans, NJ	Treponema ruminis SP nov., a spirochaete isolated from the bovine rumen	INT J SYST EVOL MICR	1466-5026	2017	10.1099/ijsem.0.001812	3/1/2022
Nidhina, N; Bhavya, ML; Bhaskar, N; Muthukumar, SP; Murthy, PS	Aflatoxin production BY Aspergillus flavus in rumen liquor and its implications	FOOD CONTROL	0956-7135	2017	10.1016/j.foodcont.2016.05.051	3/1/2022
Palevich, N; Kelly, WJ; Leahy, SC; Altermann, E; Rakonjac, J; Attwood, GT	The complete genome sequence of the rumen bacterium Butyrivibrio hungatei MB2003	STAND GENOMIC SCI	1944-3277	2017	10.1186/s40793-017-0285-8	3/1/2022
Pang, J; Liu, ZY; Hao, M; Zhang, YF; QI, QS	AN isolated cellulolytic Escherichia coli from bovine rumen produces ethanol and hydrogen from corn straw	BIOTECHNOL BIOFUELS	1754-6834	2017	10.1186/s13068-017-0852-7	3/1/2022
Podlesny, M; Jarocki, P; Wyrostek, J; Czernecki, T; Kucharska, J; Nowak, A; Targonski, Z	Enterobacter SP LU1 as a novel succinic acid producer - CO-utilization of glycerol and lactose	MICROB BIOTECHNOL	1751-7915	2017	10.1111/1751-7915.12458	3/1/2022
Priji, P; Sajith, S; Unni, KN; Anderson, RC; Benjamin, S	Pseudomonas SP BUP6, a novel isolate from Malabari goat produces AN efficient rhamnolipid type biosurfactant	J BASIC MICROB	0233-111X	2017	10.1002/jobm.201600158	3/1/2022
Sharma, D; Mal, G; Kannan, A; Bhar, R; Sharma, R; Singh, B	Degradation of euptox A BY tannase-producing rumen bacteria from migratory goats	J APPL MICROBIOL	1364-5072	2017	10.1111/jam.13563	3/1/2022

Wang, XW; Liu, XZ; Groenewald, JZ	Phylogeny of anaerobic fungi (phylum Neocallimastigomycota), with contributions from yak in China	ANTON LEEUW INT J G	0003-6072	2017	10.1007/s10482-016-0779-1	3/1/2022
Wei, YQ; Yang, HJ; Long, RJ; Wang, ZY; Cao, BB; Ren, QC; Wu, TT	Characterization of natural CO-cultures of Piromyces with Methanobrevibacter ruminantium from yaks grazing on the Qinghai-Tibetan Plateau: a microbial consortium with high potential in plant biomass degradation	AMB EXPRESS	2191-0855	2017	10.1186/s13568-017-0459-1	3/1/2022
Bohra, V; Dafale, NA; Purohit, HJ	Paenibacillus polymyxa ND25: candidate genome for lignocellulosic biomass utilization	3 BIOTECH	2190-572X	2018	10.1007/s13205-018-1274-3	3/1/2022
Boonsaen, P; Kinjo, M; Sawanon, S; Suzuki, Y; Koike, S; Kobayashi, Y	Partial characterization of phylogeny, ecology and function of the fibrolytic bacterium Ruminococcus flavefaciens OS14, newly isolated from the rumen of swamp buffalo	ANIM SCI J	1344-3941	2018	10.1111/asj.12927	3/1/2022
Cipriano-Salazar, M; Rojas-Hernandez, S; Olivares-Perez, J; Jimenez-Guillen, R; Cruz-Lagunas, B; Camacho-Diaz, LM; Ugbogu, AE	Antibacterial activities of tannic acid against isolated ruminal bacteria from sheep	MICROB PATHOGENESIS	0882-4010	2018	10.1016/j.micpath.2018.01.045	3/1/2022
Dollhofer, V; Dandikas, V; Dorn-In, S; Bauer, C; Lebuhn, M; Bauer, J	Accelerated biogas production from lignocellulosic biomass after pre-treatment with Neocallimastix frontalis	BIORESOURCE TECHNOL	0960-8524	2018	10.1016/j.biortech.2018.05.068	3/1/2022
Hanafy, RA; Elshahed, MS; Youssef, NH	Feramyces austinii, gen. Nov., SP nov., AN anaerobic gut fungus from rumen and fecal samples of wild Barbary sheep and fallow deer	MYCOLOGIA	0027-5514	2018	10.1080/00275514.2018.1466610	3/1/2022
