

Itzhak Mizrahi

List of Publications by Year in descending order

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Version: 2024-02-01

69
papers

6,428
citations

126907

33
h-index

106344

65
g-index

81
all docs

81
docs citations

81
times ranked

6645
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Exploring the bovine rumen bacterial community from birth to adulthood. ISME Journal, 2013, 7, 1069-1079. | 9.8 | 799 |
| 2 | Specific microbiome-dependent mechanisms underlie the energy harvest efficiency of ruminants. ISME Journal, 2016, 10, 2958-2972. | 9.8 | 564 |
| 3 | Composition and Similarity of Bovine Rumen Microbiota across Individual Animals. PLoS ONE, 2012, 7, e33306. | 2.5 | 508 |
| 4 | Potential Role of the Bovine Rumen Microbiome in Modulating Milk Composition and Feed Efficiency. PLoS ONE, 2014, 9, e85423. | 2.5 | 417 |
| 5 | Tracking heavy water (D ₂ O) incorporation for identifying and sorting active microbial cells. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E194-203. | 7.1 | 359 |
| 6 | FEAST: fast expectation-maximization for microbial source tracking. Nature Methods, 2019, 16, 627-632. | 19.0 | 275 |
| 7 | Addressing Global Ruminant Agricultural Challenges Through Understanding the Rumen Microbiome: Past, Present, and Future. Frontiers in Microbiology, 2018, 9, 2161. | 3.5 | 255 |
| 8 | A heritable subset of the core rumen microbiome dictates dairy cow productivity and emissions. Science Advances, 2019, 5, eaav8391. | 10.3 | 218 |
| 9 | Calcium Handling in Human Induced Pluripotent Stem Cell Derived Cardiomyocytes. PLoS ONE, 2011, 6, e18037. | 2.5 | 165 |
| 10 | Towards lactic acid bacteria-based biorefineries. Biotechnology Advances, 2014, 32, 1216-1236. | 11.7 | 152 |
| 11 | Insights into the bovine rumen plasmidome. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5452-5457. | 7.1 | 145 |
| 12 | The rumen microbiome: balancing food security and environmental impacts. Nature Reviews Microbiology, 2021, 19, 553-566. | 28.6 | 143 |
| 13 | Emergence of plasmid stability under non-selective conditions maintains antibiotic resistance. Nature Communications, 2019, 10, 2595. | 12.8 | 141 |
| 14 | Man-made microbial resistances in built environments. Nature Communications, 2019, 10, 968. | 12.8 | 128 |
| 15 | Recycler: an algorithm for detecting plasmids from <i>de novo</i> assembly graphs. Bioinformatics, 2017, 33, 475-482. | 4.1 | 117 |
| 16 | Stochasticity constrained by deterministic effects of diet and age drive rumen microbiome assembly dynamics. Nature Communications, 2020, 11, 1904. | 12.8 | 117 |
| 17 | Host genetic selection for cold tolerance shapes microbiome composition and modulates its response to temperature. ELife, 2018, 7, . | 6.0 | 113 |
| 18 | Heritable Bovine Rumen Bacteria Are Phylogenetically Related and Correlated with the Cow's Capacity To Harvest Energy from Its Feed. MBio, 2017, 8, . | 4.1 | 110 |

