Seferina Mavroudi

List of Publications by Year
in descending order

42 papers	426 citations	840776 11 h-index	794594 19 g-index
44 all docs	44 docs citations	44 times ranked	472 citing authors

#	ARTICLE	IF	CITATIONS
1	Ischemia detection with a self-organizing map supplemented by supervised learning. IEEE Transactions on Neural Networks, 2001, 12, 503-515.	4.2	54
2	Where we stand, where we are moving: Surveying computational techniques for identifying miRNA genes and uncovering their regulatory role. Journal of Biomedical Informatics, 2013, 46, 563-573.	4.3	41
3	ScalaLab and GroovyLab: Comparing Scala and Groovy for Scientific Computing. Scientific Programming, 2015, 2015, 1-13.	0.7	40
4	YamiPred: A Novel Evolutionary Method for Predicting Pre-miRNAs and Selecting Relevant Features. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 1183-1192.	3.0	28
5	A PROBABILISTIC SYMMETRIC ENCRYPTION SCHEME FOR VERY FAST SECURE COMMUNICATION BASED ON CHAOTIC SYSTEMS OF DIFFERENCE EQUATIONS. International Journal of Bifurcation and Chaos in Applied Sciences and Engineering, 2001, 11, 3107-3115.	1.7	27
6	Computational Approaches for the Prediction of Protein-Protein Interactions: A Survey. Current Bioinformatics, 2011, 6, 398-414.	1.5	27
7	Predicting protein complexes from weighted protein–protein interaction graphs with a novel unsupervised methodology: Evolutionary enhanced Markov clustering. Artificial Intelligence in Medicine, 2015, 63, 181-189.	6.5	26
8	Gene expression data analysis with a dynamically extended self-organized map that exploits class information. Bioinformatics, 2002, 18, 1446-1453.	4.1	22
9	EnsembleGASVR: a novel ensemble method for classifying missense single nucleotide polymorphisms. Bioinformatics, 2014, 30, 2324-2333.	4.1	17
10	On the human taste perception: Molecular-level understanding empowered by computational methods. Trends in Food Science and Technology, 2021, 116, 445-459.	15.1	17
11	Discovery of stroke-related blood biomarkers from gene expression network models. BMC Medical Genomics, 2019, 12, 118.	1.5	14
12	ScalaLab: An Effective Scala-Based Scientific Programming Environment for Java. Computing in Science and Engineering, 2011, 13, 43-55.	1.2	11
13	An Adaptive Pipeline To Maximize Isobaric Tagging Data in Large-Scale MS-Based Proteomics. Journal of Proteome Research, 2018, 17, 2165-2173.	3.7	11
14	Scientific Scripting for the Java Platform with jLab. Computing in Science and Engineering, 2009, 11, 50-60.	1.2	9
15	The Supervised Network Self-Organizing Map for Classification of Large Data Sets. Applied Intelligence, 2002, 16, 185-203.	5.3	8
16	Predicting overlapping protein complexes from weighted protein interaction graphs by gradually expanding dense neighborhoods. Artificial Intelligence in Medicine, 2016, 71, 62-69.	6.5	8
17	<p>Reducing Opioid Prescriptions by Identifying Responders on Topical Analgesic Treatment Using an Individualized Medicine and Predictive Analytics Approach</p>. Journal of Pain Research, 2020, Volume 13, 1255-1266.	2.0	8
18	A Hybrid Support Vector Fuzzy Inference System for the Classification of Leakage Current Waveforms Portraying Discharges. Electric Power Components and Systems, 2014, 42, 180-189.	1.8	7

