

Martin Tompa

List of Publications by Year in descending order

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26
papers

3,952
citations

394421

19
h-index

642732

23
g-index

27
all docs

27
docs citations

27
times ranked

3726
citing authors

#	ARTICLE	IF	CITATIONS
1	Assessing computational tools for the discovery of transcription factor binding sites. <i>Nature Biotechnology</i> , 2005, 23, 137-144.	17.5	1,121
2	Rv3133c/dosR is a transcription factor that mediates the hypoxic response of <i>Mycobacterium tuberculosis</i> . <i>Molecular Microbiology</i> , 2003, 48, 833-843.	2.5	674
3	Identification of 22 candidate structured RNAs in bacteria using the CMfinder comparative genomics pipeline. <i>Nucleic Acids Research</i> , 2007, 35, 4809-4819.	14.5	292
4	Discovery of Regulatory Elements by a Computational Method for Phylogenetic Footprinting. <i>Genome Research</i> , 2002, 12, 739-748.	5.5	268
5	YMF: a program for discovery of novel transcription factor binding sites by statistical overrepresentation. <i>Nucleic Acids Research</i> , 2003, 31, 3586-3588.	14.5	203
6	Discovery of novel transcription factor binding sites by statistical overrepresentation. <i>Nucleic Acids Research</i> , 2002, 30, 5549-5560.	14.5	171
7	PhyME: a probabilistic algorithm for finding motifs in sets of orthologous sequences. <i>BMC Bioinformatics</i> , 2004, 5, 170.	2.6	158
8	FootPrinter: a program designed for phylogenetic footprinting. <i>Nucleic Acids Research</i> , 2003, 31, 3840-3842.	14.5	143
9	Algorithms for Phylogenetic Footprinting. <i>Journal of Computational Biology</i> , 2002, 9, 211-223.	1.6	138
10	Evolutionarily conserved sequence elements that positively regulate IFN- γ expression in T cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12622-12627.	7.1	124
11	Space-bounded hierarchies and probabilistic computations. <i>Journal of Computer and System Sciences</i> , 1984, 28, 216-230.	1.2	108
12	Finding motifs using random projections. , 2001, , .		101
13	Two Applications of Inductive Counting for Complementation Problems. <i>SIAM Journal on Computing</i> , 1989, 18, 559-578.	1.0	100
14	A Computational Pipeline for High- Throughput Discovery of cis-Regulatory Noncoding RNA in Prokaryotes. <i>PLoS Computational Biology</i> , 2007, 3, e126.	3.2	77
15	Analysis of computational approaches for motif discovery. <i>Algorithms for Molecular Biology</i> , 2006, 1, 8.	1.2	58
16	Discovery of regulatory elements in vertebrates through comparative genomics. <i>Nature Biotechnology</i> , 2005, 23, 1249-1256.	17.5	48
17	Time-space tradeoffs for computing functions, using connectivity properties of their circuits. <i>Journal of Computer and System Sciences</i> , 1980, 20, 118-132.	1.2	47
18	A New Pebble Game that Characterizes Parallel Complexity Classes. <i>SIAM Journal on Computing</i> , 1989, 18, 533-549.	1.0	31

#	ARTICLE	IF	CITATIONS
19	MicroFootPrinter: a tool for phylogenetic footprinting in prokaryotic genomes. Nucleic Acids Research, 2006, 34, W366-W368.	14.5	25
20	Two Familiar Transitive Closure Algorithms Which Admit No Polynomial Time, Sublinear Space Implementations. SIAM Journal on Computing, 1982, 11, 130-137.	1.0	22
21	Communication-Space Tradeoffs for Unrestricted Protocols. SIAM Journal on Computing, 1994, 23, 652-661.	1.0	14
22	Trade-offs between communication and space. Journal of Computer and System Sciences, 1992, 45, 296-315.	1.2	8
23	A Time-Space Tradeoff for Undirected Graph Traversal by Walking Automata. SIAM Journal on Computing, 1998, 28, 1051-1072.	1.0	8
24	The effect of number of Hamiltonian paths on the complexity of a vertex-coloring problem. , 1981, , .		4
25	Figures of merit: the sequel. ACM SIGACT News, 1990, 21, 78-81.	0.1	0
26	Computational motif discovery. , 2005, , .		0