Robert Wallace

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8469518/publications.pdf

Version: 2024-02-01

21 papers

2,400 citations

20 h-index

361045

752256 20 g-index

21 all docs

21 docs citations

times ranked

21

2698 citing authors

#	Article	IF	Citations
1	Impact and legacy of the highly cited paper by Blaxter and Clapperton (1965) Prediction of the amount of methane produced by ruminants. <i>Br. J. Nutr.</i> 19, 511-522. British Journal of Nutrition, 2022, , 1-10.	1.2	O
2	The rumen microbiome: balancing food security and environmental impacts. Nature Reviews Microbiology, 2021, 19, 553-566.	13.6	143
3	A heritable subset of the core rumen microbiome dictates dairy cow productivity and emissions. Science Advances, 2019, 5, eaav8391.	4.7	218
4	The ruminal microbiome associated with methane emissions from ruminant livestock. Journal of Animal Science and Biotechnology, 2017, 8, 7.	2.1	246
5	A Review of Bioinformatics Tools for Bio-Prospecting from Metagenomic Sequence Data. Frontiers in Genetics, 2017, 8, 23.	1.1	137
6	Taxon abundance, diversity, co-occurrence and network analysis of the ruminal microbiota in response to dietary changes in dairy cows. PLoS ONE, 2017, 12, e0180260.	1.1	84
7	Simple and Versatile Turbidimetric Monitoring of Bacterial Growth in Liquid Cultures Using a Customized 3D Printed Culture Tube Holder and a Miniaturized Spectrophotometer: Application to Facultative and Strictly Anaerobic Bacteria. Frontiers in Microbiology, 2016, 7, 1381.	1.5	29
8	Oral Samples as Non-Invasive Proxies for Assessing the Composition of the Rumen Microbial Community. PLoS ONE, 2016, 11, e0151220.	1.1	70
9	Bovine Host Genetic Variation Influences Rumen Microbial Methane Production with Best Selection Criterion for Low Methane Emitting and Efficiently Feed Converting Hosts Based on Metagenomic Gene Abundance. PLoS Genetics, 2016, 12, e1005846.	1.5	267
10	Metabolism of $\langle i \rangle \hat{l} \pm \langle i \rangle$ -linolenic acid during incubations with strained bovine rumen contents: products and mechanisms. British Journal of Nutrition, 2016, 115, 2093-2105.	1.2	28
11	Risks associated with endotoxins in feed additives produced by fermentation. Environmental Health, 2016, 15, 5.	1.7	36
12	The rumen microbial metagenome associated with high methane production in cattle. BMC Genomics, 2015, 16, 839.	1.2	306
13	Essential oils have different effects on human pathogenic and commensal bacteria in mixed faecal fermentations compared with pure cultures. Microbiology (United Kingdom), 2015, 161, 441-449.	0.7	26
14	Diversity and Community Composition of Methanogenic Archaea in the Rumen of Scottish Upland Sheep Assessed by Different Methods. PLoS ONE, 2014, 9, e106491.	1.1	32
15	Hydrogen and methane emissions from beef cattle and their rumen microbial community vary with diet, time after feeding and genotype. British Journal of Nutrition, 2014, 112, 398-407.	1.2	95
16	Effect of DNA extraction and sample preservation method on rumen bacterial population. Anaerobe, 2014, 29, 80-84.	1.0	81
17	Archaeal abundance in post-mortem ruminal digesta may help predict methane emissions from beef cattle. Scientific Reports, 2014, 4, 5892.	1.6	88
18	Sensitivity of pathogenic and commensal bacteria from the human colon to essential oils. Microbiology (United Kingdom), 2012, 158, 2870-2877.	0.7	66

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#	Article	lF	CITATIONS
19	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. International Journal of Systematic and Evolutionary Microbiology, 2011, 61, 795-803.	0.8	121
20	Metabolism of conjugated linoleic acids and 18 : 1 fatty acids by ruminal bacteria: products and mechanisms. Microbiology (United Kingdom), 2010, 156, 579-588.	0.7	124
21	16S rDNA library-based analysis of ruminal bacterial diversity. Antonie Van Leeuwenhoek, 2004, 86, 263-281.	0.7	203