

Tolga Ãan

List of Publications by Year in descending order

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Version: 2024-02-01

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	A C-terminal truncated eIF2B^3 protein encoded by an intronically polyadenylated isoform introduces unfavorable eIF2B^3 - eIF2^3 interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 889-897.	2.6	1
2	Targeting HIF1-alpha/miR-326/ITGA5 axis potentiates chemotherapy response in triple-negative breast cancer. <i>Breast Cancer Research and Treatment</i> , 2022, 193, 331-348.	2.5	18
3	MotifGenie: a Python application for searching transcription factor binding sequences using ChIP-Seq datasets. <i>Bioinformatics</i> , 2021, 37, 4238-4239.	4.1	3
4	A CpG island promoter drives the CXXC5 gene expression. <i>Scientific Reports</i> , 2021, 11, 15655.	3.3	2
5	A prelude to the proximity interaction mapping of CXXC5. <i>Scientific Reports</i> , 2021, 11, 17587.	3.3	4
6	Identification of an mRNA isoform switch for HNRNPA1 in breast cancers. <i>Scientific Reports</i> , 2021, 11, 24444.	3.3	5
7	JOA: Joint Overlap Analysis of multiple genomic interval sets. <i>BMC Bioinformatics</i> , 2019, 20, 121.	2.6	2
8	Abstract 2360: Deregulated APA and cancer specific APA isoforms. , 2018, , .		0
9	Alternative Polyadenylation Patterns for Novel Gene Discovery and Classification in Cancer. <i>Neoplasia</i> , 2017, 19, 574-582.	5.3	13
10	Comparison of tissue/disease specific integrated networks using directed graphlet signatures. <i>BMC Bioinformatics</i> , 2017, 18, 135.	2.6	9
11	A multiplex primer design algorithm for target amplification of continuous genomic regions. <i>BMC Bioinformatics</i> , 2017, 18, 306.	2.6	2
12	Abstract 3374: APA isoform diversity in triple negative breast cancers. , 2017, , .		0
13	Comparison of tissue/disease specific integrated networks using directed graphlet signatures. , 2016, , .		1
14	Alternative Polyadenylation: Another Foe in Cancer. <i>Molecular Cancer Research</i> , 2016, 14, 507-517.	3.4	51
15	SUMONA: A supervised method for optimizing network alignment. <i>Computational Biology and Chemistry</i> , 2016, 63, 41-51.	2.3	7
16	The CHEMDNER corpus of chemicals and drugs and its annotation principles. <i>Journal of Cheminformatics</i> , 2015, 7, S2.	6.1	166
17	Unsupervised identification of redundant domain entries in InterPro database using clustering techniques. , 2015, , .		0
18	Reconstruction of the temporal signaling network in Salmonella-infected human cells. <i>Frontiers in Microbiology</i> , 2015, 6, 730.	3.5	21

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19	3'UTR shortening and EGF signaling: implications for breast cancer. Human Molecular Genetics, 2015, 24, ddv391.	2.9	42
20	Informatics Olympiads in Turkey: Team Selection and Training. Olympiads in Informatics, 2015, 9, 225-232.	0.1	0
21	Div-BLAST: Diversification of Sequence Search Results. PLoS ONE, 2014, 9, e115445.	2.5	1
22	GPCRs 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
23	Introduction to Bioinformatics. Methods in Molecular Biology, 2014, 1107, 51-71.	0.9	50
24	Identification of Novel Reference Genes Based on MeSH Categories. PLoS ONE, 2014, 9, e93341.	2.5	12
25	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
26	Estrogen-induced upregulation and 3'UTR shortening of CDC6. Nucleic Acids Research, 2012, 40, 10679-10688.	14.5	76
27	M4B: A novel method for designing and ordering of the genetic devices. , 2012, , .		1
28	Large-Scale Signaling Network Reconstruction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1696-1708.	3.0	15
29	The effect of representative training dataset selection on the classification performance of the promoter sequences. , 2011, , .		0
30	Constructing signaling pathways from RNAi data using genetic algorithms. , 2011, , .		0
31	Parallelization of the functional flow algorithm for prediction of protein function using protein-protein interaction networks. , 2011, , .		0
32	ProSVM and ProK-means: Novel methods for promoter prediction. , 2011, , .		0
33	Parallel SPICi. , 2011, , .		0
34	A design goal and design pattern based approach for development of game engines for mobile platforms. , 2011, , .		4
35	Metadata Management and Semantics in Microarray Repositories. Balkan Journal of Medical Genetics, 2011, 14, 49-64.	0.5	0
36	Using network context as a filter for miRNA target prediction. BioSystems, 2011, 105, 201-209.	2.0	14

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37	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
38	Coevolution based prediction of protein-protein interactions with reduced training data. , 2010, , .		1
39	Accurate and Scalable Techniques for the Complex/Pathway Membership Problem in Protein Networks. Advances in Bioinformatics, 2009, 2009, 1-9.	5.7	1
40	RRW: repeated random walks on genome-scale protein networks for local cluster discovery. BMC Bioinformatics, 2009, 10, 283.	2.6	158
41	Integration of topological measures for eliminating non-specific interactions in protein interaction networks. Discrete Applied Mathematics, 2009, 157, 2416-2424.	0.9	4
42	Text classification in the Turkish marketing domain for context sensitive ad distribution. , 2009, , .		1
43	Discovering functional interaction patterns in protein-protein interaction networks. BMC Bioinformatics, 2008, 9, 276.	2.6	13
44	Efficient molecular surface generation using level-set methods. Journal of Molecular Graphics and Modelling, 2006, 25, 442-454.	2.4	62
45	Integrating multi-attribute similarity networks for robust representation of the protein space. Bioinformatics, 2006, 22, 1585-1592.	4.1	19
46	Analysis of protein-protein interaction networks using random walks. , 2005, , .		47
47	DECISION TREE BASED INFORMATION INTEGRATION FOR AUTOMATED PROTEIN CLASSIFICATION. Journal of Bioinformatics and Computational Biology, 2005, 03, 717-742.	0.8	20
48	Automated protein classification using consensus decision. , 2004, , 224-35.		4
49	PROTEIN STRUCTURE ALIGNMENT AND FAST SIMILARITY SEARCH USING LOCAL SHAPE SIGNATURES. Journal of Bioinformatics and Computational Biology, 2004, 02, 215-239.	0.8	6
50	FPV: fast protein visualization using Java 3DTM. Bioinformatics, 2003, 19, 913-922.	4.1	24
51	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
52	CTSS: a robust and efficient method for protein structure alignment based on local geometrical and biological features. , 0, , .		38