

# Seferina Mavroudi

## List of Publications by Year in descending order

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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	Pharmacoeigenomics circuits induced by a novel retinoid-polyamine conjugate in human immortalized keratinocytes. <i>Pharmacogenomics Journal</i> , 2021, 21, 638-648.	2.0	3
2	On the human taste perception: Molecular-level understanding empowered by computational methods. <i>Trends in Food Science and Technology</i> , 2021, 116, 445-459.	15.1	17
3	&lt;p&gt;Reducing Opioid Prescriptions by Identifying Responders on Topical Analgesic Treatment Using an Individualized Medicine and Predictive Analytics Approach&lt;p&gt;. <i>Journal of Pain Research</i> , 2020, Volume 13, 1255-1266.	2.0	8
4	Discovery of stroke-related blood biomarkers from gene expression network models. <i>BMC Medical Genomics</i> , 2019, 12, 118.	1.5	14
5	A precision medicine approach for non-opioid pain therapy using a combination of multi-objective optimization and support vector regression. , 2019, , .		0
6	An Adaptive Pipeline To Maximize Isobaric Tagging Data in Large-Scale MS-Based Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 2165-2173.	3.7	11
7	Non-coding RNA Sequences Identification and Classification Using a Multi-class and Multi-label Ensemble Technique. <i>IFIP Advances in Information and Communication Technology</i> , 2018, , 179-188.	0.7	1
8	InSyBio ncRNASeq: A web tool for analyzing non-coding RNAs. <i>EMBnet Journal</i> , 2017, 23, 882.	0.6	2
9	Superclusteroid 2.0: A Web Tool for Processing Big Biological Networks. <i>IFIP Advances in Information and Communication Technology</i> , 2016, , 623-633.	0.7	0
10	Predicting overlapping protein complexes from weighted protein interaction graphs by gradually expanding dense neighborhoods. <i>Artificial Intelligence in Medicine</i> , 2016, 71, 62-69.	6.5	8
11	InSyBio BioNets: an efficient tool for network-based biomarker discovery. <i>EMBnet Journal</i> , 2016, 22, 871.	0.6	4
12	Predicting and classifying short non-coding RNAs using a multiclass evolutionary methodology. , 2015, , .		0
13	Quo vadis1 computational analysis of PPI data or why the future isn't here yet. <i>Frontiers in Genetics</i> , 2015, 6, 289.	2.3	1
14	ScalaLab and GroovyLab: Comparing Scala and Groovy for Scientific Computing. <i>Scientific Programming</i> , 2015, 2015, 1-13.	0.7	40
15	ncRNAclass: A Web Platform for Non-Coding RNA Feature Calculation and MicroRNAs and Targets Prediction. <i>International Journal on Artificial Intelligence Tools</i> , 2015, 24, 1540002.	1.0	4
16	Predicting protein complexes from weighted proteinâ€“protein interaction graphs with a novel unsupervised methodology: Evolutionary enhanced Markov clustering. <i>Artificial Intelligence in Medicine</i> , 2015, 63, 181-189.	6.5	26
17	YamiPred: A Novel Evolutionary Method for Predicting Pre-miRNAs and Selecting Relevant Features. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 1183-1192.	3.0	28
18	Predicting human miRNA target genes using a novel computational intelligent framework. <i>Information Sciences</i> , 2015, 294, 576-585.	6.9	6

#	ARTICLE	IF	CITATIONS
19	MATLAB-Like Scripting of Java Scientific Libraries in ScalaLab. <i>Scientific Programming</i> , 2014, 22, 187-199.	0.7	0
20	The Human Interactome Knowledge Base (HINT-KB): an integrative human protein interaction database enriched with predicted protein-protein interaction scores using a novel hybrid technique. <i>Artificial Intelligence Review</i> , 2014, 42, 427-443.	15.7	5
21	A Hybrid Support Vector Fuzzy Inference System for the Classification of Leakage Current Waveforms Portraying Discharges. <i>Electric Power Components and Systems</i> , 2014, 42, 180-189.	1.8	7
22	EnsembleGASVR: a novel ensemble method for classifying missense single nucleotide polymorphisms. <i>Bioinformatics</i> , 2014, 30, 2324-2333.	4.1	17
23	A New Framework for Bridging the Gap from Protein-Protein Interactions to Biological Process Interactions. <i>IFIP Advances in Information and Communication Technology</i> , 2014, , 196-204.	0.7	0
24	Where we stand, where we are moving: Surveying computational techniques for identifying miRNA genes and uncovering their regulatory role. <i>Journal of Biomedical Informatics</i> , 2013, 46, 563-573.	4.3	41
25	Efficient Computational Prediction and Scoring of Human Protein-Protein Interactions Using a Novel Gene Expression Programming Methodology. <i>Communications in Computer and Information Science</i> , 2012, , 472-481.	0.5	1
26	Computational Methods and Algorithms for Mass Spectrometry Based Differential Proteomics: Recent Advances, Perspectives and Open Problems. <i>Current Proteomics</i> , 2012, 9, 143-159.	0.3	0
27	The Software Architecture for Performing Scientific Computation with the JLAPACK Libraries in ScalaLab. <i>Scientific Programming</i> , 2012, 20, 379-391.	0.7	3
28	ncRNA-Class Web Tool: Non-coding RNA Feature Extraction and Pre-miRNA Classification Web Tool. <i>International Federation for Information Processing</i> , 2012, , 632-641.	0.4	2
29	HINT-KB: The Human Interactome Knowledge Base. <i>International Federation for Information Processing</i> , 2012, , 612-621.	0.4	1
30	Computational Approaches for the Prediction of Protein-Protein Interactions: A Survey. <i>Current Bioinformatics</i> , 2011, 6, 398-414.	1.5	27
31	ScalaLab: An Effective Scala-Based Scientific Programming Environment for Java. <i>Computing in Science and Engineering</i> , 2011, 13, 43-55.	1.2	11
32	Scientific Scripting for the Java Platform with jLab. <i>Computing in Science and Engineering</i> , 2009, 11, 50-60.	1.2	9
33	Revealing the Structure of Childhood Abdominal Pain Data and Supporting Diagnostic Decision Making. <i>Communications in Computer and Information Science</i> , 2009, , 165-177.	0.5	1
34	Computational Methods and Algorithms for Mass-Spectrometry Based Differential Proteomics. <i>Current Proteomics</i> , 2007, 4, 223-234.	0.3	4
35	MUTUAL INFORMATION CLUSTERING FOR EFFICIENT MINING OF FUZZY ASSOCIATION RULES WITH APPLICATION TO GENE EXPRESSION DATA ANALYSIS. <i>International Journal on Artificial Intelligence Tools</i> , 2006, 15, 227-250.	1.0	6
36	Som-Based Class Discovery Exploring the ICA-Reduced Features of Microarray Expression Profiles. <i>Comparative and Functional Genomics</i> , 2004, 5, 596-616.	2.0	3

#	ARTICLE	IF	CITATIONS
37	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
38	Gene expression data analysis with a dynamically extended self-organized map that exploits class information. Bioinformatics, 2002, 18, 1446-1453.	4.1	22
39	The Supervised Network Self-Organizing Map for Classification of Large Data Sets. Applied Intelligence, 2002, 16, 185-203.	5.3	8
40	Title is missing!. Applied Intelligence, 2002, 16, 223-234.	5.3	1
41	Ischemia detection with a self-organizing map supplemented by supervised learning. IEEE Transactions on Neural Networks, 2001, 12, 503-515.	4.2	54
42	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