Mehmet Koyuturk

List of Publications by Year
in descending order

93 papers	2,668 citations	218677 26 h-index	206112 48 g-index
101 all docs	101 docs citations	101 times ranked	3566 citing authors

#	Article	IF	Citations
1	Circulating microbial content in myeloid malignancy patients is associated with disease subtypes and patient outcomes. Nature Communications, 2022, 13, 1038.	12.8	13
2	Uncovering complementary sets of variants for predicting quantitative phenotypes. Bioinformatics, 2022, 38, 908-917.	4.1	1
3	Protein Biomarkers in Monocytes and CD4 Lymphocytes for Predicting Lithium Treatment Response of Bipolar Disorder: a Feasibility Study with Tyramine-Based Signal-Amplified Flow Cytometry.. Psychopharmacology Bulletin, 2022, 52, 8-35.	0.0	1
4	Identification of intimate partner violence from free text descriptions in social media. Journal of Computational Social Science, 2022, 5, 1207-1233.	2.4	5
5	Functional characterization of co-phosphorylation networks. Bioinformatics, 2022, 38, 3785-3793.	4.1	5
6	Co-phosphorylation networks reveal subtype-specific signaling modules in breast cancer. Bioinformatics, 2021, 37, 221-228.	4.1	7
7	Robust inference of kinase activity using functional networks. Nature Communications, 2021, 12, 1177.	12.8	36
8	Data-driven identification of subtypes of intimate partner violence. Scientific Reports, 2021, 11, 6736.	3.3	3
9	Fast computation of Katz index for efficient processing of link prediction queries. Data Mining and Knowledge Discovery, 2021, 35, 1342-1368.	3.7	2
10	Node similarity-based graph convolution for link prediction in biological networks. Bioinformatics, 2021, 37, 4501-4508.	4.1	31
11	Integrated querying and version control of context-specific biological networks. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	4
12	Identifying health correlates of intimate partner violence against pregnant women. Health Information Science and Systems, 2020, 8, 36.	5.2	2
13	Interplay between traumatic brain injury and intimate partner violence: data driven analysis utilizing electronic health records. BMC Women's Health, 2020, 20, 269.	2.0	9
14	Generalized and Mechanistic PV Module Performance Prediction From Computer Vision and Machine Learning on Electroluminescence Images. IEEE Journal of Photovoltaics, 2020, 10, 878-887.	2.5	35
15	Co-occurrence Patterns of Intimate Partner Violence. , 2020, , .		5
16	Cross-population analysis for functional characterization of type II diabetes variants. BMC Bioinformatics, 2019, 20, 320.	2.6	2
17	Characterizing human genomic coevolution in locus-gene regulatory interactions. BioData Mining, 2019, 12, 8.	4.0	0
18	CoPhosK: A method for comprehensive kinase substrate annotation using co-phosphorylation analysis. PLoS Computational Biology, 2019, 15, e1006678.	3.2	30

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19	Querying of Disparate Association and Interaction Data in Biomedical Applications. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1052-1065.	3.0	2
20	Linearity of network proximity measures: implications for set-based queries and significance testing. Bioinformatics, 2017, 33, 1354-1361.	4.1	7
21	Visually Meaningful Histopathological Features for Automatic Grading of Prostate Cancer. IEEE Journal of Biomedical and Health Informatics, 2017, 21, 1027-1038.	6.3	33
22	Drug Response Prediction as a Link Prediction Problem. Scientific Reports, 2017, 7, 40321.	3.3	64
23	Phosphoproteomics Profiling of Nonsmall Cell Lung Cancer Cells Treated with a Novel Phosphatase Activator. Proteomics, 2017, 17, 1700214.	2.2	21
24	Effects of emotion and topic area on topic shifts in social media discussions. Social Network Analysis and Mining, 2017, 7, 1.	2.8	2
25	Prioritizing tests of epistasis through hierarchical representation of genomic redundancies. Nucleic Acids Research, 2017, 45, e131-e131.	14.5	15
26	The KSEA App: a web-based tool for kinase activity inference from quantitative phosphoproteomics. Bioinformatics, 2017, 33, 3489-3491.	4.1	181
27	Mining Electronic Health Records Data: Domestic Violence and Adverse Health Effects. Journal of Family Violence, 2017, 32, 79-87.	3.3	44
28	Pluribusâ€"Exploring the Limits of Error Correction Using a Suffix Tree. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1378-1388.	3.0	2
29	NETWORK MAP OF ADVERSE HEALTH EFFECTS AMONG VICTIMS OF INTIMATE PARTNER VIOLENCE. , 2017, 22, 324-335.		7
30	Emotion -and area-driven topic shift analysis in social media discussions. , 2016, , .		10
31	Disease gene prioritization by integrating tissue-specific molecular networks using a robust multi-network model. BMC Bioinformatics, 2016, 17, 453.	2.6	31
32	Efficient Processing of Network Proximity Queries via Chebyshev Acceleration. , 2016, , .		18
33	PoCos: Population Covering Locus Sets for Risk Assessment in Complex Diseases. PLoS Computational Biology, 2016, 12, e1005195.	3.2	4
34	Assessing the collective disease association of multiple genomic loci. , 2015, , .		2
35	Sets Visualization using their Graph Representation. , 2015, , .		0
36	Network-Based Integration of Disparate Omic Data To Identify "Silent Players" in Cancer. PLoS Computational Biology, 2015, 11, e1004595.	3.2	60

