

# Kamal Taha

## List of Publications by Year in descending order

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Version: 2024-02-01

79  
papers

1,157  
citations

643344

15  
h-index

466096

32  
g-index

81  
all docs

81  
docs citations

81  
times ranked

1395  
citing authors

#	ARTICLE	IF	CITATIONS
1	Inferring the densest multi-profiled cross-community for a user. Knowledge-Based Systems, 2022, 237, 107681.	4.0	2
2	Detecting implicit cross-communities to which an active user belongs. PLoS ONE, 2022, 17, e0264771.	1.1	0
3	Personizing the prediction of future susceptibility to a specific disease. PLoS ONE, 2021, 16, e0243127.	1.1	3
4	R <sup>2</sup> BN: An Adaptive Model for Keystroke-Dynamics-Based Educational Level Classification. IEEE Transactions on Cybernetics, 2020, 50, 525-535.	6.2	15
5	Detecting Disjoint Communities in a Social Network based on the Degrees of Association between Edges and Influential Nodes. IEEE Transactions on Knowledge and Data Engineering, 2020, , 1-1.	4.0	3
6	Inferring Causation in Yeast Gene Association Networks With Kernel Logistic Regression. Evolutionary Bioinformatics, 2020, 16, 117693432092031.	0.6	2
7	Methods That Optimize Multi-Objective Problems: A Survey and Experimental Evaluation. IEEE Access, 2020, 8, 80855-80878.	2.6	18
8	IMPACT: Impersonation Attack Detection via Edge Computing Using Deep Autoencoder and Feature Abstraction. IEEE Access, 2020, 8, 65520-65529.	2.6	60
9	Static and Dynamic Community Detection Methods That Optimize a Specific Objective Function: A Survey and Experimental Evaluation. IEEE Access, 2020, 8, 98330-98358.	2.6	9
10	An effective approach for identifying defective critical fabrication path. Cogent Engineering, 2019, 6, .	1.1	3
11	Predicting the Functions of Proteins from their Co-occurrences with Implicit and Explicit Functional Terms in Texts. , 2019, , .		1
12	DEMISe. , 2019, , .		20
13	Shortlisting the Influential Members of Criminal Organizations and Identifying Their Important Communication Channels. IEEE Transactions on Information Forensics and Security, 2019, 14, 1988-1999.	4.5	13
14	Analyzing a co-occurrence gene-interaction network to identify disease-gene association. BMC Bioinformatics, 2019, 20, 70.	1.2	27
15	Predicting protein functions by applying predicate logic to biomedical literature. BMC Bioinformatics, 2019, 20, 71.	1.2	3
16	Employing the Inference Rules of Predicate Logic for Predicting Protein Functions. , 2019, , .		1
17	Detecting Overlapping Communities of Nodes with Multiple Attributes from Heterogeneous Networks. Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering, 2019, , 760-779.	0.2	4
18	CDID: A System for Identifying the Root Cause of a Defect in Semiconductor Wafer Fabrication. IEEE Transactions on Semiconductor Manufacturing, 2018, 31, 221-231.	1.4	5

#	ARTICLE	IF	CITATIONS
19	Inferring the Functions of Proteins from the Interrelationships between Functional Categories. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 157-167.	1.9	4
20	A Forensic System for Identifying the Suspects of a Crime with No Solid Material Evidences. , 2018, , .		0
21	Clustering the Dominant Defective Patterns in Semiconductor Wafer Maps. IEEE Transactions on Semiconductor Manufacturing, 2018, 31, 156-165.	1.4	23
22	Disjoint Community Detection in Networks Based on the Relative Association of Members. IEEE Transactions on Computational Social Systems, 2018, 5, 493-507.	3.2	15
23	CRS. , 2018, , 553-570.		0
24	An Effective Approach for Associating the Sources of Defect Signatures to Process Zones. IEEE Transactions on Semiconductor Manufacturing, 2017, 30, 176-184.	1.4	5
25	Constructing Genetic Networks using Biomedical Literature and Rare Event Classification. Scientific Reports, 2017, 7, 15784.	1.6	7
26	Using the Spanning Tree of a Criminal Network for Identifying Its Leaders. IEEE Transactions on Information Forensics and Security, 2017, 12, 445-453.	4.5	32
27	Identifying wafer fabrication defect signatures. , 2017, , .		0
28	Constructing yeast genetic interaction network using biomedical literature and logistic regression. , 2017, , .		1
29	SIIMCO: A Forensic Investigation Tool for Identifying the Influential Members of a Criminal Organization. IEEE Transactions on Information Forensics and Security, 2016, 11, 811-822.	4.5	29
30	Applying Monte Carlo Simulation to Biomedical Literature to Approximate Genetic Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 494-504.	1.9	14
31	A Knowledge Base Visual Analytics Technique for Semantic Web. , 2016, , .		2
32	Predicting the functions of a protein from its ability to associate with other molecules. BMC Bioinformatics, 2016, 17, 34.	1.2	6
33	Data Randomization and Cluster-Based Partitioning for Botnet Intrusion Detection. IEEE Transactions on Cybernetics, 2016, 46, 1796-1806.	6.2	109
34	Extracting Useful Information from Mobile Communication Data for Forensic Investigation. Advanced Science Letters, 2016, 22, 3100-3104.	0.2	0
35	Clustering a Network Based on the Dynamics and Interactions of Its Members. Advanced Science Letters, 2016, 22, 3071-3075.	0.2	0
36	iFPFi: A System for Improving Protein Function Prediction through Cumulative Iterations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 825-836.	1.9	7

