Tamer Kahveci

List of Publications by Year in descending order

44 papers	2,940 citations	706676 14 h-index	445137 33 g-index
47 all docs	47 docs citations	47 times ranked	7421 citing authors

#	Article	IF	Citations
1	Motifs in Biological Networks. , 2021, , 101-123.		1
2	Evaluation of crop model prediction and uncertainty using Bayesian parameter estimation and Bayesian model averaging. Agricultural and Forest Meteorology, 2021, 311, 108686.	1.9	13
3	Comparison of three calibration methods for modeling rice phenology. Agricultural and Forest Meteorology, 2020, 280, 107785.	1.9	40
4	Replication timing networks reveal a link between transcription regulatory circuits and replication timing control. Genome Research, 2019, 29, 1415-1428.	2.4	12
5	Identification of co-evolving temporal networks. BMC Genomics, 2019, 20, 434.	1.2	8
6	Co-evolving Patterns in Temporal Networks of Varying Evolution. , 2019, , .		12
7	Counting motifs in dynamic networks. BMC Systems Biology, 2018, 12, 6.	3.0	11
8	Index Structures for Biological Sequences. , 2018, , 1845-1850.		0
9	Motif centrality in food web networks. Journal of Complex Networks, 2017, 5, 641-664.	1.1	12
10	Motifs in the assembly of food web networks. Oikos, 2016, 125, 480-491.	1.2	39
11	Identification of large disjoint motifs in biological networks. BMC Bioinformatics, 2016, 17, 408.	1.2	20
12	Integrating Domain Specific Knowledge and Network Analysis to Predict Drug Sensitivity of Cancer Cell Lines. PLoS ONE, 2016, 11, e0162173.	1.1	15
13	Computing interaction probabilities in signaling networks. Eurasip Journal on Bioinformatics and Systems Biology, 2015, 2015, 10.	1.4	5
14	Indexing a protein-protein interaction network expedites network alignment. BMC Bioinformatics, 2015, 16, 326.	1.2	8
15	Dynamic changes in replication timing and gene expression during lineage specification of human pluripotent stem cells. Genome Research, 2015, 25, 1091-1103.	2.4	145
16	Incremental network querying in biological networks. , 2014, , .		4
17	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	13.7	1,444
18	Topologically associating domains are stable units of replication-timing regulation. Nature, 2014, 515, 402-405.	13.7	779

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19	Network-based Prediction of Cancer under Genetic Storm. Cancer Informatics, 2014, 13s3, CIN.S14025.	0.9	6
20	Probabilistic Biological Network Alignment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 109-121.	1.9	26
21	Color distribution can accelerate network alignment. , 2013, , .		7
22	TOPAC: ALIGNMENT OF GENE REGULATORY NETWORKS USING TOPOLOGY-AWARE COLORING. Journal of Bioinformatics and Computational Biology, 2012, 10, 1240001.	0.3	11
23	Metabolic network alignment in large scale by network compression. BMC Bioinformatics, 2012, 13, S2.	1.2	9
24	Mining Biological Networks for Similar Patterns. Intelligent Systems Reference Library, 2012, , 63-99.	1.0	0
25	SubMAP: Aligning Metabolic Pathways with Subnetwork Mappings. Journal of Computational Biology, 2011, 18, 219-235.	0.8	66
26	RINQ: Reference-based Indexing for Network Queries. Bioinformatics, 2011, 27, i149-i158.	1.8	9
27	GBA Manager: An Online Tool for Querying Low-Complexity Regions in Proteins. Journal of Computational Biology, 2010, 17, 73-77.	0.8	0
28	Finding steady states of large scale regulatory networks through partitioning. , 2010, , .		2
29	SubMAP: Aligning Metabolic Pathways with Subnetwork Mappings. Lecture Notes in Computer Science, 2010, , 15-30.	1.0	9
30	Scalable Steady State Analysis of Boolean Biological Regulatory Networks. PLoS ONE, 2009, 4, e7992.	1.1	60
31	A FAST AND ACCURATE ALGORITHM FOR COMPARATIVE ANALYSIS OF METABOLIC PATHWAYS. Journal of Bioinformatics and Computational Biology, 2009, 07, 389-428.	0.3	16
32	Double iterative optimisation for metabolic network-based drug target identification. International Journal of Data Mining and Bioinformatics, 2009, 3, 124.	0.1	11
33	Index Structures for Biological Sequences. , 2009, , 1428-1432.		0
34	Reference-based indexing for metric spaces with costly distance measures. VLDB Journal, 2008, 17, 1231-1251.	2.7	21
35	CONSISTENT ALIGNMENT OF METABOLIC PATHWAYS WITHOUT ABSTRACTION. , 2008, , .		10
36	Consistent alignment of metabolic pathways without abstraction. Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference, 2008, 7, 237-48.	0.4	3

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37	An iterative algorithm for metabolic network-based drug target identification. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2007, , 88-99.	0.7	12
38	A Novel algorithm for identifying low-complexity regions in a protein sequence. Bioinformatics, 2006, 22, 2980-2987.	1.8	27
39	Finding Data Broadness Via Generalized Nearest Neighbors. Lecture Notes in Computer Science, 2006, , 645-663.	1.0	2
40	INDEX-BASED SIMILARITY SEARCH FOR PROTEIN STRUCTURE DATABASES. Journal of Bioinformatics and Computational Biology, 2004, 02, 99-126.	0.3	11
41	Speeding up whole-genome alignment by indexing frequency vectors. Bioinformatics, 2004, 20, 2122-2134.	1.8	15
42	PSI: indexing protein structures for fast similarity search. Bioinformatics, 2003, 19, i81-i83.	1.8	27
43	MAP: searching large genome databases. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2003, , 303-14.	0.7	2
44	MAP: SEARCHING LARGE GENOME DATABASES. , 2002, , .		6