Hoang, VT; Hoang, DH; Pham, ND; Tran, HM; Bui, HTV; Ngo, TA	Hydrogen production BY newly isolated Clostridium species from cow rumen in pure-and CO-cultures on a broad range of carbon sources	AIMS ENERGY	2333-8326	2018	10.3934/energy.2018.5.846	3/1/2022
Hoedt, EC; Parks, DH; Volmer, JG; Rosewarne, CP; Denman, SE; Mcsweeney, CS; Muir, JG; Gibson, PR; Cuiv, PO; Hugenholtz, P; Tyson, GW; Morrison, M	Culture- and metagenomics-enabled analyses of the Methanosphaera genus reveals their monophyletic origin and differentiation according to genome size	ISME JOURNAL	1751-7362	2018	10.1038/s41396-018-0225-7	3/1/2022
Intanoo, M; Kongkeitkajorn, MB; Pattarajinda, V; Bernard, JK; Callaway, TR; Suriyasathaporn, W; Phasuk, Y	Isolation and screening of aflatoxin-detoxifying yeast and bacteria from ruminal fluids to reduce aflatoxin B-1 contamination in dairy cattle feed	J APPL MICROBIOL	1364-5072	2018	10.1111/jam.14060	3/1/2022
Joshi, A; Lanjekar, V; Dhakephalkar, PK; Dagar, SS	Cultivation of multiple genera of hydrogenotrophic methanogens from different environmental niches	ANAEROBE	1075-9964	2018	10.1016/j.anaerobe.2018.02.001	3/1/2022
Jung, DH; Chung, WH; Seo, DH; Nam, YD; Yoon, S; Park, CS	Complete genome sequence of Bifidobacterium choerinum FMB-1, a resistant starch-degrading bacterium	J BIOTECHNOL	0168-1656	2018	10.1016/j.jbiotec.2018.03.009	3/1/2022
Jung, DH; Seo, DH; Kim, GY; Nam, YD; Song, EJ; Yoon, S; Park, CS	The effect of resistant starch (RS) on the bovine rumen microflora and isolation of RS-degrading bacteria	APPL MICROBIOL BIOT	0175-7598	2018	10.1007/s00253-018-8971-z	3/1/2022

Kalawong, R; Wakayama, M; Anuntalabhochai, S; Wongsawad, C; Sangwijit, K	Comparison and Characterization of Purified Cellulase and Xylanase from Bacillus amyloliquefaciens CX1 and Bacillus subtilis B4	CHIANG MAI J SCI	0125-2526	2018		3/1/2022
Kim, MK; Kim, ET; Kim, SB; Jeong, HY; Park, BY; Srinivasan, S	Kurthia ruminicola SP nov., isolated from the rumen contents of a Holstein cow	J MICROBIOL	1225-8873	2018	10.1007/s12275-018-7285-2	3/1/2022
Ladha, G; Jeevaratnam, K	Probiotic Potential of Pediococcus pentosaceus LJR1, a Bacteriocinogenic Strain Isolated from Rumen Liquor of Goat (Capra aegagrus hircus)	FOOD BIOTECHNOL	0890-5436	2018	10.1080/08905436.2017.1414700	3/1/2022
Li, JF; Yuan, XJ; Desta, ST; Dong, ZH; Mugabe, W; Shao, T	Characterization of Enterococcus faecalis JF85 and Enterococcus faecium Y83 isolated from Tibetan yak (Bos grunniens) for ensiling Pennisetum sinese	BIORESOURCE TECHNOL	0960-8524	2018	10.1016/j.biortech.2018.02.070	3/1/2022
Park, T; Seo, S; Shin, T; Cho, BW; Cho, S; Kim, B; Lee, S; Ha, JK; Seo, J	Molecular cloning, purification, expression, and characterization of beta-1, 4-endoglucanase gene (Cel5A) from Eubacterium cellulosolvens SP isolated from Holstein steers' rumen	ASIAN AUSTRAL J ANIM	1011-2367	2018	10.5713/ajas.17.0552	3/1/2022
Ranjan, R; Pandit, RJ; Duggirala, SM; Joshi, CG; Sharma, S; Patil, NV	Genome sequencing of Pediococcus acidilactici (NRCC1), a novel isolate from dromedary camel (Camelus dromedarius) rumen fluid	ANN MICROBIOL	1590-4261	2018	10.1007/s13213-017-1320-0	3/1/2022