#	ARTICLE	IF	CITATIONS
37	Semantic rules for extracting proteins functions information from biomedical abstracts. , 2015, , .		0
38	Predicting protein function from biomedical text. , 2015, 2015, 3275-8.		1
39	An information extraction system for protein function prediction. , 2015, , .		1
40	A System for Analyzing Criminal Social Networks. , 2015, , .		7
41	Extracting Various Classes of Data From Biological Text Using the Concept of Existence Dependency. IEEE Journal of Biomedical and Health Informatics, 2015, 19, 1918-1928.	3.9	11
42	CISRI: A Crime Investigation System Using the Relative Importance of Information Spreaders in Networks Depicting Criminals Communications. IEEE Transactions on Information Forensics and Security, 2015, 10, 2196-2211.	4.5	24
43	Efficient Machine Learning for Big Data: A Review. Big Data Research, 2015, 2, 87-93.	2.6	425
44	Randomized Subspace Learning for Proline Cis-Trans Isomerization Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 763-769.	1.9	4
45	Simplified Subspaced Regression Network for Identification of Defect Patterns in Semiconductor Wafer Maps. IEEE Transactions on Industrial Informatics, 2015, 11, 1267-1276.	7.2	71
46	RGFinder: A System for Determining Semantically Related Genes Using GO Graph Minimum Spanning Tree. IEEE Transactions on Nanobioscience, 2015, 14, 24-37.	2.2	4
47	Integrating supply chain data standards in healthcare operations and Electronic Health Records. , 2015, , .		3
48	BioHCDP: A Hybrid Constituency-Dependency Parser for Biological NLP information extraction. , 2014, , .		1
49	Determining Semantically Related Significant Genes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 1119-1130.	1.9	17
50	Inferring the relationships among genes from weighted GO graph. , 2014, , .		0
51	Intelligent Consensus Modeling for Proline Cis-Trans Isomerization Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 26-32.	1.9	5
52	CRS. Advances in Educational Technologies and Instructional Design Book Series, 2014, , 177-193.	0.2	1
53	XEngine: An XML Search Engine for Social Groups. Lecture Notes in Social Networks, 2014, , 305-337.	0.8	0
54	A Classifier System for Determining the Functions of Un-Annotated Proteins Based on Their Semantic Similarities with Gene Ontology Annotation Terms. Advanced Science, Engineering and Medicine, 2014, 6, 879-883.	0.3	0

#	ARTICLE	IF	CITATIONS
55	GRank: a middleware search engine for ranking genes by relevance to given genes. BMC Bioinformatics, 2013, 14, 251.	1.2	12
56	GRtoGR: A System for Mapping GO Relations to Gene Relations. IEEE Transactions on Nanobioscience, 2013, 12, 289-297.	2.2	12
57	Determining the Semantic Similarities Among Gene Ontology Terms. IEEE Journal of Biomedical and Health Informatics, 2013, 17, 512-525.	3.9	17
58	Visual analytics in the web of data. , 2013, , .		0
59	GOseek: A gene ontology search engine using enhanced keywords. , 2013, 2013, 1502-5.		2
60	Determining the semantic similarities of GO terms based on their existence dependencies. , 2012, , .		0
61	Automatic Academic Advisor. , 2012, , .		11
62	GOcSim: GO context-driven similarity. , 2012, , .		6
63	RGRank: Ranking Semantically Related Genes. , 2012, , .		3
64	Personalization with Dynamic Group Profile. , 2012, , .		1
65	IRTG: A Grid Middleware for Bioinformatics. , 2011, , .		0
66	GMB: an efficient query processor for biological data. Journal of Integrative Bioinformatics, 2011, 8, 165.	1.0	1
67	XTEngine. , 2011, , 174-213.		0
68	BusSEngine: a business search engine. Knowledge and Information Systems, 2010, 23, 153-197.	2.1	16
69	SPGProfile: Speak Group Profile. Information Systems, 2010, 35, 774-790.	2.4	8
70	XCDSearch: An XML Context-Driven Search Engine. IEEE Transactions on Knowledge and Data Engineering, 2010, 22, 1781-1796.	4.0	17
71	OOXKSearch. Journal of Database Management, 2009, 20, 18-50.	1.0	7
72	Pitfalls of non context-driven XML search systems. , 2009, , .		0

#	ARTICLE	IF	CITATIONS
73	XML with Recursive Querying. , 2009, , .		0
74	KSRQuerying: XML Keyword with Recursive Querying. Lecture Notes in Computer Science, 2009, , 33-52.	1.0	1
75	CXLEngine. , 2008, , .		18
76	XPCache: An Efficient Query Processor for Client-Server Architecture. , 2007, , .		1
77	OOXSearch: A Search Engine for Answering Loosely Structured XML Queries Using OO Programming. Lecture Notes in Computer Science, 2007, , 82-100.	1.0	5
78	Social Search and Personalization Through Demographic Filtering. , 0, , 183-203.		1
79	SEEC. , 0, , 57-81.		0