

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	GNPS Dashboard: collaborative exploration of mass spectrometry data in the web browser. <i>Nature Methods</i> , 2022, 19, 134-136.	19.0	35
2	Generating lineage-resolved, complete metagenome-assembled genomes from complex microbial communities. <i>Nature Biotechnology</i> , 2022, 40, 711-719.	17.5	99
3	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
4	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
5	Mammalian gut metabolomes mirror microbiome composition and host phylogeny. <i>ISME Journal</i> , 2022, 16, 1262-1274.	9.8	12
6	Auto-deconvolution and molecular networking of gas chromatography-mass spectrometry data. <i>Nature Biotechnology</i> , 2021, 39, 169-173.	17.5	78
7	A method to the madness. <i>EMBO Reports</i> , 2021, 22, e52269.	4.5	2
8	The rumen microbiome: balancing food security and environmental impacts. <i>Nature Reviews Microbiology</i> , 2021, 19, 553-566.	28.6	143
9	SCAPP: an algorithm for improved plasmid assembly in metagenomes. <i>Microbiome</i> , 2021, 9, 144.	11.1	31
10	Unravelling plasmidome distribution and interaction with its hosting microbiome. <i>Environmental Microbiology</i> , 2020, 22, 32-44.	3.8	22
11	Antibiotic effect and microbiome persistence vary along the European seabass gut. <i>Scientific Reports</i> , 2020, 10, 10003.	3.3	31
12	Context-dependent dynamics lead to the assembly of functionally distinct microbial communities. <i>Nature Communications</i> , 2020, 11, 1440.	12.8	73
13	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
14	Stochasticity constrained by deterministic effects of diet and age drive rumen microbiome assembly dynamics. <i>Nature Communications</i> , 2020, 11, 1904.	12.8	117
15	PlasClass improves plasmid sequence classification. <i>PLoS Computational Biology</i> , 2020, 16, e1007781.	3.2	67
16	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
17	Modeling the temporal dynamics of the gut microbial community in adults and infants. <i>PLoS Computational Biology</i> , 2019, 15, e1006960.	3.2	42
18	A heritable subset of the core rumen microbiome dictates dairy cow productivity and emissions. <i>Science Advances</i> , 2019, 5, eaav8391.	10.3	218

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19	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
20	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
21	Cell-surface display of designer cellulosomes by <i>Lactobacillus plantarum</i> . <i>Methods in Enzymology</i> , 2019, 617, 241-263.	1.0	6
22	The Road Not Taken: The Rumen Microbiome, Functional Groups, and Community States. <i>Trends in Microbiology</i> , 2019, 27, 538-549.	7.7	92
23	FEAST: fast expectation-maximization for microbial source tracking. <i>Nature Methods</i> , 2019, 16, 627-632.	19.0	275
24	Emergence of plasmid stability under non-selective conditions maintains antibiotic resistance. <i>Nature Communications</i> , 2019, 10, 2595.	12.8	141
25	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
26	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
27	Man-made microbial resistances in built environments. <i>Nature Communications</i> , 2019, 10, 968.	12.8	128
28	Segregational Drift and the Interplay between Plasmid Copy Number and Evolvability. <i>Molecular Biology and Evolution</i> , 2019, 36, 472-486.	8.9	46
29	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
30	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
31	Addressing Global Ruminant Agricultural Challenges Through Understanding the Rumen Microbiome: Past, Present, and Future. <i>Frontiers in Microbiology</i> , 2018, 9, 2161.	3.5	255
32	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
33	Insights Into Culturomics of the Rumen Microbiome. <i>Frontiers in Microbiology</i> , 2018, 9, 1999.	3.5	35
34	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
35	Host genetic selection for cold tolerance shapes microbiome composition and modulates its response to temperature. <i>ELife</i> , 2018, 7, .	6.0	113
36	Recycler: an algorithm for detecting plasmids from <i>de novo</i> assembly graphs. <i>Bioinformatics</i> , 2017, 33, 475-482.	4.1	117