Salem, AZM; Khusro, A; Elghandour, Mmy; Olivares-Perez, J; Rojas-Hernandez, S; Jimenez-Guillen, R	Susceptibility of ruminal bacteria isolated from large and small ruminant to multiple conventional antibiotics	MICROB PATHOGENESIS	0882-4010	2018	10.1016/j.micpath.2018.05.013	3/1/2022
Simunek, J; Killer, J; Sechovcova, H; Simunek, J; Pechar, R; Rada, V; Svec, P; Sedlacek, I	Characterization of a xylanolytic bacterial strain C10 isolated from the rumen of a red deer (Cervus elaphus) closely related of the recently described species Actinomyces succiniciruminis, A-glycerinitolerans, and A-ruminicola	FOLIA MICROBIOL	0015-5632	2018	10.1007/s12223-017-0577-9	3/1/2022
Sugiharto, S; Yudiarti, T; Isroli, I; Widiastuti, E; Wahyuni, HI; Suprijatna, E	The potential of Bacillus strains isolated from the rumen content of dairy cows as natural antibacterial and antioxidant agents for broilers	J INDONES TROP ANIM AGR	2087-8273	2018	10.14710/jitaa.43.2.115-123	3/1/2022
Yang, Y; Zhou, MX; Hardwidge, PR; Cui, HM; Zhu, GQ	Isolation and Characterization of N-acyl Homoserine Lactone-Producing Bacteria From Cattle Rumen and Swine Intestines	FRONT CELL INFECT MI	2235-2988	2018	10.3389/fcimb.2018.00155	3/1/2022
Zhang, HY; Shen, NK; Qin, Y; Zhu, L; Li, Y; Wu, JF; Jiang, MG	Complete Genome Sequence of Actinobacillus succinogenes GXAS137, a Highly Efficient Producer of Succinic Acid	MICROBIOLOGY RESOURCE ANNOUNCEMENTS	2576-098X	2018	10.1128/genomea.01562-17	3/1/2022
Zhang, YH; Zhang, ZY; Dai, L; Liu, Y; Cheng, MJ; Chen, LJ	Isolation and characterization of a novel gossypol-degrading bacteria Bacillus subtilis strain Rumen Bacillus Subtilis	ASIAN AUSTRAL J ANIM	1011-2367	2018	10.5713/ajas.17.0018	3/1/2022
Aphale, D; Natu, A; Laldas, S; Kulkarni, A	Administration of Streptococcus bovis isolated from sheep rumen digesta on rumen function and physiology as evaluated in a rumen simulation technique system	VETERINARY WORLD	0972-8988	2019	10.14202/vetworld.2019.1362-1371	3/1/2022
Battumur, U; Lee, M; Bae, GS; Kim, CH	Isolation and characterization of a new Methanoculleus bourgensis strain KOR-2 from the rumen of Holstein steers	ASIAN AUSTRAL J ANIM	1011-2367	2019	10.5713/ajas.18.0409	3/1/2022

Bohra, V; Tikariha, H; Dafale, NA	Genomically Defined Paenibacillus polymyxa ND24 for Efficient Cellulase Production Utilizing Sugarcane Bagasse as a Substrate	APPL BIOCHEM BIOTECH	0273-2289	2019	10.1007/s12010-018-2820-5	3/1/2022
Boonsaen, P; Poonko, S; Kanjanapruetipong, J; Wongchawalit, J; Phiriyangkul, P; Sawanon, S	Isolation and partial characterization of ruminococcus flavefaciens from the rumen of swamp buffalo	BUFFALO BULL	0125-6726	2019		3/1/2022
Dadheech, T; Jakhesara, S; Chauhan, PS; Pandit, R; Hinsu, A; Kunjadiya, A; Rank, D; Joshi, C	Draft genome analysis of lignocellulolytic enzymes producing Aspergillus terreus with structural insight of beta-glucosidases through molecular docking approach	INT J BIOL MACROMOL	0141-8130	2019	10.1016/j.ijbiomac.2018.12.020	3/1/2022
