

Jorge Frias-Lopez

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

3,687
citations

236925

25
h-index

377865

34
g-index

37
all docs

37
docs citations

37
times ranked

4977
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic and Biochemical Characterization of the Na ⁺ /H ⁺ Antiporters of <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2021, 203, e0028421.	2.2	2
2	Long-term dynamics of the human oral microbiome during clinical disease progression. <i>BMC Biology</i> , 2021, 19, 240.	3.8	10
3	The Oral Microbiome and Cancer. <i>Frontiers in Immunology</i> , 2020, 11, 591088.	4.8	134
4	A priori estimation of sequencing effort in complex microbial metatranscriptomes. <i>Ecology and Evolution</i> , 2020, 10, 13382-13394.	1.9	3
5	The Function of the Oral Microbiome in Health and Disease. , 2020, , 141-173.		10
6	Virulence of the Pathogen <i>Porphyromonas gingivalis</i> Is Controlled by the CRISPR-Cas Protein Cas3. <i>MSystems</i> , 2020, 5, .	3.8	19
7	The Oral Mouse Microbiome Promotes Tumorigenesis in Oral Squamous Cell Carcinoma. <i>MSystems</i> , 2019, 4, .	3.8	50
8	Metatranscriptome of the Oral Microbiome in Health and Disease. <i>Journal of Dental Research</i> , 2018, 97, 492-500.	5.2	80
9	Increased virulence of the oral microbiome in oral squamous cell carcinoma revealed by metatranscriptome analyses. <i>International Journal of Oral Science</i> , 2018, 10, 32.	8.6	88
10	The effect of the stress hormone cortisol on the metatranscriptome of the oral microbiome. <i>Npj Biofilms and Microbiomes</i> , 2018, 4, 25.	6.4	52
11	Functional profiles of coronal and dentin caries in children. <i>Journal of Oral Microbiology</i> , 2018, 10, 1495976.	2.7	33
12	Bacterial metatranscriptome of dentin caries. <i>Journal of Oral Microbiology</i> , 2017, 9, 1325194.	2.7	8
13	Potassium is a key signal in host-microbiome dysbiosis in periodontitis. <i>PLoS Pathogens</i> , 2017, 13, e1006457.	4.7	40
14	Functional signatures of oral dysbiosis during periodontitis progression revealed by microbial metatranscriptome analysis. <i>Genome Medicine</i> , 2015, 7, 27.	8.2	241
15	Targeting specific bacteria in the oral microbiome. <i>Trends in Microbiology</i> , 2015, 23, 527-528.	7.7	4
16	Beyond microbial community composition: functional activities of the oral microbiome in health and disease. <i>Microbes and Infection</i> , 2015, 17, 505-516.	1.9	137
17	Small RNA Transcriptome of the Oral Microbiome during Periodontitis Progression. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6688-6699.	3.1	28
18	The Periodontal Pathogen <i>Porphyromonas gingivalis</i> Induces Expression of Transposases and Cell Death of <i>Streptococcus mitis</i> in a Biofilm Model. <i>Infection and Immunity</i> , 2014, 82, 3374-3382.	2.2	32

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19	Community-wide transcriptome of the oral microbiome in subjects with and without periodontitis. <i>ISME Journal</i> , 2014, 8, 1659-1672.	9.8	295
20	Biofilm Control Strategies in Dental Health. Springer Series on Biofilms, 2014, , 291-326.	0.1	0
21	Lessons learned and unlearned in periodontal microbiology. <i>Periodontology 2000</i> , 2013, 62, 95-162.	13.4	268
22	Transplantation-Associated Long-Term Immunosuppression Promotes Oral Colonization by Potentially Opportunistic Pathogens without Impacting Other Members of the Salivary Bacteriome. <i>Vaccine Journal</i> , 2013, 20, 920-930.	3.1	54
23	Effect of Periodontal Pathogens on the Metatranscriptome of a Healthy Multispecies Biofilm Model. <i>Journal of Bacteriology</i> , 2012, 194, 2082-2095.	2.2	85
24	Correlation Network Analysis Applied to Complex Biofilm Communities. <i>PLoS ONE</i> , 2011, 6, e28438.	2.5	108
25	Temporal dynamics of <i>Prochlorococcus</i> ecotypes in the Atlantic and Pacific oceans. <i>ISME Journal</i> , 2010, 4, 1252-1264.	9.8	221
26	UV hyper-resistance in <i>Prochlorococcus</i> MED4 results from a single base pair deletion just upstream of an operon encoding nudix hydrolase and photolyase. <i>Environmental Microbiology</i> , 2010, 12, 1978-1988.	3.8	29
27	Use of stable isotope-labelled cells to identify active grazers of picocyanobacteria in ocean surface waters. <i>Environmental Microbiology</i> , 2009, 11, 512-525.	3.8	138
28	Microbial community gene expression in ocean surface waters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3805-3810.	7.1	699
29	Bacterial communities inhabiting the healthy tissues of two Caribbean reef corals: interspecific and spatial variation. <i>Coral Reefs</i> , 2005, 24, 129-137.	2.2	60
30	Bacterial Community Associated with Black Band Disease in Corals. <i>Applied and Environmental Microbiology</i> , 2004, 70, 5955-5962.	3.1	124
31	Identification of Differential Gene Expression in Bacteria Associated with Coral Black Band Disease by Using RNA-Arbitrarily Primed PCR. <i>Applied and Environmental Microbiology</i> , 2004, 70, 3687-3694.	3.1	22
32	Partitioning of bacterial communities between travertine depositional facies at Mammoth Hot Springs, Yellowstone National Park, U.S.A.. <i>Canadian Journal of Earth Sciences</i> , 2003, 40, 1531-1548.	1.3	78
33	Cyanobacteria Associated with Coral Black Band Disease in Caribbean and Indo-Pacific Reefs. <i>Applied and Environmental Microbiology</i> , 2003, 69, 2409-2413.	3.1	127
34	Partitioning of Bacterial Communities between Seawater and Healthy, Black Band Diseased, and Dead Coral Surfaces. <i>Applied and Environmental Microbiology</i> , 2002, 68, 2214-2228.	3.1	386
35	Identification of cell wall proteins of <i>Bacteroides fragilis</i> to which bacteriophage B40-8 binds specifically The PIR accession numbers for the sequences reported in this paper are A59325 (BactA) and B59325 (BactB).. <i>Microbiology (United Kingdom)</i> , 2001, 147, 281-288.	1.8	12