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|----|--|------|-----------|
| 19 | Generating lineage-resolved, complete metagenome-assembled genomes from complex microbial communities. <i>Nature Biotechnology</i> , 2022, 40, 711-719. | 17.5 | 99 |
| 20 | Core gut microbial communities are maintained by beneficial interactions and strain variability in fish. <i>Nature Microbiology</i> , 2019, 4, 2456-2465. | 13.3 | 98 |
| 21 | The Road Not Taken: The Rumen Microbiome, Functional Groups, and Community States. <i>Trends in Microbiology</i> , 2019, 27, 538-549. | 7.7 | 92 |
| 22 | Islands in the stream: from individual to communal fiber degradation in the rumen ecosystem. <i>FEMS Microbiology Reviews</i> , 2019, 43, 362-379. | 8.6 | 88 |
| 23 | Auto-deconvolution and molecular networking of gas chromatography–mass spectrometry data. <i>Nature Biotechnology</i> , 2021, 39, 169-173. | 17.5 | 78 |
| 24 | Context-dependent dynamics lead to the assembly of functionally distinct microbial communities. <i>Nature Communications</i> , 2020, 11, 1440. | 12.8 | 73 |
| 25 | PlasClass improves plasmid sequence classification. <i>PLoS Computational Biology</i> , 2020, 16, e1007781. | 3.2 | 67 |
| 26 | Microbiome niche modification drives diurnal rumen community assembly, overpowering individual variability and diet effects. <i>ISME Journal</i> , 2018, 12, 2446-2457. | 9.8 | 66 |
| 27 | Diet-induced changes of redox potential underlie compositional shifts in the rumen archaeal community. <i>Environmental Microbiology</i> , 2017, 19, 174-184. | 3.8 | 53 |
| 28 | Similarity of the ruminal bacteria across individual lactating cows. <i>Anaerobe</i> , 2012, 18, 338-343. | 2.1 | 49 |
| 29 | Segregational Drift and the Interplay between Plasmid Copy Number and Evolvability. <i>Molecular Biology and Evolution</i> , 2019, 36, 472-486. | 8.9 | 46 |
| 30 | Compositional and functional dynamics of the bovine rumen methanogenic community across different developmental stages. <i>Environmental Microbiology</i> , 2017, 19, 3365-3373. | 3.8 | 43 |
| 31 | Transcriptome Analysis Reveals Common and Differential Response to Low Temperature Exposure Between Tolerant and Sensitive Blue Tilapia (<i>Oreochromis aureus</i>). <i>Frontiers in Genetics</i> , 2019, 10, 100. | 2.3 | 43 |
| 32 | Establishment of a Simple <i>Lactobacillus plantarum</i> Cell Consortium for Cellulase-Xylanase Synergistic Interactions. <i>Applied and Environmental Microbiology</i> , 2013, 79, 5242-5249. | 3.1 | 42 |
| 33 | Modeling the temporal dynamics of the gut microbial community in adults and infants. <i>PLoS Computational Biology</i> , 2019, 15, e1006960. | 3.2 | 42 |
| 34 | A combined cell-consortium approach for lignocellulose degradation by specialized <i>Lactobacillus plantarum</i> cells. <i>Biotechnology for Biofuels</i> , 2014, 7, 112. | 6.2 | 40 |
| 35 | A method for purifying high quality and high yield plasmid DNA for metagenomic and deep sequencing approaches. <i>Journal of Microbiological Methods</i> , 2013, 95, 272-279. | 1.6 | 38 |
| 36 | Insights Into Culturomics of the Rumen Microbiome. <i>Frontiers in Microbiology</i> , 2018, 9, 1999. | 3.5 | 35 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 37 | GNPS Dashboard: collaborative exploration of mass spectrometry data in the web browser. <i>Nature Methods</i> , 2022, 19, 134-136. | 19.0 | 35 |
| 38 | Rumen Symbioses. , 2013, , 533-544. | | 33 |
| 39 | Assembly of Synthetic Functional Cellulosomal Structures onto the Cell Surface of <i>Lactobacillus plantarum</i> , a Potent Member of the Gut Microbiome. <i>Applied and Environmental Microbiology</i> , 2018, 84, . | 3.1 | 33 |
| 40 | Broad phylogeny and functionality of cellulosomal components in the bovine rumen microbiome. <i>Environmental Microbiology</i> , 2017, 19, 185-197. | 3.8 | 32 |
| 41 | Short- and long-term low-salinity acclimation effects on the branchial and intestinal gene expression in the European seabass (<i>Dicentrarchus labrax</i>). <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2019, 231, 11-18. | 1.8 | 32 |
| 42 | Evaluation of Automated Ribosomal Intergenic Spacer Analysis for Bacterial Fingerprinting of Rumen Microbiome Compared to Pyrosequencing Technology. <i>Pathogens</i> , 2014, 3, 109-120. | 2.8 | 31 |
| 43 | Antibiotic effect and microbiome persistence vary along the European seabass gut. <i>Scientific Reports</i> , 2020, 10, 10003. | 3.3 | 31 |
| 44 | SCAPP: an algorithm for improved plasmid assembly in metagenomes. <i>Microbiome</i> , 2021, 9, 144. | 11.1 | 31 |
| 45 | On the oligomeric state of chloroplast chaperonin 10 and chaperonin 20. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2003, 1651, 76-84. | 2.3 | 28 |
| 46 | Effect of feeding ensiled mixture of pomegranate pulp and drier feeds on digestibility and milk performance in dairy cows. <i>Journal of Dairy Research</i> , 2016, 83, 35-41. | 1.4 | 25 |
| 47 | Protozoa populations are ecosystem engineers that shape prokaryotic community structure and function of the rumen microbial ecosystem. <i>ISME Journal</i> , 2022, 16, 1187-1197. | 9.8 | 25 |
| 48 | Unravelling plasmidome distribution and interaction with its hosting microbiome. <i>Environmental Microbiology</i> , 2020, 22, 32-44. | 3.8 | 22 |
| 49 | Differential effects of co-chaperonin homologs on cpn60 oligomers. <i>Cell Stress and Chaperones</i> , 2009, 14, 509-519. | 2.9 | 20 |
| 50 | Dietary salt levels affect digestibility, intestinal gene expression, and the microbiome, in Nile tilapia (<i>Oreochromis niloticus</i>). <i>PLoS ONE</i> , 2018, 13, e0202351. | 2.5 | 20 |
| 51 | Involvement of the Pta-AckA pathway in protein folding and aggregation. <i>Research in Microbiology</i> , 2009, 160, 80-84. | 2.1 | 19 |
| 52 | Lysozyme activity of the <i>Uminococcus champanellensis</i> cellulosome. <i>Environmental Microbiology</i> , 2016, 18, 5112-5122. | 3.8 | 19 |
| 53 | Requirement for the acetyl phosphate pathway in <i>Escherichia coli</i> ATP-dependent proteolysis. <i>Molecular Microbiology</i> , 2006, 62, 201-211. | 2.5 | 16 |
| 54 | Concepts and Consequences of a Core Gut Microbiota for Animal Growth and Development. <i>Annual Review of Animal Biosciences</i> , 2022, 10, 177-201. | 7.4 | 16 |