Dubrovin, A; Dunyashev, T; Ilina, L; Filippova, V; Laishev, K	Isolation of cellulolytic bacterial strains from rangifer tarandus rumen microflora	RES RURAL DEV	1691-4031	2019	10.22616/rrd.25.2019.041	3/1/2022
Fernandes, T; Carvalho, BF; Mantovani, HC; Schwan, RF; Avila, CLS	Identification and characterization of yeasts from bovine rumen for potential use as probiotics	J APPL MICROBIOL	1364-5072	2019	10.1111/jam.14350	3/1/2022
Guder, DG; Krishna, MSR	Isolation and Characterization of Potential Cellulose Degrading Bacteria from Sheep Rumen	J PURE APPL MICROBIO	0973-7510	2019	10.22207/JPAM.13.3.60	3/1/2022
Jaglan, N; Kumar, S; Choudhury, PK; Tyagi, B; Tyagi, AK	Isolation, characterization and conjugated linoleic acid production potential of bifidobacterial isolates from ruminal fluid samples of Murrah buffaloes	ANAEROBE	1075-9964	2019	10.1016/j.anaerobe.2019.02.001	3/1/2022
Kang, S; Denman, S; Mcsweeney, C	Draft Genome Sequence and Annotation of Oribacterium SP. Strain C9, Isolated from a Cattle Rumen	MICROBIOLOGY RESOURCE ANNOUNCEMENTS	2576-098X	2019	10.1128/MRA.01562-18	3/1/2022
Kang, S; Denman, S; Tahmasbi, R; Mcsweeney, C	Draft Genome Sequence and Annotation of Sporanaerobacter acetigenes Strain F-12, Isolated from a Cattle Rumen	MICROBIOLOGY RESOURCE ANNOUNCEMENTS	2576-098X	2019	10.1128/MRA.00634-19	3/1/2022
Liu, JG; Liu, ZY; Liu, YC; Hao, M; Hou, XZ	Analysis of Cellulolytic Bacterial Flora in the Rumen of Inner Mongolian Sheep	BIORESOURCES	1930-2126	2019	10.15376/biores.14.4.9544-9556	3/1/2022
Lunar, L; Hernandez, D; Silva, HV; Cobos, MA; Gonzalez, SS; Cortez, C; Pinto, R; Ramirez, E; Pinos, JM; Vargas, JM	Isolation, biochemical characterization, and phylogeny of a cellulose-degrading ruminal bacterium	REV COLOMB CIENC PEC	0120-0690	2019	10.17533/udea.rccp.v32n2a05	3/1/2022
Miguel, MA; Lee, SS; Mamuad, LL; Choi, YJ; Jeong, CD; Son, AR; Cho, KK; Kim, ET; Kim, SB; Suk, S	Enhancing Butyrate Production, Ruminal Fermentation and Microbial Population through Supplementation with Clostridium saccharobutylicum	J MICROBIOL BIOTECHN	1017-7825	2019	10.4014/jmb.1905.05016	3/1/2022
Pimentel, MFA; Paula, DAJ; Riet-Correa, F; Dutra, V; Nakazato, L	Detection and Characterization of Bovine Rumen Microorganisms Resistant to Sodium Fluoroacetate	ACTA SCI VET	1678-0345	2019	10.22456/1679-9216.89907	3/1/2022
Raza, A; Bashir, S; Tabassum, R	Evaluation of Cellulases and Xylanases Production from Bacillus spp. Isolated from Buffalo Digestive System	KAFKAS UNIV VET FAK	1300-6045	2019	10.9775/kvfd.2018.20280	3/1/2022

Sabino, YNV; Fochat, RC; Lima, JCF; Ribeiro, MT; Arcuri, PB; Carneiro, JD; Machado, MA; Reis, DRD; Machado, ABF; Hungaro, HM; Ribeiro, JB; Paiva, AD	Antibacterial activity and lantibiotic post-translational modification genes in Streptococcus spp. Isolated from ruminal fluid	ANN MICROBIOL	1590-4261	2019	10.1007/s13213-018-1407-2	3/1/2022
Sedighi, R; Alipour, D	Assessment of probiotic effects of isolated Megasphaera elsdenii strains in Mehraban sheep and Holstein lactating cows	ANIM FEED SCI TECH	0377-8401	2019	10.1016/j.anifeedsci.2019.01.007	3/1/2022
