Marcio Dorn

List of Publications by Year
in descending order

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70 papers	788 citations	623574 14 h-index	580701 25 g-index
72 all docs	72 docs citations	72 times ranked	736 citing authors

#	Article	IF	Citations
1	Three-dimensional protein structure prediction: Methods and computational strategies. Computational Biology and Chemistry, 2014, 53, 251-276.	1.1	160
2	CuMiDa: An Extensively Curated Microarray Database for Benchmarking and Testing of Machine Learning Approaches in Cancer Research. Journal of Computational Biology, 2019, 26, 376-386.	0.8	46
3	Aromatic Rings Commonly Used in Medicinal Chemistry: Force Fields Comparison and Interactions With Water Toward the Design of New Chemical Entities. Frontiers in Pharmacology, 2018, 9, 395.	1.6	40
4	APL: An angle probability list to improve knowledge-based metaheuristics for the three-dimensional protein structure prediction. Computational Biology and Chemistry, 2015, 59, 142-157.	1.1	38
5	Hemogram data as a tool for decision-making in COVID-19 management: applications to resource scarcity scenarios. PeerJ, 2020, 8, e9482.	0.9	32
6	A GMDH polynomial neural network-based method to predict approximate three-dimensional structures of polypeptides. Expert Systems With Applications, 2012, 39, 12268-12279.	4.4	29
7	Neuroevolution as a tool for microarray gene expression pattern identification in cancer research. Journal of Biomedical Informatics, 2019, 89, 122-133.	2.5	27
8	The tale of a versatile enzyme: Alpha-amylase evolution, structure, and potential biotechnological applications for the bioremediation of n-alkanes. Chemosphere, 2020, 250, 126202.	4.2	25
9	A Memetic Algorithm for 3D Protein Structure Prediction Problem. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 690-704.	1.9	24
10	A Memetic Algorithm Based on an NSGA-II Scheme for Phylogenetic Tree Inference. IEEE Transactions on Evolutionary Computation, 2019, 23, 776-787.	7.5	22
11	NIAS-Server: Neighbors Influence of Amino acids and Secondary Structures in Proteins. Journal of Computational Biology, 2017, 24, 255-265.	0.8	19
12	Three-dimensional protein structure prediction based on memetic algorithms. Computers and Operations Research, 2018, 91, 160-177.	2.4	18
13	Relevance aggregation for neural networks interpretability and knowledge discovery on tabular data. Information Sciences, 2021, 559, 111-129.	4.0	18
14	A multi-objective gene clustering algorithm guided by apriori biological knowledge with intensification and diversification strategies. BioData Mining, 2018, 11, 16.	2.2	17
15	Evaluation of drug repositioning by molecular docking of pharmaceutical resources available in the Brazilian healthcare system against SARS-CoV-2. Informatics in Medicine Unlocked, 2021, 23, 100539.	1.9	15
16	Multi-Approach Bioinformatics Analysis of Curated Omics Data Provides a Gene Expression Panorama for Multiple Cancer Types. Frontiers in Genetics, 2020, 11, 586602.	1.1	14
17	A3N: An artificial neural network n-gram-based method to approximate 3-D polypeptides structure prediction. Expert Systems With Applications, 2010, 37, 7497-7508.	4.4	13
18	A multi-population memetic algorithm for the 3-D protein structure prediction problem. Swarm and Evolutionary Computation, 2020, 55, 100677.	4.5	13

