Richard M Karp

List of Publications by Year
in descending order

80 papers	19,642 citations	94433 37 h-index	91884 69 g-index
81 all docs	81 docs citations	81 times ranked	10127 citing authors

#	Article	IF	Citations
1	Optimization criteria and biological process enrichment in homologous multiprotein modules. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 10872-10877.	7.1	5
2	The Implicit Hitting Set Approach to Solve Combinatorial Optimization Problems with an Application to Multigenome Alignment. Operations Research, 2013, 61, 453-468.	1.9	23
3	Algorithmic methodologies for ultra-efficient inexact architectures for sustaining technology scaling. , 2012, , .		29
4	Comparing Pedigree Graphs. Journal of Computational Biology, 2012, 19, 998-1014.	1.6	12
5	Algorithms to Detect Multiprotein Modularity Conserved during Evolution. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1046-1058.	3.0	9
6	Understanding Science Through the Computational Lens. Journal of Computer Science and Technology, 2011, 26, 569-577.	1.5	20
7	Heuristic algorithms in computational molecular biology. Journal of Computer and System Sciences, 2011, 77, 122-128.	1.2	17
8	Pedigree Reconstruction Using Identity by Descent. Journal of Computational Biology, 2011, 18, 1481-1493.	1.6	25
9	Haplotype Inference in Complex Pedigrees. Journal of Computational Biology, 2010, 17, 269-280.	1.6	7
10	Topology-Free Querying of Protein Interaction Networks. Journal of Computational Biology, 2010, 17, 237-252.	1.6	99
11	Torque: topology-free querying of protein interaction networks. Nucleic Acids Research, 2009, 37, W106-W108.	14.5	30
12	Genome-Wide Association Data Reveal a Global Map of Genetic Interactions among Protein Complexes. PLoS Genetics, 2009, 5, e1000782.	3.5	52
13	On the Price of Heterogeneity in Parallel Systems. Theory of Computing Systems, 2009, 45, 280-301.	1.1	1
14	Topology-Free Querying of Protein Interaction Networks. Lecture Notes in Computer Science, 2009, , 74-89.	1.3	15
15	Haplotype Inference in Complex Pedigrees. Lecture Notes in Computer Science, 2009, , 108-120.	1.3	1
16	George Dantzig's impact on the theory of computation. Discrete Optimization, 2008, 5, 174-185.	0.9	7
17	Probabilistic Analysis of Linear Programming Decoding. IEEE Transactions on Information Theory, 2008, 54, 3565-3578.	2.4	50
18	Association Mapping and Significance Estimation via the Coalescent. American Journal of Human Genetics, 2008, 83, 675-683.	6.2	11

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19	eQED: an efficient method for interpreting eQTL associations using protein networks. Molecular Systems Biology, 2008, 4, 162.	7.2	117
20	Detecting Disease-Specific Dysregulated Pathways Via Analysis of Clinical Expression Profiles. Lecture Notes in Computer Science, 2008, , 347-359.	1.3	37
21	A Randomization Test for Controlling Population Stratification in Whole-Genome Association Studies. American Journal of Human Genetics, 2007, 81, 895-905.	6.2	48
22	Comparing Protein Interaction Networks via a Graph Match-and-Split Algorithm. Journal of Computational Biology, 2007, 14, 892-907.	1.6	61
23	Efficient Algorithms for Detecting Signaling Pathways in Protein Interaction Networks. Journal of Computational Biology, 2006, 13, 133-144.	1.6	225
24	The minimum-entropy set cover problem. Theoretical Computer Science, 2005, 348, 240-250.	0.9	28
25	Conserved patterns of protein interaction in multiple species. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1974-1979.	7.1	714
26	Identification of Protein Complexes by Comparative Analysis of Yeast and Bacterial Protein Interaction Data. Journal of Computational Biology, 2005, 12, 835-846.	1.6	161
27	Efficient Algorithms for Detecting Signaling Pathways in Protein Interaction Networks. Lecture Notes in Computer Science, 2005, , 1-13.	1.3	14
28	Identification of protein complexes by comparative analysis of yeast and bacterial protein interaction data. , 2004, , .		19
29	MotifPrototyper: A Bayesian profile model for motif families. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 10523-10528.	7.1	30
30	LOGOS: A MODULAR BAYESIAN MODEL FOR DE NOVO MOTIF DETECTION. Journal of Bioinformatics and Computational Biology, 2004, 02, 127-154.	0.8	38
31	The Restriction Scaffold Problem. Journal of Computational Biology, 2003, 10, 385-398.	1.6	16
32	CREME: a framework for identifying cis-regulatory modules in human-mouse conserved segments. Bioinformatics, 2003, 19, i283-i291.	4.1	94
33	Conserved pathways within bacteria and yeast as revealed by global protein network alignment. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 11394-11399.	7.1	466
34	EFFICIENT RECONSTRUCTION OF HAPLOTYPE STRUCTURE VIA PERFECT PHYLOGENY. Journal of Bioinformatics and Computational Biology, 2003, 01, 1-20.	0.8	100
35	The restriction scaffold problem. , 2002, , .		0
36	Algorithms for graph partitioning on the planted partition model. Random Structures and Algorithms, 2001, 18, 116-140.	1.1	240

