Tolga Ãn

List of Publications by Year
in descending order

52 papers	938 citations	623734 14 h-index	501196 28 g-index
52 all docs	52 docs citations	52 times ranked	1252 citing authors

#	Article	IF	Citations
1	The CHEMDNER corpus of chemicals and drugs and its annotation principles. Journal of Cheminformatics, 2015, 7, S2.	6.1	166
2	RRW: repeated random walks on genome-scale protein networks for local cluster discovery. BMC Bioinformatics, 2009, 10, 283.	2.6	158
3	Estrogen-induced upregulation and 3â€²-UTR shortening of CDC6. Nucleic Acids Research, 2012, 40, 10679-10688.	14.5	76
4	Efficient molecular surface generation using level-set methods. Journal of Molecular Graphics and Modelling, 2006, 25, 442-454.	2.4	62
5	Alternative Polyadenylation: Another Foe in Cancer. Molecular Cancer Research, 2016, 14, 507-517.	3.4	51
6	Introduction to Bioinformatics. Methods in Molecular Biology, 2014, 1107, 51-71.	0.9	50
7	Analysis of protein-protein interaction networks using random walks. , 2005, , .		47
8	3â€²UTR shortening and EGF signaling: implications for breast cancer. Human Molecular Genetics, 2015, 24, ddv391.	2.9	42
9	CTSS: a robust and efficient method for protein structure alignment based on local geometrical and biological features. , 0, , .		38
10	FPV: fast protein visualization using Java 3DTM. Bioinformatics, 2003, 19, 913-922.	4.1	24
11	Reconstruction of the temporal signaling network in Salmonella-infected human cells. Frontiers in Microbiology, 2015, 6, 730.	3.5	21
12	DECISION TREE BASED INFORMATION INTEGRATION FOR AUTOMATED PROTEIN CLASSIFICATION. Journal of Bioinformatics and Computational Biology, 2005, 03, 717-742.	0.8	20
13	Integrating multi-attribute similarity networks for robust representation of the protein space. Bioinformatics, 2006, 22, 1585-1592.	4.1	19
14	Targeting HIF1-alpha/miR-326/ITGA5 axis potentiates chemotherapy response in triple-negative breast cancer. Breast Cancer Research and Treatment, 2022, 193, 331-348.	2.5	18
15	Large-Scale Signaling Network Reconstruction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1696-1708.	3.0	15
16	Using network context as a filter for miRNA target prediction. BioSystems, 2011, 105, 201-209.	2.0	14
17	Discovering functional interaction patterns in protein-protein interaction networks. BMC Bioinformatics, 2008, 9, 276.	2.6	13
18	Alternative Polyadenylation Patterns for Novel Gene Discovery and Classification in Cancer. Neoplasia, 2017, 19, 574-582.	5.3	13

#	Article	IF	Citations
19	Identification of Novel Reference Genes Based on MeSH Categories. PLoS ONE, 2014, 9, e93341.	2.5	12
20	Comparison of tissue/disease specific integrated networks using directed graphlet signatures. BMC Bioinformatics, 2017, 18, 135.	2.6	9
21	A Divide and Conquer Approach for Construction of Large-Scale Signaling Networks from PPI and RNAi Data Using Linear Programming. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 869-883.	3.0	7
22	SUMONA: A supervised method for optimizing network alignment. Computational Biology and Chemistry, 2016, 63, 41-51.	2.3	7
23	PROTEIN STRUCTURE ALIGNMENT AND FAST SIMILARITY SEARCH USING LOCAL SHAPE SIGNATURES. Journal of Bioinformatics and Computational Biology, 2004, 02, 215-239.	0.8	6
24	Bi-k-bi clustering: mining large scale gene expression data using two-level biclustering. International Journal of Data Mining and Bioinformatics, 2010, 4, 701.	0.1	5
25	CTSS: a robust and efficient method for protein structure alignment based on local geometrical and biological features. Proceedings, 2003, 2, 169-79.	0.1	5
26	Identification of an mRNA isoform switch for HNRNPA1 in breast cancers. Scientific Reports, 2021, 11, 24444.	3.3	5
27	Automated protein classification using consensus decision. , 2004, , 224-35.		4
28	Integration of topological measures for eliminating non-specific interactions in protein interaction networks. Discrete Applied Mathematics, 2009, 157, 2416-2424.	0.9	4
29	A design goal and design pattern based approach for development of game engines for mobile platforms. , 2011, , .		4
30	A prelude to the proximity interaction mapping of CXXC5. Scientific Reports, 2021, 11, 17587.	3.3	4
31	GPCRsortâ€"Responding to the Next Generation Sequencing Data Challenge: Prediction of G Protein-Coupled Receptor Classes Using Only Structural Region Lengths. OMICS A Journal of Integrative Biology, 2014, 18, 636-644.	2.0	3
32	MotifGenie: a Python application for searching transcription factor binding sequences using ChIP-Seq datasets. Bioinformatics, 2021, 37, 4238-4239.	4.1	3
33	A multiplex primer design algorithm for target amplification of continuous genomic regions. BMC Bioinformatics, 2017, 18, 306.	2.6	2
34	JOA: Joint Overlap Analysis of multiple genomic interval sets. BMC Bioinformatics, 2019, 20, 121.	2.6	2
35	A CpG island promoter drives the CXXC5 gene expression. Scientific Reports, 2021, 11, 15655.	3.3	2
36	Accurate and Scalable Techniques for the Complex/Pathway Membership Problem in Protein Networks. Advances in Bioinformatics, 2009, 2009, 1-9.	5.7	1

#	Article	IF	Citations
37	Text classification in the Turkish marketing domain for context sensitive ad distribution. , 2009, , .		1
38	Coevolution based prediction of protein-protein interactions with reduced training data. , 2010, , .		1
39	M4B: A novel method for designing and ordering of the genetic devices. , 2012, , .		1
40	Div-BLAST: Diversification of Sequence Search Results. PLoS ONE, 2014, 9, e115445.	2.5	1
41	Comparison of tissue/disease specific integrated networks using directed graphlet signatures. , 2016, , .		1
42	A Câ€term truncated <scp>EIF2BÎ³</scp> protein encoded by an intronically polyadenylated isoform introduces unfavorable <scp>EIF2BÎ³â€"EIF2Î³</scp> interactions. Proteins: Structure, Function and Bioinformatics, 2022, 90, 889-897.	2.6	1
43	The effect of representative training dataset selection on the classification performance of the promoter sequences. , 2011, , .		0
44	Constructing signaling pathways from RNAI data using genetic algorithms. , 2011, , .		0
45	Parallelization of the functional flow algorithm for prediction of protein function using protein-protein interaction networks. , 2011, , .		0
46	ProSVM and ProK-means: Novel methods for promoter prediction. , 2011, , .		0
47	Parallel SPICi. , 2011, , .		0
48	Metadata Management and Semantics in Microarray Repositories. Balkan Journal of Medical Genetics, 2011, 14, 49-64.	0.5	0
49	Unsupervised identification of redundant domain entries in InterPro database using clustering techniques. , 2015, , .		0
50	Informatics Olympiads in Turkey: Team Selection and Training. Olympiads in Informatics, 2015, 9, 225-232.	0.1	0
51	Abstract 3374: APA isoform diversity in triple negative breast cancers. , 2017, , .		0
52	Abstract 2360: Deregulated APA and cancer specific APA isoforms. , 2018, , .		0