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37	Integrated querying of disparate association and interaction data in biomedical applications. , 2015, , .		2
38	Link Prediction in Large Networks by Comparing the Global View of Nodes in the Network. , 2015, , .		11
39	MOBAS: identification of disease-associated protein subnetworks using modularity-based scoring. Eurasip Journal on Bioinformatics and Systems Biology, 2015, 2015, 7.	1.4	17
40	Whole-exome sequencing enhances prognostic classification of myeloid malignancies. Journal of Biomedical Informatics, 2015, 58, 104-113.	4.3	9
41	Omics and Biomarkers Development for Intestinal Tumorigenesis. , 2015, , 365-389.		0
42	Prioritization of genomic locus pairs for testing epistasis. , 2014, , .		5
43	DB2: a probabilistic approach for accurate detection of tandem duplication breakpoints using paired-end reads. BMC Genomics, 2014, 15, 175.	2.8	7
44	Discovery of common sequences absent in the human reference genome using pooled samples from next generation sequencing. BMC Genomics, 2014, 15, 685.	2.8	24
45	Comprehensive Evaluation of Composite Gene Features in Cancer Outcome Prediction. Cancer Informatics, 2014, 13s3, CIN.S14028.	1.9	2
46	Efficiently Enumerating All Connected Induced Subgraphs of a Large Molecular Network. Lecture Notes in Computer Science, 2014, , 171-182.	1.3	15
47	Suffix-Tree Based Error Correction of NGS Reads Using Multiple Manifestations of an Error. , 2013, , .		4
48	Network Signatures of Survival in Glioblastoma Multiforme. PLoS Computational Biology, 2013, 9, e1003237.	3.2	71
49	Guest Editorial for Special Section on BIOKDD. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1199-1200.	3.0	0
50	Accurate estimation of short read mapping quality for next-generation genome sequencing. Bioinformatics, 2012, 28, i349-i355.	4.1	29
51	Network biology methods integrating biological data for translational science. Briefings in Bioinformatics, 2012, 13, 446-459.	6.5	57
52	Algorithms for detecting complementary SNPs within a region of interest that are associated with diseases. , 2012, , .		1
53	Network-based approaches for extending the Wnt signalling pathway and identifying context-specific sub-networks. International Journal of Computational Biology and Drug Design, 2012, 5, 185.	0.3	2
54	Gene interaction enrichment and network analysis to identify dysregulated pathways and their interactions in complex diseases. BMC Systems Biology, 2012, 6, 65.	3.0	47