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|----|--|-----|-----------|
| 55 | Scalable Production of Cardiomyocytes Derived from c-Myc Free Induced Pluripotent Stem Cells. Tissue Engineering - Part A, 2011, 17, 1027-1037. | 3.1 | 15 |
| 56 | Involvement of dietary salt in shaping bacterial communities in European sea bass (<i>Dicentrarchus labrax</i>). <i>Journal of Applied Microbiology</i> , 2012, 112, 107-115. | 3.3 | 14 |
| 57 | Functional phylotyping approach for assessing intraspecific diversity of <i>Ruminococcus albus</i> within the rumen microbiome. <i>FEMS Microbiology Letters</i> , 2015, 362, 1-10. | 1.8 | 12 |
| 58 | Mammalian gut metabolomes mirror microbiome composition and host phylogeny. <i>ISME Journal</i> , 2022, 16, 1262-1274. | 9.8 | 12 |
| 59 | Diet Supplementation With Pomegranate Peel Extract Altered Odorants Emission From Fresh and Incubated Calves' Feces. <i>Frontiers in Sustainable Food Systems</i> , 2018, 2, . | 3.9 | 11 |
| 60 | The Role of the Rumen Microbiota in Determining the Feed Efficiency of Dairy Cows. , 2012, , 203-210. | | 8 |
| 61 | The rumen plasmidome. <i>Mobile Genetic Elements</i> , 2012, 2, 152-153. | 1.8 | 7 |
| 62 | Cell-surface display of designer cellulosomes by <i>Lactobacillus plantarum</i> . <i>Methods in Enzymology</i> , 2019, 617, 241-263. | 1.0 | 6 |
| 63 | Potential Use of Toxic Thermolabile Proteins To Study Protein Quality Control Systems. <i>Applied and Environmental Microbiology</i> , 2007, 73, 5951-5953. | 3.1 | 5 |
| 64 | Rapid adaptation for fibre degradation by changes in plasmid stoichiometry within <i>Lactobacillus plantarum</i> at the synthetic community level. <i>Microbial Biotechnology</i> , 2020, 13, 1748-1764. | 4.2 | 5 |
| 65 | Nanoscale resolution of microbial fiber degradation in action. <i>ELife</i> , 0, 11, . | 6.0 | 5 |
| 66 | Rumen Plasmids. , 2013, , 105-120. | | 3 |
| 67 | A method to the madness. <i>EMBO Reports</i> , 2021, 22, e52269. | 4.5 | 2 |
| 68 | Host-rumen microbiome interactions and influences on feed conversion efficiency (FCE), methane production and other productivity traits. <i>Burleigh Dodds Series in Agricultural Science</i> , 2020, , 547-566. | 0.2 | 2 |
| 69 | Tools for the study of protein quality control systems: Use of truncated homoserine trans-succinylase as a model substrate for ATP-dependent proteolysis in <i>Escherichia coli</i> . <i>Journal of Microbiological Methods</i> , 2007, 70, 82-85. | 1.6 | 1 |