

# Mario Inostroza-Ponta

## List of Publications by Year in descending order

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Version: 2024-02-01

41  
papers

915  
citations

758635

12  
h-index

839053

18  
g-index

41  
all docs

41  
docs citations

41  
times ranked

1502  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide analysis of long noncoding RNA stability. <i>Genome Research</i> , 2012, 22, 885-898.	2.4	471
2	Is there more than one proctitis syndrome? A revisitaton using data from the TROG 96.01 trial. <i>Radiotherapy and Oncology</i> , 2009, 90, 400-407.	0.3	70
3	A Transcription Factor Map as Revealed by a Genome-Wide Gene Expression Analysis of Whole-Blood mRNA Transcriptome in Multiple Sclerosis. <i>PLoS ONE</i> , 2010, 5, e14176.	1.1	51
4	APL: An angle probability list to improve knowledge-based metaheuristics for the three-dimensional protein structure prediction. <i>Computational Biology and Chemistry</i> , 2015, 59, 142-157.	1.1	38
5	(GTC)5 MSP-PCR Fingerprinting as a Technique for Discrimination of Wine Associated Yeasts?. <i>PLoS ONE</i> , 2014, 9, e105870.	1.1	33
6	Comparison of Phylogenetic Tree Topologies for Nitrogen Associated Genes Partially Reconstruct the Evolutionary History of <i>Saccharomyces cerevisiae</i> . <i>Microorganisms</i> , 2020, 8, 32.	1.6	26
7	A Memetic Algorithm for 3D Protein Structure Prediction Problem. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 690-704.	1.9	24
8	A Memetic Algorithm Based on an NSGA-II Scheme for Phylogenetic Tree Inference. <i>IEEE Transactions on Evolutionary Computation</i> , 2019, 23, 776-787.	7.5	22
9	QAPgrid: A Two Level QAP-Based Approach for Large-Scale Data Analysis and Visualization. <i>PLoS ONE</i> , 2011, 6, e14468.	1.1	22
10	NIAS-Server: Neighbors Influence of Amino acids and Secondary Structures in Proteins. <i>Journal of Computational Biology</i> , 2017, 24, 255-265.	0.8	19
11	A multi-objective gene clustering algorithm guided by apriori biological knowledge with intensification and diversification strategies. <i>BioData Mining</i> , 2018, 11, 16.	2.2	17
12	An automatic graph layout procedure to visualize correlated data. , 2006, , 179-188.		16
13	An Integrated QAP-Based Approach to Visualize Patterns of Gene Expression Similarity. , 2007, , 156-167.		15
14	A New Strategy to Evaluate Technical Efficiency in Hospitals Using Homogeneous Groups of Casemix. <i>Journal of Medical Systems</i> , 2016, 40, 103.	2.2	14
15	Clustering Nodes in Large-Scale Biological Networks Using External Memory Algorithms. <i>Lecture Notes in Computer Science</i> , 2011, , 375-386.	1.0	12
16	A memetic algorithm for the quadratic assignment problem with parallel local search. , 2015, , .		8
17	Molecular Modeling of Epithiospecifier and Nitrile-Specifier Proteins of Broccoli and Their Interaction with Aglycones. <i>Molecules</i> , 2020, 25, 772.	1.7	8
18	A knowledge-based genetic algorithm to predict three-dimensional structures of polypeptides. , 2013, , .		5

#	ARTICLE	IF	CITATIONS
19	Application of different multi-objective decision making techniques in the phylogenetic inference problem. , 2017, , .		5
20	Evaluating Memory Schemas in a Memetic Algorithm for the Quadratic Assignment Problem. , 2011, , .		4
21	Understanding the Relationship Between Decision and Objective Space in the Multi-Objective Phylogenetic Inference Problem. , 2018, , .		4
22	A bi-objective model for gene clustering combining expression data and external biological knowledge. , 2016, , .		3
23	Evaluating the use of local search strategies for a memetic algorithm for the protein-ligand docking problem. , 2017, , .		3
24	Performance Comparison of Multi-Objective Local Search Strategies to Infer Phylogenetic Trees. , 2018, , .		3
25	A multimodal multi-objective optimisation approach to deal with the phylogenetic inference problem. , 2020, , .		3
26	Exploring the high selectivity of 3-D protein structures using distributed memetic algorithms. Journal of Computational Science, 2020, 41, 101087.	1.5	3
27	A Memetic Algorithm for Protein Structure Prediction based on Conformational Preferences of Aminoacid Residues. , 2015, , .		2
28	An evolutionary multi-agent algorithm to explore the high degree of selectivity in three-dimensional protein structures. , 2017, , .		2
29	Tackling the bi-objective quadratic assignment problem by characterizing different memory strategies in a memetic algorithm. , 2017, , .		2
30	A Genetic Algorithm Based on Restricted Tournament Selection for the 3D-PSP Problem. , 2018, , .		2
31	Total evidence or taxonomic congruence? A comparison of methods for combining biological evidence. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050040.	0.3	2
32	A multi-modal algorithm based on an NSGA-II scheme for phylogenetic tree inference. BioSystems, 2022, 213, 104606.	0.9	2
33	Evaluation of a combined energy fitness function for a distributed memetic algorithm to tackle the 3D protein structure prediction problem. , 2016, , .		1
34	Using local search strategies to improve the performance of NSGA-II for the Multi-Criteria Minimum Spanning Tree problem. , 2017, , .		1
35	Unsupervised Pattern Recognition for Geographical Clustering of Seismic Events Post M<sub>W</sub> 7.8 Ecuador Earthquake. , 2018, , .		1
36	Influence of the go-based semantic similarity measures in multi-objective gene clustering algorithm performance. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050038.	0.3	1

#	ARTICLE	IF	CITATIONS
37	Using the QAPgrid Visualization Approach for Biomarker Identification of Cell-Specific Transcriptomic Signatures. <i>Methods in Molecular Biology</i> , 2017, 1526, 271-297.	0.4	0
38	Visualizing Products and Consumers: A Gestalt Theory Inspired Method. , 2019, , 661-689.		0
39	A multi-objective optimisation evolutionary approach for the Multidimensional Scaling Problem. , 2019, , .		0
40	Evaluating the categorisation of the public hospitals in Chile according to case-mix complexity: a genetic algorithm approach. , 2020, , .		0
41	A multi-objective approach for the protein structure prediction problem. , 2021, , .		0