Vaidya, JD; Hornung, BVH; Smidt, H; Edwards, JE; Plugge, CM	Propionibacterium ruminifibrarum SP. Nov., isolated from cow rumen fibrous content	INT J SYST EVOL MICR	1466-5026	2019	10.1099/ijsem.0.003544	3/1/2022
Astriani, M; Zubaidah, S; Abadi, AL; Suarsini, E	Isolation and identification of phosphate solubilizing bacteria from indigenous microorganisms (IMO) of cow rumen in East Java, Indonesia as eco-friendly biofertilizer	MALAYS J MICROBIOL	1823-8262	2020	10.21161/mjm.190536	3/1/2022
Cao, LB; MA, YM; Deng, DD; Jiang, HC; Wang, JX; Liu, Y	Electricity production of microbial fuel cells BY degrading cellulose coupling with CR(VI) removal	J HAZARD MATER	0304-3894	2020	10.1016/j.jhazmat.2020.122184	3/1/2022
Friedersdorff, JCA; Kingston-Smith, AH; Pachebat, JA; Cookson, AR; Rooke, D; Creevey, CJ	The Isolation and Genome Sequencing of Five Novel Bacteriophages From the Rumen Active againstbutyrivibrio fibrisolvens	FRONT MICROBIOL	1664-302X	2020	10.3389/fmicb.2020.01588	3/1/2022
Guo, LN; Yao, DD; Li, DX; Lin, YL; Bureenok, S; Ni, KK; Yang, FY	Effects of Lactic Acid Bacteria Isolated From Rumen Fluid and Feces of Dairy Cows on Fermentation Quality, Microbial Community, and in vitro Digestibility of Alfalfa Silage	FRONT MICROBIOL	1664-302X	2020	10.3389/fmicb.2019.02998	3/1/2022
Hailemariam, S; Zhao, SG; Wang, JQ	Complete Genome Sequencing and Transcriptome Analysis of Nitrogen Metabolism ofsuccinivibrio dextrinosolvensstrain Z6 Isolated From Dairy Cow Rumen	FRONT MICROBIOL	1664-302X	2020	10.3389/fmicb.2020.01826	3/1/2022
Hanafy, RA; Johnson, B; Youssef, NH; Elshahed, MS	Assessing anaerobic gut fungal diversity in herbivores usingd1/d2large ribosomal subunit sequencing and multi-year isolation	ENVIRON MICROBIOL	1462-2912	2020	10.1111/1462-2920.15164	3/1/2022
Hanafy, RA; Lanjekar, VB; Dhakephalkar, PK; Callaghan, TM; Dagar, SS; Griffith, GW; Elshahed, MS; Youssef, NH	Seven new Neocallimastigomycota genera from wild, zoo-housed, and domesticated herbivores greatly expand the taxonomic diversity of the phylum	MYCOLOGIA	0027-5514	2020	10.1080/00275514.2019.1696619	3/1/2022
Hong, SJ; Kim, DH; Jung, DJS; Hague, MN; Baik, M	Complete genome analysis of a novel mucolytic bacterium, Prevotella mucinisolvens SP. Nov., isolated from bovine rumen epithelium	J ANIM SCI	0021-8812	2020	10.1093/jas/skaa278.711	3/1/2022
Kang, S; Khan, S; Webb, R; Denman, S; Mcsweeney, C	Characterization and survey in cattle of a rumen Pyrimadobacter SP. Which degrades the plant toxin fluoroacetate	FEMS MICROBIOL ECOL	0168-6496	2020	10.1093/femsec/fiaa077	3/1/2022
Kim, SH; Mamuad, LL; Islam, M; Lee, SS	Reductive acetogens isolated from ruminants and their effect on in vitro methane mitigation and milk performance in Holstein cows	J ANIM SCI AND TECHNOLOGY	2672-0191	2020	10.5187/jast.2020.62.1.1	3/1/2022
Kuppusamy, P; Kim, D; Soundharrajan, I; Park, HS; Jung, JS; Yang, SH; Choi, KC	Low-Carbohydrate Tolerant LAB Strains Identified from Rumen Fluid: Investigation of	MICROORGANISMS	2076-2607	2020	10.3390/microorganisms8071044	3/1/2022

	Probiotic Activity and Legume Silage Fermentation					
Li, Y; Guo, BZ; Li, C; Wang, WW; Wu, ZK; Liu, GH; Cai, HY	Isolation of a Highly Efficient Antigenic-Protein-degradingbacillus amyloliquefaciensand Assessment of Its Safety	ANIMALS	2076-2615	2020	10.3390/ani10071144	3/1/2022
