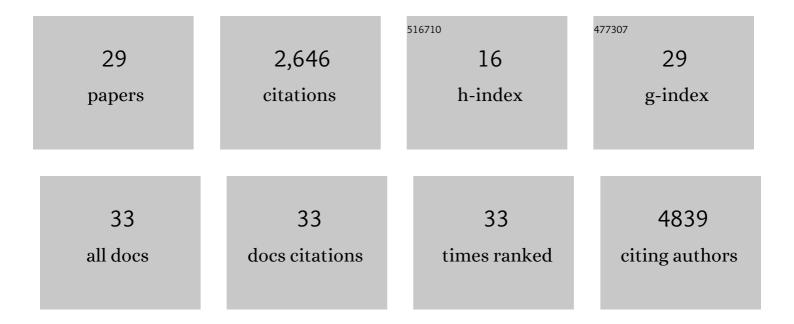
LÃ-Â-via Soares Zaramela

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2905256/publications.pdf

Version: 2024-02-01



#	Article	IF	CITATIONS
1	Linking anaerobic gut bacteria and cardiovascular disease. Nature Microbiology, 2022, 7, 14-15.	13.3	3
2	The Ubiquitous Human Skin Commensal Staphylococcus hominis Protects against Opportunistic Pathogens. MBio, 2022, 13, .	4.1	24
3	Host DNA Depletion in Saliva Samples for Improved Shotgun Metagenomics. Methods in Molecular Biology, 2021, 2327, 87-92.	0.9	1
4	The sum is greater than the parts: exploiting microbial communities to achieve complex functions. Current Opinion in Biotechnology, 2021, 67, 149-157.	6.6	25
5	A comparison of DNA/RNA extraction protocols for high-throughput sequencing of microbial communities. BioTechniques, 2021, 70, 149-159.	1.8	17
6	Combining Functional Genomics and Whole-Genome Sequencing to Detect Antibiotic Resistance Genes in Bacterial Strains Co-Occurring Simultaneously in a Brazilian Hospital. Antibiotics, 2021, 10, 419.	3.7	3
7	Intestinal α1-2-Fucosylation Contributes to Obesity and Steatohepatitis in Mice. Cellular and Molecular Gastroenterology and Hepatology, 2021, 12, 293-320.	4.5	14
8	Transcriptional profiling of lung macrophages identifies a predictive signature for inflammatory lung disease in preterm infants. Communications Biology, 2020, 3, 259.	4.4	25
9	Genomic and Transcriptomic Evidence Supports Methane Metabolism in <i>Archaeoglobi</i> . MSystems, 2020, 5, .	3.8	33
10	Interplay of Staphylococcal and Host Proteases Promotes Skin Barrier Disruption in Netherton Syndrome. Cell Reports, 2020, 30, 2923-2933.e7.	6.4	56
11	Environmental stimuli drive a transition from cooperation to competition in synthetic phototrophic communities. Nature Microbiology, 2019, 4, 2184-2191.	13.3	54
12	Gut bacteria responding to dietary change encode sialidases that exhibit preference for red meat-associated carbohydrates. Nature Microbiology, 2019, 4, 2082-2089.	13.3	56
13	Establishing microbial composition measurement standards with reference frames. Nature Communications, 2019, 10, 2719.	12.8	428
14	Deciphering the microbiome and virome composition of patients with Atopic Dermatitis and Eczema Herpeticum (ADEH+). Journal of Allergy and Clinical Immunology, 2019, 143, AB302.	2.9	2
15	The impact of skin care products on skin chemistry and microbiome dynamics. BMC Biology, 2019, 17, 47.	3.8	101
16	A multi-omics evaluation of the non-lesional skin surface identifies atopic dermatitis with food allergy (AD FA+) as a unique endotype. Journal of Allergy and Clinical Immunology, 2019, 143, AB125.	2.9	2
17	Quorum sensing between bacterial species on the skin protects against epidermal injury in atopic dermatitis. Science Translational Medicine, 2019, 11, .	12.4	185
18	The nonlesional skin surface distinguishes atopic dermatitis with food allergy as a unique endotype. Science Translational Medicine, 2019, 11, .	12.4	159

LÃÂVIA SOARES ZARAMELA

#	Article	IF	CITATIONS
19	Identification of potential target genes associated with the reversion of androgen-dependent skeletal muscle atrophy. Archives of Biochemistry and Biophysics, 2019, 663, 173-182.	3.0	6
20	The social network of microorganisms — how auxotrophies shape complex communities. Nature Reviews Microbiology, 2018, 16, 383-390.	28.6	311
21	Optimization of carbon and energy utilization through differential translational efficiency. Nature Communications, 2018, 9, 4474.	12.8	35
22	Internal RNAs overlapping coding sequences can drive the production of alternative proteins in archaea. RNA Biology, 2018, 15, 1-14.	3.1	14
23	American Gut: an Open Platform for Citizen Science Microbiome Research. MSystems, 2018, 3, .	3.8	604
24	Improving saliva shotgun metagenomics by chemical host DNA depletion. Microbiome, 2018, 6, 42.	11.1	218
25	Metabolic capability and in situ activity of microorganisms in an oil reservoir. Microbiome, 2018, 6, 5.	11.1	70
26	Elucidation of complexity and prediction of interactions in microbial communities. Microbial Biotechnology, 2017, 10, 1500-1522.	4.2	117
27	Development of New Modular Genetic Tools for Engineering the Halophilic Archaeon Halobacterium salinarum. PLoS ONE, 2015, 10, e0129215.	2.5	9
28	Sense overlapping transcripts in IS <i>1341</i> -type transposase genes are functional non-coding RNAs in archaea. RNA Biology, 2015, 12, 490-500.	3.1	27
29	Transcription Start Site Associated RNAs (TSSaRNAs) Are Ubiquitous in All Domains of Life. PLoS ONE,	2.5	14