

# Martin Tompa

## List of Publications by Year in descending order

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Version: 2024-02-01

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	A Computational Pipeline for High- Throughput Discovery of cis-Regulatory Noncoding RNA in Prokaryotes. PLoS Computational Biology, 2007, 3, e126.	3.2	77
2	Identification of 22 candidate structured RNAs in bacteria using the CMfinder comparative genomics pipeline. Nucleic Acids Research, 2007, 35, 4809-4819.	14.5	292
3	Analysis of computational approaches for motif discovery. Algorithms for Molecular Biology, 2006, 1, 8.	1.2	58
4	MicroFootPrinter: a tool for phylogenetic footprinting in prokaryotic genomes. Nucleic Acids Research, 2006, 34, W366-W368.	14.5	25
5	Assessing computational tools for the discovery of transcription factor binding sites. Nature Biotechnology, 2005, 23, 137-144.	17.5	1,121
6	Discovery of regulatory elements in vertebrates through comparative genomics. Nature Biotechnology, 2005, 23, 1249-1256.	17.5	48
7	Computational motif discovery. , 2005, , .		0
8	Evolutionarily conserved sequence elements that positively regulate IFN- $\gamma$ expression in T cells. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 12622-12627.	7.1	124
9	PhyME: a probabilistic algorithm for finding motifs in sets of orthologous sequences. BMC Bioinformatics, 2004, 5, 170.	2.6	158
10	Rv3133c/dosR is a transcription factor that mediates the hypoxic response of Mycobacterium tuberculosis. Molecular Microbiology, 2003, 48, 833-843.	2.5	674
11	YMF: a program for discovery of novel transcription factor binding sites by statistical overrepresentation. Nucleic Acids Research, 2003, 31, 3586-3588.	14.5	203
12	FootPrinter: a program designed for phylogenetic footprinting. Nucleic Acids Research, 2003, 31, 3840-3842.	14.5	143
13	Algorithms for Phylogenetic Footprinting. Journal of Computational Biology, 2002, 9, 211-223.	1.6	138
14	Discovery of novel transcription factor binding sites by statistical overrepresentation. Nucleic Acids Research, 2002, 30, 5549-5560.	14.5	171
15	Discovery of Regulatory Elements by a Computational Method for Phylogenetic Footprinting. Genome Research, 2002, 12, 739-748.	5.5	268
16	Finding motifs using random projections. , 2001, , .		101
17	A Time-Space Tradeoff for Undirected Graph Traversal by Walking Automata. SIAM Journal on Computing, 1998, 28, 1051-1072.	1.0	8
18	Communication-Space Tradeoffs for Unrestricted Protocols. SIAM Journal on Computing, 1994, 23, 652-661.	1.0	14

#	ARTICLE	IF	CITATIONS
19	Trade-offs between communication and space. Journal of Computer and System Sciences, 1992, 45, 296-315.	1.2	8
20	Figures of merit: the sequel. ACM SIGACT News, 1990, 21, 78-81.	0.1	0
21	A New Pebble Game that Characterizes Parallel Complexity Classes. SIAM Journal on Computing, 1989, 18, 533-549.	1.0	31
22	Two Applications of Inductive Counting for Complementation Problems. SIAM Journal on Computing, 1989, 18, 559-578.	1.0	100
23	Space-bounded hierarchies and probabilistic computations. Journal of Computer and System Sciences, 1984, 28, 216-230.	1.2	108
24	Two Familiar Transitive Closure Algorithms Which Admit No Polynomial Time, Sublinear Space Implementations. SIAM Journal on Computing, 1982, 11, 130-137.	1.0	22
25	The effect of number of Hamiltonian paths on the complexity of a vertex-coloring problem. , 1981, , .		4
26	Time-space tradeoffs for computing functions, using connectivity properties of their circuits. Journal of Computer and System Sciences, 1980, 20, 118-132.	1.2	47