Mishra, P; Tulsani, NJ; Jakhesara, SJ; Dafale, NA; Patil, NV; Purohit, HJ; Koringa, PG; Joshi, CG	Exploring the eukaryotic diversity in rumen of Indian camel (Camelus dromedarius) using 18S rrna amplicon sequencing	ARCH MICROBIOL	0302-8933	2020	10.1007/s00203-020-01897-w	3/1/2022
Peters, M; Wohlsein, P	The deliberate killing of a sheep with a fire extinguisher: a case report and experimental reconstruction study	FORENSIC SCI MED PAT	1547-769X	2020	10.1007/s12024-020-00245-0	3/1/2022
Ratnakomala, S; Perwitasari, U; Yopi	The amylase production BY Actinobacteria isolated from rumen fluid	INTERNATIONAL SYMPOSIUM OF INNOVATIVE BIO-PRODUCTION INDONESIA ON BIOTECHNOLOGY AND BIOENGINEERING 2019	1755-1307	2020	10.1088/1755-1315/439/1/012019	3/1/2022
Stabel, M; Hanafy, RA; Schweitzer, T; Greif, M; Aliyu, H; Flad, V; Young, D; Lebuhn, M; Elshahed, MS; Ochsenreither, K; Youssef, NH	Aestipascuomycesdupliciliberans gen. Nov, SP. Nov., the First Cultured Representative of the Uncultured SK4 Clade from Aoudad Sheep and Alpaca	MICROORGANISMS	2076-2607	2020	10.3390/microorganisms8111734	3/1/2022
Szczerba, H; Komon-Janczara, E; Dudziak, K; Wasko, A; Targonski, Z	A novel biocatalyst,Enterobacter aerogeneslu2, for efficient production of succinic acid using whey permeate as a cost-effective carbon source	BIOTECHNOL BIOFUELS	1754-6834	2020	10.1186/s13068-020-01739-3	3/1/2022
Tyagi, AK; Kumar, S; Choudhury, PK; Tyagi, B; Tyagi, N	Conjugated linoleic acid producing potential of lactobacilli isolated from goat (AXB) rumen fluid samples	ASIAN AUSTRAL J ANIM	1011-2367	2020	10.5713/ajas.19.0080	3/1/2022
Alves, JMD; Rocha, PJD; Duarte, ER; Maia, HAR; Freitas, CES; Pimenta, MAS; Valerio, HM	Enzymatic profiles of hydrolysis of lignocellulosic materials from Aspergillus terreus strains isolated from the rumen of beef cattle from Brazil	BIOCATAL AGRI BIOTECH	1878-8181	2021	10.1016/j.bcab.2021.102143	3/1/2022
Avchar, R; Lanjekar, V; Kshirsagar, P; Dhakephalkar, PK; Dagar, SS; Baghela, A	Buffalo rumen harbours diverse thermotolerant yeasts capable of producing second-generation bioethanol from lignocellulosic biomass	RENEW ENERG	0960-1481	2021	10.1016/j.renene.2021.04.002	3/1/2022
Badejo, OA; Olaniyi, OO; Ayodeji, AO; Lawal, OT	Biochemical properties of partially purified surfactant-tolerant alkalophilic endo beta-1,4 xylanase and acidophilic beta-mannanase from bacteria resident in ruminants' guts	BIOCATAL AGRI BIOTECH	1878-8181	2021	10.1016/j.bcab.2021.101982	3/1/2022
DE Sousa, BL; Azevedo, AC; Oliveira, IMF; Bento, CBP; Santana, MF; Bazzolli, DMS; Mantovani, HC	PCR screening reveals abundance of bovicin-like bacteriocins among ruminal Streptococcus spp. Isolated from beef and dairy cattle	J APPL MICROBIOL	1364-5072	2021	10.1111/jam.15069	3/1/2022

Duarte, ER; Maia, HAR; Freitas, CES; Alves, JMD; Valerio, HM; Cota, J	Hydrolysis of lignocellulosic forages BY Trichoderma longibrachiatum isolate from bovine rumen	BIOCATAL AGRI BIOTECH	1878-8181	2021	10.1016/j.bcab.2021.102135	3/1/2022
