

Tamer Kahveci

List of Publications by Year in descending order

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Version: 2024-02-01

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	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	13.7	1,444
2	Topologically associating domains are stable units of replication-timing regulation. <i>Nature</i> , 2014, 515, 402-405.	13.7	779
3	Dynamic changes in replication timing and gene expression during lineage specification of human pluripotent stem cells. <i>Genome Research</i> , 2015, 25, 1091-1103.	2.4	145
4	SubMAP: Aligning Metabolic Pathways with Subnetwork Mappings. <i>Journal of Computational Biology</i> , 2011, 18, 219-235.	0.8	66
5	Scalable Steady State Analysis of Boolean Biological Regulatory Networks. <i>PLoS ONE</i> , 2009, 4, e7992.	1.1	60
6	Comparison of three calibration methods for modeling rice phenology. <i>Agricultural and Forest Meteorology</i> , 2020, 280, 107785.	1.9	40
7	Motifs in the assembly of food web networks. <i>Oikos</i> , 2016, 125, 480-491.	1.2	39
8	PSI: indexing protein structures for fast similarity search. <i>Bioinformatics</i> , 2003, 19, i81-i83.	1.8	27
9	A Novel algorithm for identifying low-complexity regions in a protein sequence. <i>Bioinformatics</i> , 2006, 22, 2980-2987.	1.8	27
10	Probabilistic Biological Network Alignment. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 109-121.	1.9	26
11	Reference-based indexing for metric spaces with costly distance measures. <i>VLDB Journal</i> , 2008, 17, 1231-1251.	2.7	21
12	Identification of large disjoint motifs in biological networks. <i>BMC Bioinformatics</i> , 2016, 17, 408.	1.2	20
13	A FAST AND ACCURATE ALGORITHM FOR COMPARATIVE ANALYSIS OF METABOLIC PATHWAYS. <i>Journal of Bioinformatics and Computational Biology</i> , 2009, 07, 389-428.	0.3	16
14	Speeding up whole-genome alignment by indexing frequency vectors. <i>Bioinformatics</i> , 2004, 20, 2122-2134.	1.8	15
15	Integrating Domain Specific Knowledge and Network Analysis to Predict Drug Sensitivity of Cancer Cell Lines. <i>PLoS ONE</i> , 2016, 11, e0162173.	1.1	15
16	Evaluation of crop model prediction and uncertainty using Bayesian parameter estimation and Bayesian model averaging. <i>Agricultural and Forest Meteorology</i> , 2021, 311, 108686.	1.9	13
17	Motif centrality in food web networks. <i>Journal of Complex Networks</i> , 2017, 5, 641-664.	1.1	12
18	Replication timing networks reveal a link between transcription regulatory circuits and replication timing control. <i>Genome Research</i> , 2019, 29, 1415-1428.	2.4	12

#	ARTICLE	IF	CITATIONS
19	Co-evolving Patterns in Temporal Networks of Varying Evolution. , 2019, , .		12
20	An iterative algorithm for metabolic network-based drug target identification. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2007, , 88-99.	0.7	12
21	INDEX-BASED SIMILARITY SEARCH FOR PROTEIN STRUCTURE DATABASES. Journal of Bioinformatics and Computational Biology, 2004, 02, 99-126.	0.3	11
22	Double iterative optimisation for metabolic network-based drug target identification. International Journal of Data Mining and Bioinformatics, 2009, 3, 124.	0.1	11
23	TOPAC: ALIGNMENT OF GENE REGULATORY NETWORKS USING TOPOLOGY-AWARE COLORING. Journal of Bioinformatics and Computational Biology, 2012, 10, 1240001.	0.3	11
24	Counting motifs in dynamic networks. BMC Systems Biology, 2018, 12, 6.	3.0	11
25	CONSISTENT ALIGNMENT OF METABOLIC PATHWAYS WITHOUT ABSTRACTION. , 2008, , .		10
26	RINQ: Reference-based Indexing for Network Queries. Bioinformatics, 2011, 27, i149-i158.	1.8	9
27	Metabolic network alignment in large scale by network compression. BMC Bioinformatics, 2012, 13, S2.	1.2	9
28	SubMAP: Aligning Metabolic Pathways with Subnetwork Mappings. Lecture Notes in Computer Science, 2010, , 15-30.	1.0	9
29	Indexing a protein-protein interaction network expedites network alignment. BMC Bioinformatics, 2015, 16, 326.	1.2	8
30	Identification of co-evolving temporal networks. BMC Genomics, 2019, 20, 434.	1.2	8
31	Color distribution can accelerate network alignment. , 2013, , .		7
32	Network-based Prediction of Cancer under Genetic Storm. Cancer Informatics, 2014, 13s3, CIN.S14025.	0.9	6
33	MAP: SEARCHING LARGE GENOME DATABASES. , 2002, , .		6
34	Computing interaction probabilities in signaling networks. Eurasip Journal on Bioinformatics and Systems Biology, 2015, 2015, 10.	1.4	5
35	Incremental network querying in biological networks. , 2014, , .		4
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

#	ARTICLE	IF	CITATIONS
37	Finding steady states of large scale regulatory networks through partitioning. , 2010, , .		2
38	Finding Data Broadness Via Generalized Nearest Neighbors. Lecture Notes in Computer Science, 2006, , 645-663.	1.0	2
39	MAP: searching large genome databases. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2003, , 303-14.	0.7	2
40	Motifs in Biological Networks. , 2021, , 101-123.		1
41	GBA Manager: An Online Tool for Querying Low-Complexity Regions in Proteins. Journal of Computational Biology, 2010, 17, 73-77.	0.8	0
42	Index Structures for Biological Sequences. , 2009, , 1428-1432.		0
43	Mining Biological Networks for Similar Patterns. Intelligent Systems Reference Library, 2012, , 63-99.	1.0	0
44	Index Structures for Biological Sequences. , 2018, , 1845-1850.		0