

Felipe Cabarcas Jaramillo

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

493
citations

933447

10
h-index

794594

19
g-index

26
all docs

26
docs citations

26
times ranked

686
citing authors

#	ARTICLE	IF	CITATIONS
1	Assessment of the microbial community and biocide resistance profile in production and injection waters from an Andean oil reservoir in Colombia. <i>International Biodeterioration and Biodegradation</i> , 2021, 157, 105137.	3.9	5
2	<i>Cryptosporidium hominis</i> Phylogenomic Analysis Reveals Separate Lineages With Continental Segregation. <i>Frontiers in Genetics</i> , 2021, 12, 740940.	2.3	3
3	Metagenomic Analysis of Biocide-Treated Neotropical Oil Reservoir Water Unveils Microdiversity of Thermophile <i>Tepidiphilus</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 741555.	3.5	4
4	Annual microbial community dynamics in a full-scale anaerobic sludge digester from a wastewater treatment plant in Colombia. <i>Science of the Total Environment</i> , 2020, 726, 138479.	8.0	23
5	Comparative genomic analysis of the principal <i>Cryptosporidium</i> species that infect humans. <i>PeerJ</i> , 2020, 8, e10478.	2.0	7
6	DATMA: Distributed AuTomatic Metagenomic Assembly and annotation framework. <i>PeerJ</i> , 2020, 8, e9762.	2.0	2
7	Metagenomic assessment of the microbial community and methanogenic pathways in biosolids from a municipal wastewater treatment plant in Medellín, Colombia. <i>Science of the Total Environment</i> , 2019, 648, 572-581.	8.0	26
8	Differential determinants of virulence in two <i>Mycobacterium tuberculosis</i> Colombian clinical isolates of the LAM09 family. <i>Virulence</i> , 2019, 10, 695-710.	4.4	36
9	Efficient public-key operation in multivariate schemes. <i>Advances in Mathematics of Communications</i> , 2019, 13, 343-371.	0.7	1
10	CLAME: a new alignment-based binning algorithm allows the genomic description of a novel <i>Xanthomonadaceae</i> from the Colombian Andes. <i>BMC Genomics</i> , 2018, 19, 858.	2.8	2
11	Early-Onset Invasive Infection Due to <i>Corynespora cassiicola</i> Associated with Compound Heterozygous <i>CARD9</i> Mutations in a Colombian Patient. <i>Journal of Clinical Immunology</i> , 2018, 38, 794-803.	3.8	40
12	Inherited p40phox deficiency differs from classic chronic granulomatous disease. <i>Journal of Clinical Investigation</i> , 2018, 128, 3957-3975.	8.2	99
13	Microbiota bacteriana asociada al papel moneda de circulación en Colombia. <i>Infectio</i> , 2016, 20, 218-224.	0.4	2
14	Transcriptome profiling of the cysticercus stage of the laboratory model <i>Taenia crassiceps</i> , strain ORF. <i>Acta Tropica</i> , 2016, 154, 50-62.	2.0	13
15	On the simulation of large-scale architectures using multiple application abstraction levels. <i>Transactions on Architecture and Code Optimization</i> , 2012, 8, 1-20.	2.0	33
16	DMA++: On the Fly Data Realignment for On-Chip Memories. <i>IEEE Transactions on Computers</i> , 2012, 61, 237-250.	3.4	2
17	Scalable multicore architectures for long DNA sequence comparison. <i>Concurrency Computation Practice and Experience</i> , 2011, 23, 2205-2219.	2.2	1
18	Parametrizing multicore architectures for multiple sequence alignment. , 2011, , .		0

#	ARTICLE	IF	CITATIONS
19	Breaking the bandwidth wall in chip multiprocessors. , 2011, , .		5
20	Trace-driven simulation of multithreaded applications. , 2011, , .		33
21	The SARC Architecture. IEEE Micro, 2010, 30, 16-29.	1.8	39
22	Comparing last-level cache designs for CMP architectures. , 2010, , .		2
23	Task Superscalar: An Out-of-Order Task Pipeline. , 2010, , .		86
24	Interleaving granularity on high bandwidth memory architecture for CMPs. , 2010, , .		1
25	Long DNA Sequence Comparison on Multicore Architectures. Lecture Notes in Computer Science, 2010, , 247-259.	1.3	10
26	Approaching the Slepianâ€™Wolf boundary using practical channel codes. Signal Processing, 2006, 86, 3096-3101.	3.7	18