Felipe Cabarcas Jaramillo

List of Publications by Year
in descending order

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	Inherited p40phox deficiency differs from classic chronic granulomatous disease. Journal of Clinical Investigation, 2018, 128, 3957-3975.	8.2	99
2	Task Superscalar: An Out-of-Order Task Pipeline. , 2010, , .		86
3	Early-Onset Invasive Infection Due to Corynespora cassiicola Associated with Compound Heterozygous CARD9 Mutations in a Colombian Patient. Journal of Clinical Immunology, 2018, 38, 794-803.	3.8	40
4	The SARC Architecture. IEEE Micro, 2010, 30, 16-29.	1.8	39
5	Differential determinants of virulence in two Mycobacterium tuberculosis Colombian clinical isolates of the LAM09 family. Virulence, 2019, 10, 695-710.	4.4	36
6	Trace-driven simulation of multithreaded applications. , 2011, , .		33
7	On the simulation of large-scale architectures using multiple application abstraction levels. Transactions on Architecture and Code Optimization, 2012, 8, 1-20.	2.0	33
8	Metagenomic assessment of the microbial community and methanogenic pathways in biosolids from a municipal wastewater treatment plant in Medellín, Colombia. Science of the Total Environment, 2019, 648, 572-581.	8.0	26
9	Annual microbial community dynamics in a full-scale anaerobic sludge digester from a wastewater treatment plant in Colombia. Science of the Total Environment, 2020, 726, 138479.	8.0	23
10	Approaching the Slepian–Wolf boundary using practical channel codes. Signal Processing, 2006, 86, 3096-3101.	3.7	18
11	Transcriptome profiling of the cysticercus stage of the laboratory model Taenia crassiceps, strain ORF. Acta Tropica, 2016, 154, 50-62.	2.0	13
12	Long DNA Sequence Comparison on Multicore Architectures. Lecture Notes in Computer Science, 2010, , 247-259.	1.3	10
13	Comparative genomic analysis of the principal <i>Cryptosporidium</i> species that infect humans. PeerJ, 2020, 8, e10478.	2.0	7
14	Breaking the bandwidth wall in chip multiprocessors. , 2011, , .		5
15	Assessment of the microbial community and biocide resistance profile in production and injection waters from an Andean oil reservoir in Colombia. International Biodeterioration and Biodegradation, 2021, 157, 105137.	3.9	5
16	Metagenomic Analysis of Biocide-Treated Neotropical Oil Reservoir Water Unveils Microdiversity of Thermophile Tepidiphilus. Frontiers in Microbiology, 2021, 12, 741555.	3.5	4
17	Cryptosporidium hominis Phylogenomic Analysis Reveals Separate Lineages With Continental Segregation. Frontiers in Genetics, 2021, 12, 740940.	2.3	3
18	Comparing last-level cache designs for CMP architectures. , 2010, , .		2

#	Article	IF	Citations
19	DMA++: On the Fly Data Realignment for On-Chip Memories. IEEE Transactions on Computers, 2012, 61, 237-250.	3.4	2
20	Microbiota bacteriana asociada al papel moneda de circulaciÃ³n en Colombia. Infectio, 2016, 20, 218-224.	0.4	2
21	CLAME: a new alignment-based binning algorithm allows the genomic description of a novel Xanthomonadaceae from the Colombian Andes. BMC Genomics, 2018, 19, 858.	2.8	2
22	DATMA: Distributed AuTomatic Metagenomic Assembly and annotation framework. PeerJ, 2020, 8, e9762.	2.0	2
23	Interleaving granularity on high bandwidth memory architecture for CMPs. , 2010, , .		1
24	Scalable multicore architectures for long DNA sequence comparison. Concurrency Computation Practice and Experience, 2011, 23, 2205-2219.	2.2	1
25	Efficient public-key operation in multivariate schemes. Advances in Mathematics of Communications, 2019, 13, 343-371.	0.7	1
26	Parametrizing multicore architectures for multiple sequence alignment. , 2011, , .		0