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37	Heritable Bovine Rumen Bacteria Are Phylogenetically Related and Correlated with the Cow's Capacity To Harvest Energy from Its Feed. <i>MBio</i> , 2017, 8, .	4.1	110
38	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
39	Broad phylogeny and functionality of cellulosomal components in the bovine rumen microbiome. <i>Environmental Microbiology</i> , 2017, 19, 185-197.	3.8	32
40	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
41	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
42	Specific microbiome-dependent mechanisms underlie the energy harvest efficiency of ruminants. <i>ISME Journal</i> , 2016, 10, 2958-2972.	9.8	564
43	Lysozyme activity of the <i>Ruminococcus champanellensis</i> cellulosome. <i>Environmental Microbiology</i> , 2016, 18, 5112-5122.	3.8	19
44	Tracking heavy water (D ₂ O) incorporation for identifying and sorting active microbial cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E194-203.	7.1	359
45	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
46	Potential Role of the Bovine Rumen Microbiome in Modulating Milk Composition and Feed Efficiency. <i>PLoS ONE</i> , 2014, 9, e85423.	2.5	417
47	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
48	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
49	Towards lactic acid bacteria-based biorefineries. <i>Biotechnology Advances</i> , 2014, 32, 1216-1236.	11.7	152
50	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
51	Rumen Symbioses. , 2013, , 533-544.		33
52	Exploring the bovine rumen bacterial community from birth to adulthood. <i>ISME Journal</i> , 2013, 7, 1069-1079.	9.8	799
53	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
54	Involvement of dietary salt in shaping bacterial communities in European sea bass (<i>Dicentrarchus labrax</i>). <i>Journal of Applied Microbiology</i> , 2013, 115, 100-108.	3.3	14

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55	Rumen Plasmids. , 2013, , 105-120.		3
56	The rumen plasmidome. Mobile Genetic Elements, 2012, 2, 152-153.	1.8	7
57	The Role of the Rumen Microbiota in Determining the Feed Efficiency of Dairy Cows. , 2012, , 203-210.		8
58	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
59	Similarity of the ruminal bacteria across individual lactating cows. Anaerobe, 2012, 18, 338-343.	2.1	49
60	Composition and Similarity of Bovine Rumen Microbiota across Individual Animals. PLoS ONE, 2012, 7, e33306.	2.5	508
61	Scalable Production of Cardiomyocytes Derived from c-Myc Free Induced Pluripotent Stem Cells. Tissue Engineering - Part A, 2011, 17, 1027-1037.	3.1	15
62	Calcium Handling in Human Induced Pluripotent Stem Cell Derived Cardiomyocytes. PLoS ONE, 2011, 6, e18037.	2.5	165
63	Differential effects of co-chaperonin homologs on cpn60 oligomers. Cell Stress and Chaperones, 2009, 14, 509-519.	2.9	20
64	Involvement of the Pta-AckA pathway in protein folding and aggregation. Research in Microbiology, 2009, 160, 80-84.	2.1	19
65	Potential Use of Toxic Thermolabile Proteins To Study Protein Quality Control Systems. Applied and Environmental Microbiology, 2007, 73, 5951-5953.	3.1	5
66	Tools for the study of protein quality control systems: Use of truncated homoserine trans-succinylase as a model substrate for ATP-dependent proteolysis in Escherichia coli. Journal of Microbiological Methods, 2007, 70, 82-85.	1.6	1
67	Requirement for the acetyl phosphate pathway in Escherichia coli ATP-dependent proteolysis. Molecular Microbiology, 2006, 62, 201-211.	2.5	16
68	On the oligomeric state of chloroplast chaperonin 10 and chaperonin 20. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2003, 1651, 76-84.	2.3	28
69	Nanoscale resolution of microbial fiber degradation in action. ELife, 0, 11, .	6.0	5