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37	Algorithms for graph partitioning on the planted partition model. , 2001, 18, 116.		38
38	Parallel Sorting with Limited Bandwidth. SIAM Journal on Computing, 2000, 29, 1997-2015.	1.0	2
39	Error-resilient DNA computation. Random Structures and Algorithms, 1999, 15, 450-466.	1.1	4
40	DISCOVERY OF REGULATORY INTERACTIONS THROUGH PERTURBATION: INFERENCE AND EXPERIMENTAL DESIGN. , 1999, , 305-16.		111
41	Error Checking and Graphical Representation of Multiple–Complete–Digest (MCD) Restriction-Fragment Maps. Genome Research, 1999, 9, 79-90.	5.5	7
42	An algorithmic approach to multiple complete digest mapping. , 1997, , .		4
43	LogP. Communications of the ACM, 1996, 39, 78-85.	4.5	226
44	Bounded branching process and and/or tree evaluation. Random Structures and Algorithms, 1995, 7, 97-116.	1.1	10
45	When Is the Assignment Bound Tight for the Asymmetric Traveling-Salesman Problem?. SIAM Journal on Computing, 1995, 24, 484-493.	1.0	11
46	A Graph-Theoretic Game and Its Application to the k-Server Problem. SIAM Journal on Computing, 1995, 24, 78-100.	1.0	235
47	Probabilistic recurrence relations. Journal of the ACM, 1994, 41, 1136-1150.	2.2	47
48	Average Case Analysis of a Heuristic for the Assignment Problem. Mathematics of Operations Research, 1994, 19, 513-522.	1.3	20
49	Probabilistic Analysis of Network Flow Algorithms. Mathematics of Operations Research, 1993, 18, 71-97.	1.3	10
50	An introduction to randomized algorithms. Discrete Applied Mathematics, 1991, 34, 165-201.	0.9	74
51	Competitive paging algorithms. Journal of Algorithms, 1991, 12, 685-699.	0.9	356
52	The transitive closure of a random digraph. Random Structures and Algorithms, 1990, 1, 73-93.	1.1	163
53	Parallel Algorithms for Shared-Memory Machines. , 1990, , 869-941.		279
54	Monte-Carlo approximation algorithms for enumeration problems. Journal of Algorithms, 1989, 10, 429-448.	0.9	242

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55	The complexity of parallel search. Journal of Computer and System Sciences, 1988, 36, 225-253.	1.2	71
56	Efficient randomized pattern-matching algorithms. IBM Journal of Research and Development, 1987, 31, 249-260.	3.1	899
57			

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73	The Traveling-Salesman Problem and Minimum Spanning Trees. Operations Research, 1970, 18, 1138-1162.	1.9	1,056
74	Parallel program schemata. Journal of Computer and System Sciences, 1969, 3, 147-195.	1.2	768
75	The Organization of Computations for Uniform Recurrence Equations. Journal of the ACM, 1967, 14, 563-590.	2.2	470
76	Parallel program schemata: A mathematical model for parallel computation. , 1967, , .		21
77	Finite-State Processes and Dynamic Programming. SIAM Journal on Applied Mathematics, 1967, 15, 693-718.	1.8	128
78	Properties of a Model for Parallel Computations: Determinacy, Termination, Queueing. SIAM Journal on Applied Mathematics, 1966, 14, 1390-1411.	1.8	318
79	Assembly-Line Balancing—Dynamic Programming with Precedence Constraints. Operations Research, 1963, 11, 442-459.	1.9	136
80	A Dynamic Programming Approach to Sequencing Problems. Journal of the Society for Industrial and Applied Mathematics, 1962, 10, 196-210.	0.5	787