

Richard Hughey

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

2,384
citations

758635

12
h-index

940134

16
g-index

21
all docs

21
docs citations

21
times ranked

2775
citing authors

#	ARTICLE	IF	CITATIONS
1	Power/Energy Minimization Techniques for Variability-Aware High-Performance 16-nm 6T-SRAM. IEEE Access, 2016, 4, 594-613.	2.6	14
2	Confronting the Variability Issues Affecting the Performance of Next-Generation SRAM Design to Optimize and Predict the Speed and Yield. IEEE Access, 2014, 2, 577-601.	2.6	18
3	Finding the Next Computational Model: Experience with the UCSC Kestrel. Journal of Signal Processing Systems, 2008, 53, 171-186.	1.4	1
4	The UCSC Kestrel Application-Unspecific Processor. , 2006, , .		3
5	Optimizing neural networks on SIMD parallel computers. Parallel Computing, 2005, 31, 97-115.	1.3	9
6	Alkaline hemolysis fragility is dependent on cell shape: Results from a morphology tracker. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2005, 65A, 116-123.	1.1	14
7	A Range-Compaction Heuristic for Graph Coloring. Journal of Heuristics, 2003, 9, 489-506.	1.1	2
8	Bioinformatics: A New Field in Engineering Education. Journal of Engineering Education, 2003, 92, 101-104.	1.9	10
9	Assignment of homology to genome sequences using a library of hidden Markov models that represent all proteins of known structure. Journal of Molecular Biology, 2001, 313, 903-919.	2.0	1,092
10	What is the value added by human intervention in protein structure prediction?. Proteins: Structure, Function and Bioinformatics, 2001, 45, 86-91.	1.5	104
11	Molecular Fingerprinting on the SIMD Parallel Processor Kestrel. , 2000, , 323-34.		2
12	Sequence Analysis With the Kestrel SIMD Parallel Processor. , 2000, , 263-74.		10
13	High-Performance Computing for Computational Biology. , 2000, , .		0
14	Predicting protein structure using only sequence information. Proteins: Structure, Function and Bioinformatics, 1999, 37, 121-125.	1.5	76
15	Predicting protein structure using only sequence information. , 1999, 37, 121.		1
16	Predicting protein structure using only sequence information. Proteins: Structure, Function and Bioinformatics, 1999, Suppl 3, 121-5.	1.5	52
17	Kestrel: A Programmable Array for Sequence Analysis. Journal of Signal Processing Systems, 1998, 19, 115-126.	1.0	20
18	Sequence comparisons using multiple sequences detect three times as many remote homologues as pairwise methods. Journal of Molecular Biology, 1998, 284, 1201-1210.	2.0	498

#	ARTICLE	IF	CITATIONS
19	Predicting protein structure using hidden Markov models. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 134-139.	1.5	110
20	Predicting protein structure using hidden Markov models. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 134-139.	1.5	31
21	Stochastic context-free grammars for tRNA modeling. <i>Nucleic Acids Research</i> , 1994, 22, 5112-5120.	6.5	317