Gaffney, J; Embree, J; Gilmore, S; Embree, M	Ruminococcus bovis SP. Nov., a novel species of amylolytic Ruminococcus isolated from the rumen of a dairy cow	INT J SYST EVOL MICR	1466-5026	2021	10.1099/ijsem.0.004924	3/1/2022
Li, J; Tang, X; Zhao, J; Chen, S; Wang, S; Shao, T	Improvement of fermentation quality and cellulose convertibility of Napier grass silage BY inoculation of cellulolytic bacteria from Tibetan yak (Bos grunniens)	J APPL MICROBIOL	1364-5072	2021	10.1111/jam.14917	3/1/2022
Mahoney-Kurpe, SC; Palevich, N; Noel, SJ; Kumar, S; Gagic, D; Biggs, PJ; Janssen, PH; Attwood, GT; Moon, CD	Complete Genome Sequences of Three Clostridiales R-7 Group Strains Isolated from the Bovine Rumen in New Zealand	MICROBIOLOGY RESOURCE ANNOUNCEMENTS	2576-098X	2021	10.1128/MRA.00310-21	3/1/2022
Medhi, D; Ali, E; Choudhury, LC; Baruah, KK; Santra, A; Dubey, S; Agarwal, P; Chakravarty, P	Isolation, identification and characterization of rumen bacteria and estimation of their fibre degradable enzymes in yak (Bos grunniens)	INDIAN J ANIM SCIS	0367-8318	2021		3/1/2022
NA, SW; Chun, BH; Beak, SH; Khan, SA; Haque, MN; Lee, JS; Jeon, CO; Lee, SS; Baik, M	Pseudoprevotella muciniphila gen. Nov., SP. Nov., a mucin-degrading bacterium attached to the bovine rumen epithelium	PLOS ONE	1932-6203	2021	10.1371/journal.pone.0251791	3/1/2022
Pang, J; Liu, LH; Liu, XP; Wang, Y; Chen, B; Wu, SR; Yao, JH; Xu, XR	A novel identified Pseudomonas aeruginosa, which exhibited nitrate- and nitrite-dependent methane oxidation abilities, could alleviate the disadvantages caused BY nitrate supplementation in rumen fluid fermentation	MICROB BIOTECHNOL	1751-7915	2021	10.1111/1751-7915.13726	3/1/2022
Park, T; Wijeratne, S; Meulia, T; Firkins, JL; Yu, ZT	Original The macronuclear genome of anaerobic ciliate Entodinium caudatum reveals its biological features adapted to the distinct rumen environment	GENOMICS	0888-7543	2021	10.1016/j.ygeno.2021.03.014	3/1/2022
Srivastava, S; Dafale, NA; Jakhesara, SJ; Joshi, CG; Patil, NV; Purohit, HJ	Unraveling the camel rumen microbiome through metaculturomics approach for agriculture waste hydrolytic potential	ARCH MICROBIOL	0302-8933	2021	10.1007/s00203-020-02010-x	3/1/2022
Suntara, C; Cherdthong, A; Wanapat, M; Uriyapongson, S; Leelavatcharamas, V; Sawaengkaew, J; Chanjula, P; Foiklang, S	Isolation and Characterization of Yeasts from Rumen Fluids for Potential Use as Additives in Ruminant Feeding	VETERINARY SCIENCES	2306-7381	2021	10.3390/vetsci8030052	3/1/2022
Ticona, ARP; Ullah, SF; Hamann, PRV; Lopes, FAC; Noronha, EF	Paenibacillus barengoltzii A1_50L2 as a Source of Plant Cell Wall Degrading Enzymes and Its Use on Lignocellulosic Biomass Hydrolysis	WASTE BIOMASS VALORI	1877-2641	2021	10.1007/s12649-020-00975-w	3/1/2022
Wakai, M; Hayashi, S; Chiba, Y; Koike, S; Nagashima, K; Kobayashi, Y	Growth and morphologic response of rumen methanogenic archaea and bacteria to cashew nut shell liquid and its alkylphenol components	ANIM SCI J	1344-3941	2021	10.1111/asj.13598	3/1/2022
Wang, WK; Li, WJ; Wu, QC; Wang, YL; Li, SL; Yang, HJ	Isolation and Identification of a Rumen Lactobacillus Bacteria and Its Degradation Potential of Gossypol in Cottonseed Meal during Solid-State Fermentation	MICROORGANISMS	2076-2607	2021	10.3390/microorganisms9112200	3/1/2022