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55	Introduction to Network Biology. , 2012, , 1-13.		1
56	Gene, pathway and network frameworks to identify epistatic interactions of single nucleotide polymorphisms derived from GWAS data. BMC Systems Biology, 2012, 6, S15.	3.0	41
57	Identifying stage-specific protein subnetworks for colorectal cancer. BMC Proceedings, 2012, 6, S1.	1.6	6
58	Using Protein Interaction Networks to Understand Complex Diseases. Computer, 2012, 45, 31-38.	1.1	13
59	Molecular Networks and Complex Diseases. , 2012, , 171-199.		0
60	Comparative analysis of algorithms for next-generation sequencing read alignment. Bioinformatics, 2011, 27, 2790-2796.	4.1	195
61	Subnetwork State Functions Define Dysregulated Subnetworks in Cancer. Journal of Computational Biology, 2011, 18, 263-281.	1.6	63
62	Disease Gene Prioritization Based on Topological Similarity in Protein-Protein Interaction Networks. Lecture Notes in Computer Science, 2011, , 54-68.	1.3	4
63	DADA: Degree-Aware Algorithms for Network-Based Disease Gene Prioritization. BioData Mining, 2011, 4, 19.	4.0	148
64	Protein–protein interaction networks and subnetworks in the biology of disease. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2011, 3, 357-367.	6.6	79
65	V<scp>avien</scp>: An Algorithm for Prioritizing Candidate Disease Genes Based on Topological Similarity of Proteins in Interaction Networks. Journal of Computational Biology, 2011, 18, 1561-1574.	1.6	70
66	Functional characterization and topological modularity of molecular interaction networks. BMC Bioinformatics, 2010, 11, S35.	2.6	13
67	Algorithmic and analytical methods in network biology. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2010, 2, 277-292.	6.6	28
68	An Integrative -omics Approach to Identify Functional Sub-Networks in Human Colorectal Cancer. PLoS Computational Biology, 2010, 6, e1000639.	3.2	140
69	Weighted Matrix Ordering and Parallel Banded Preconditioners for Iterative Linear System Solvers. SIAM Journal of Scientific Computing, 2010, 32, 1201-1216.	2.8	19
70	Subnetwork State Functions Define Dysregulated Subnetworks in Cancer. Lecture Notes in Computer Science, 2010, , 80-95.	1.3	6
71	SYSTEMS BIOLOGY ANALYSES OF GENE EXPRESSION AND GENOME WIDE ASSOCIATION STUDY DATA IN OBSTRUCTIVE SLEEP APNEA. , 2010, , 14-25.		25
72	Optimization Algorithms for Identification and Genotyping of Copy Number Polymorphisms in Human Populations. Lecture Notes in Computer Science, 2010, , 74-85.	1.3	0

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73	Identification of Modules in Protein-Protein Interaction Networks. , 2010, , 253-267.		0
74	Comparative Analysis of Modularity in Biological Systems. , 2009, , .		0
75	Phylogenetic analysis of modularity in protein interaction networks. BMC Bioinformatics, 2009, 10, 333.	2.6	31
76	Efficient tag detection in RFID systems. Journal of Parallel and Distributed Computing, 2009, 69, 180-196.	4.1	40
77	An optimization framework for unsupervised identification of rare copy number variation from SNP array data. Genome Biology, 2009, 10, R119.	9.6	22
78	IDENTIFICATION OF COORDINATELY DYSREGULATED SUBNETWORKS IN COMPLEX PHENOTYPES. , 2009, , 133-144.		37
79	Semantic indexing in structured peer-to-peer networks. Journal of Parallel and Distributed Computing, 2008, 68, 64-77.	4.1	5
80	PHALANX. , 2008, , .		17
81	Functional coherence in domain interaction networks. Bioinformatics, 2008, 24, i28-i34.	4.1	28
82	Functional annotation of regulatory pathways. Bioinformatics, 2007, 23, i377-i386.	4.1	17
83	Assessing Significance of Connectivity and Conservation in Protein Interaction Networks. Journal of Computational Biology, 2007, 14, 747-764.	1.6	52
84	ANNOTATING PATHWAYS IN INTERACTION NETWORKS. , 2007, , .		0
85	Detecting Conserved Interaction Patterns in Biological Networks. Journal of Computational Biology, 2006, 13, 1299-1322.	1.6	71
86	CONQUEST: A Coarse-Grained Algorithm for Constructing Summaries of Distributed Discrete Datasets. Algorithmica, 2006, 45, 377-401.	1.3	1
87	Inferring functional information from domain co-evolution. Bioinformatics, 2006, 22, 40-49.	4.1	26
88	Nonorthogonal decomposition of binary matrices for bounded-error data compression and analysis. ACM Transactions on Mathematical Software, 2006, 32, 33-69.	2.9	30
89	Pairwise Alignment of Protein Interaction Networks. Journal of Computational Biology, 2006, 13, 182-199.	1.6	232
90	Iterative-improvement-based declustering heuristics for multi-disk databases. Information Systems, 2005, 30, 47-70.	3.6	22

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91	An efficient algorithm for detecting frequent subgraphs in biological networks. Bioinformatics, 2004, 20, i200-i207.	4.1	141
92	PROXIMUS. , 2003, , .		28
93	Consensus embedding for multiple networks: Computation and applications. Network Science, 0, , 1-17.	1.0	1