#	Article	IF	Citations
19	MUTUAL INFORMATION CLUSTERING FOR EFFICIENT MINING OF FUZZY ASSOCIATION RULES WITH APPLICATION TO GENE EXPRESSION DATA ANALYSIS. International Journal on Artificial Intelligence Tools, 2006, 15, 227-250.	1.0	6
20	Predicting human miRNA target genes using a novel computational intelligent framework. Information Sciences, 2015, 294, 576-585.	6.9	6
21	The Human Interactome Knowledge Base (HINT-KB): an integrative human protein interaction database enriched with predicted proteinâ€"protein interaction scores using a novel hybrid technique. Artificial Intelligence Review, 2014, 42, 427-443.	15.7	5
22	Computational Methods and Algorithms for Mass-Spectrometry Based Differential Proteomics. Current Proteomics, 2007, 4, 223-234.	0.3	4
23	ncRNAclass: A Web Platform for Non-Coding RNA Feature Calculation and MicroRNAs and Targets Prediction. International Journal on Artificial Intelligence Tools, 2015, 24, 1540002.	1.0	4
24	InSyBio BioNets: an efficient tool for network-based biomarker discovery. EMBnet Journal, 2016, 22, 871.	0.6	4
25	Som-Based Class Discovery Exploring the ICA-Reduced Features of Microarray Expression Profiles. Comparative and Functional Genomics, 2004, 5, 596-616.	2.0	3
26	The Software Architecture for Performing Scientific Computation with the JLAPACK Libraries in ScalaLab. Scientific Programming, 2012, 20, 379-391.	0.7	3
27	Pharmacoepigenomics circuits induced by a novel retinoid-polyamine conjugate in human immortalized keratinocytes. Pharmacogenomics Journal, 2021, 21, 638-648.	2.0	3
28	Integrating Supervised and Unsupervised Learning in Self Organizing Maps for Gene Expression Data Analysis. Lecture Notes in Computer Science, 2003, , 262-270.	1.3	3
29	ncRNA-Class Web Tool: Non-coding RNA Feature Extraction and Pre-miRNA Classification Web Tool. International Federation for Information Processing, 2012, , 632-641.	0.4	2
30	InSyBio ncRNASeq: A web tool for analyzing non-coding RNAs. EMBnet Journal, 2017, 23, 882.	0.6	2
31	Title is missing!. Applied Intelligence, 2002, 16, 223-234.	5.3	1
32	Efficient Computational Prediction and Scoring of Human Protein-Protein Interactions Using a Novel Gene Expression Programming Methodology. Communications in Computer and Information Science, 2012, , 472-481.	0.5	1
33	Quo vadis1 computational analysis of PPI data or why the future isn't here yet. Frontiers in Genetics, 2015, 6, 289.	2.3	1
34	Non-coding RNA Sequences Identification and Classification Using a Multi-class and Multi-label Ensemble Technique. IFIP Advances in Information and Communication Technology, 2018, , 179-188.	0.7	1
35	Revealing the Structure of Childhood Abdominal Pain Data and Supporting Diagnostic Decision Making. Communications in Computer and Information Science, 2009, , 165-177.	0.5	1
36	HINT-KB: The Human Interactome Knowledge Base. International Federation for Information Processing, 2012, , 612-621.	0.4	1

#	Article	IF	Citations
37	Computational Methods and Algorithms for Mass Spectrometry Based Differential Proteomics: Recent Advances, Perspectives and Open Problems. Current Proteomics, 2012, 9, 143-159.	0.3	0
38	MATLAB-Like Scripting of Java Scientific Libraries in ScalaLab. Scientific Programming, 2014, 22, 187-199.	0.7	0
39	Predicting and classifying short non-coding RNAs using a multiclass evolutionary methodology. , 2015, , .		0
40	Superclusteroid 2.0: A Web Tool for Processing Big Biological Networks. IFIP Advances in Information and Communication Technology, 2016, , 623-633.	0.7	0
41	A precision medicine approach for non-opioid pain therapy using a combination of multi-objective optimization and support vector regression. , 2019, , .		0
42	A New Framework for Bridging the Gap from Protein-Protein Interactions to Biological Process Interactions. IFIP Advances in Information and Communication Technology, 2014, , 196-204.	0.7	0