

Richard Hughey

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

2,384
citations

759233

12
h-index

940533

16
g-index

21
all docs

21
docs citations

21
times ranked

2775
citing authors

#	ARTICLE	IF	CITATIONS
1	Assignment of homology to genome sequences using a library of hidden Markov models that represent all proteins of known structure. <i>Journal of Molecular Biology</i> , 2001, 313, 903-919.	4.2	1,092
2	Sequence comparisons using multiple sequences detect three times as many remote homologues as pairwise methods. <i>Journal of Molecular Biology</i> , 1998, 284, 1201-1210.	4.2	498
3	Stochastic context-free grammars for tRNA modeling. <i>Nucleic Acids Research</i> , 1994, 22, 5112-5120.	14.5	317
4	Predicting protein structure using hidden Markov models. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 134-139.	2.6	110
5	What is the value added by human intervention in protein structure prediction?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 86-91.	2.6	104
6	Predicting protein structure using only sequence information. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 121-125.	2.6	76
7	Predicting protein structure using only sequence information. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 121-125.	2.6	52
8	Predicting protein structure using hidden Markov models. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 134-139.	2.6	31
9	Kestrel: A Programmable Array for Sequence Analysis. <i>Journal of Signal Processing Systems</i> , 1998, 19, 115-126.	1.0	20
10	Confronting the Variability Issues Affecting the Performance of Next-Generation SRAM Design to Optimize and Predict the Speed and Yield. <i>IEEE Access</i> , 2014, 2, 577-601.	4.2	18
11	Alkaline hemolysis fragility is dependent on cell shape: Results from a morphology tracker. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2005, 65A, 116-123.	1.5	14
12	Power/Energy Minimization Techniques for Variability-Aware High-Performance 16-nm 6T-SRAM. <i>IEEE Access</i> , 2016, 4, 594-613.	4.2	14
13	Bioinformatics: A New Field in Engineering Education. <i>Journal of Engineering Education</i> , 2003, 92, 101-104.	3.0	10
14	Sequence Analysis With the Kestrel SIMD Parallel Processor. , 2000, , 263-74.		10
15	Optimizing neural networks on SIMD parallel computers. <i>Parallel Computing</i> , 2005, 31, 97-115.	2.1	9
16	The UCSC Kestrel Application-Unspecific Processor. , 2006, , .		3
17	A Range-Compaction Heuristic for Graph Coloring. <i>Journal of Heuristics</i> , 2003, 9, 489-506.	1.4	2
18	Molecular Fingerprinting on the SIMD Parallel Processor Kestrel. , 2000, , 323-34.		2

#	ARTICLE	IF	CITATIONS
19	Finding the Next Computational Model: Experience with the UCSC Kestrel. Journal of Signal Processing Systems, 2008, 53, 171-186.	2.1	1
20	Predicting protein structure using only sequence information. , 1999, 37, 121.		1
21	High-Performance Computing for Computational Biology. , 2000, , .		0