Wang, Z; Wu, WQ; Cui, LC; Li, X; Kulyar, MFEA; Xiong, HQ; Zhou, NA; Yin, HH; Li, JK; Li, X	Isolation, characterization, and interaction of lignin-degrading bacteria from rumen of buffalo (Bubalus bubalis)	J BASIC MICROB	0233-111X	2021	10.1002/jobm.202100068	3/1/2022

Zada, S; Alam, S; AL Ayoubi, S; Shakeela, Q; Nisa, S; Niaz, Z; Khan, I; Ahmed, W; Bibi, Y; Ahmed, S; Qayyum, A	Biological Transformation of Zearalenone BY Some Bacterial Isolates Associated with Ruminant and Food Samples	TOXINS	2072-6651	2021	10.3390/toxins13100712	3/1/2022
Zhang, Y; Liang, S; Zhao, MD; Yang, X; Choi, SH; Li, GY	Screening and Identification of Latilactobacillus curvatus Z12 From Rumen Fluid of AN Adult Female Sika Deer as a Potential Probiotic for Feed Additives	FRONT VET SCI	2297-1769	2021	10.3389/fvets.2021.753527	3/1/2022
Zhao, J; Shao, T; Chen, S; Tao, X; Li, J	Characterization and identification of cellulase-producing Enterococcus species isolated from Tibetan yak (Bos grunniens) rumen and their application in various forage silages	J APPL MICROBIOL	1364-5072	2021	10.1111/jam.15014	3/1/2022
Zhao, JY; Jiang, YD; Gong, LM; Chen, XF; Xie, QL; Jin, Y; Du, J; Wang, SF; Liu, G	Mechanism of beta-cypermethrin metabolism BY Bacillus cereus GW-01	CHEM ENG J	1385-8947	2022	10.1016/j.cej.2021.132961	3/1/2022
Wang Y; Youssef N. H; Couger M.B; Hanafy R.A;Elshahed M.S ; Stajich J.E	Molecular Dating of the Emergence of Anaerobic Rumen Fungi and the Impact of Laterally Acquired Genes	MSYSTEMS	2379-5077	2019	10.1128/mSystems.00247-19	18/05/2022
Beijer W.H	Methane fermentation in the rumen of cattle	NATURE	0028-0836	1952	10.1038/170576a0	18/05/2022
Oppermann R.A; Nelson, W.O; Brown, R.E	In Vitro Studies on Methanogenic Rumen Bacteria	JOURNAL OF DAIRY SCIENCE	0022-0302	1957	10.3168/jds.S0022-0302(57)94554-X	18/05/2022
Smith P.H; Hungate R.E;	Isolation and characterization of Methanobacterium ruminantium n. sp	JOURNAL OF BACTERIOLOGY	0021-9193	1958	10.1128/jb.75.6.713-718.1958	18/05/2022
Rea S; Bowman J.P; Popovski S; Pimm C; Wright ADG	Methanobrevibacter millerae sp. nov. and Methanobrevibacter olleyae sp. nov., methanogens from the ovine and bovine rumen that can utilize formate for growth	INTERNATIONAL JOURNAL OF SYSTEMATIC AND EVOLUTIONARY MICROBIOLOGY	1466-5026	2007	10.1099/ijs.0.63984-0	18/05/2022
Lovley D.R;Greening R.C; Ferry J.G	Rapidly growing rumen methanogenic organism that synthesizes coenzyme M and has a high affinity for formate.	APPLIED AND ENVIRONMENTAL MICROBIOLOGY	0099-2240	1984	10.1128/aem.48.1.81-87.1984	18/05/2022
Li Y; Leahy S.C; Jeyanathan J; Henderson G; Cox F; Altermann E; Kelly W.J; Lambie S.C; Janssen P.H; Rakonjac J, Attwood G.T	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	1944-3277	2016	10.1186/s40793-016-0183-5	18/05/2022
Kelly W.J; Li D; Lambie S.C; Jeyanathan J; Cox F; Li Y; Attwood G.T; Altermann E; Leahy S.C	Complete Genome Sequence of Methanogenic Archaeon ISO4-G1, a Member of the Methanomassiliicoccales, Isolated from a Sheep Rumen	GENOMES ANNOUNCEMENTS	2169-8287	2016	10.1128/genomeA.00221-16	18/05/2022