

Mohammed H Alser

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

741
citations

840776

11
h-index

996975

15
g-index

28
all docs

28
docs citations

28
times ranked

507
citing authors

#	ARTICLE	IF	CITATIONS
1	GenStore: a high-performance in-storage processing system for genome sequence analysis. , 2022, , .		21
2	Critical Assessment of Metagenome Interpretation: the second round of challenges. Nature Methods, 2022, 19, 429-440.	19.0	133
3	SneakySnake: a fast and accurate universal genome pre-alignment filter for CPUs, GPUs and FPGAs. Bioinformatics, 2021, 36, 5282-5290.	4.1	19
4	SIMDRAM: a framework for bit-serial SIMD processing using DRAM. , 2021, , .		54
5	IChannels: Exploiting Current Management Mechanisms to Create Covert Channels in Modern Processors. , 2021, , .		6
6	GateKeeper-GPU: Fast and Accurate Pre-Alignment Filtering in Short Read Mapping. , 2021, , .		5
7	FPGA-Based Near-Memory Acceleration of Modern Data-Intensive Applications. IEEE Micro, 2021, 41, 39-48.	1.8	36
8	Technology dictates algorithms: recent developments in read alignment. Genome Biology, 2021, 22, 249.	8.8	51
9	Accelerating Genome Analysis: A Primer on an Ongoing Journey. IEEE Micro, 2020, 40, 65-75.	1.8	41
10	Metalign: efficient alignment-based metagenomic profiling via containment min hash. Genome Biology, 2020, 21, 242.	8.8	29
11	Techniques for Reducing the Connected-Standby Energy Consumption of Mobile Devices. , 2020, , .		16
12	Apollo: a sequencing-technology-independent, scalable and accurate assembly polishing algorithm. Bioinformatics, 2020, 36, 3669-3679.	4.1	26
13	GenASM: A High-Performance, Low-Power Approximate String Matching Acceleration Framework for Genome Sequence Analysis. , 2020, , .		37
14	NATSA: A Near-Data Processing Accelerator for Time Series Analysis. , 2020, , .		24
15	FlexWatts: A Power- and Workload-Aware Hybrid Power Delivery Network for Energy-Efficient Microprocessors. , 2020, , .		1
16	MiCoP: microbial community profiling method for detecting viral and fungal organisms in metagenomic samples. BMC Genomics, 2019, 20, 423.	2.8	22
17	Shouji: a fast and efficient pre-alignment filter for sequence alignment. Bioinformatics, 2019, 35, 4255-4263.	4.1	44
18	GRIM-Filter: Fast seed location filtering in DNA read mapping using processing-in-memory technologies. BMC Genomics, 2018, 19, 89.	2.8	92

#	ARTICLE	IF	CITATIONS
19	GateKeeper: a new hardware architecture for accelerating pre-alignment in DNA short read mapping. <i>Bioinformatics</i> , 2017, 33, 3355-3363.	4.1	67
20	Can you Really Anonymize the Donors of Genomic Data in Today's Digital World?. <i>Lecture Notes in Computer Science</i> , 2016, , 237-244.	1.3	1
21	A wide-range programmable frequency synthesizer based on a finite state machine filter. <i>International Journal of Electronics</i> , 2013, 100, 1546-1556.	1.4	0
22	Design and Characterization of Low Power and Low Noise Truly All-Digital Clock and Data Recovery Circuit for SERDES Devices. <i>Journal of Low Power Electronics</i> , 2013, 9, 63-72.	0.6	1
23	Design and FPGA implementation of PLL-based quarter-rate clock and data recovery circuit. , 2012, , .		2
24	Design of an All-Digital Synchronized Frequency Multiplier Based on a Dual-Loop (D/FLL) Architecture. <i>VLSI Design</i> , 2012, 2012, 1-7.	0.5	2
25	An FPGA-based design and implementation of an all-digital serializer for inter module communication in SoC. <i>IEICE Electronics Express</i> , 2011, 8, 2017-2023.	0.8	4
26	Design and modeling of low-power clockless serial link for data communication systems. , 2011, , .		4