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19	Conformational changes in 2-trans-enoyl-ACP (CoA) reductase (InhA) from M. tuberculosis induced by an inorganic complex: a molecular dynamics simulation study. Journal of Molecular Modeling, 2012, 18, 1779-1790.	0.8	12
20	Clustering Nodes in Large-Scale Biological Networks Using External Memory Algorithms. Lecture Notes in Computer Science, 2011, , 375-386.	1.0	12
21	CReF. , 2008, , .		11
22	Mining the Protein Data Bank with CReF to predict approximate 3-D structures of polypeptides. International Journal of Data Mining and Bioinformatics, 2010, 4, 281.	0.1	10
23	A biased random key genetic algorithm for the proteinâ€“ligand docking problem. Soft Computing, 2019, 23, 4155-4176.	2.1	10
24	Comparison of machine learning techniques to handle imbalanced COVID-19 CBC datasets. PeerJ Computer Science, 2021, 7, e670.	2.7	10
25	A Study on Shape-Dependent Settling of Single Particles with Equal Volume Using Surface Resolved Simulations. Computation, 2021, 9, 40.	1.0	9
26	A Hybrid Method for the Protein Structure Prediction Problem. Lecture Notes in Computer Science, 2008, , 47-56.	1.0	9
27	A hybrid genetic algorithm for the 3-D protein structure prediction problem using a path-relinking strategy. , 2011, , .		8
28	SADE-SPL: A Self-Adapting Differential Evolution algorithm with a loop Structure Pattern Library for the PSP problem. , 2017, , .		7
29	Everyone Is a Protagonist: Residue Conformational Preferences in High-Resolution Protein Structures. Journal of Computational Biology, 2018, 25, 451-465.	0.8	7
30	Perspectives and applications of machine learning for evolutionary developmental biology. Molecular Omics, 2018, 14, 289-306.	1.4	7
31	A Knowledge Based Self-Adaptive Differential Evolution Algorithm for Protein Structure Prediction. Lecture Notes in Computer Science, 2019, , 87-100.	1.0	7
32	Development of GROMOS-Compatible Parameter Set for Simulations of Chalcones and Flavonoids. Journal of Physical Chemistry B, 2019, 123, 994-1008.	1.2	7
33	Benchmarking and Testing Machine Learning Approaches with BARRA:CuRDa, a Curated RNA-Seq Database for Cancer Research. Journal of Computational Biology, 2021, 28, 931-944.	0.8	7
34	A knowledge-based genetic algorithm to predict three-dimensional structures of polypeptides. , 2013, , .		5
35	NEAT-FLEX: Predicting the conformational flexibility of amino acids using neuroevolution of augmenting topologies. Journal of Bioinformatics and Computational Biology, 2017, 15, 1750009.	0.3	5
36	Understanding the Relationship Between Decision and Objective Space in the Multi-Objective Phylogenetic Inference Problem. , 2018, , .		4

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37	A Multi-objective Swarm-Based Algorithm for the Prediction of Protein Structures. Lecture Notes in Computer Science, 2019, , 101-115.	1.0	4
38	Feature selection reveal peripheral blood parameter's changes between COVID-19 infections patients from Brazil and Ecuador. Infection, Genetics and Evolution, 2022, 98, 105228.	1.0	4
39	A cluster-DEE-based strategy to empower protein design. Expert Systems With Applications, 2013, 40, 5210-5218.	4.4	3
40	MOIRAE: A computational strategy to extract and represent structural information from experimental protein templates. Soft Computing, 2014, 18, 773-795.	2.1	3
41	D-BRKGA: A Distributed Biased Random-Key Genetic Algorithm. , 2017, , .		3
42	Evaluating the use of local search strategies for a memetic algorithm for the protein-ligand docking problem. , 2017, , .		3
43	Performance Comparison of Multi-Objective Local Search Strategies to Infer Phylogenetic Trees. , 2018, , .		3
44	A Self-adaptive Local Search Coordination in Multimeme Memetic Algorithm for Molecular Docking. Lecture Notes in Computer Science, 2019, , 145-159.	1.0	3
45	Solving fluid flow domain identification problems with adjoint lattice Boltzmann methods. Computers and Mathematics With Applications, 2020, 79, 17-33.	1.4	3
46	ConfID: an analytical method for conformational characterization of small molecules using molecular dynamics trajectories. Bioinformatics, 2020, 36, 3576-3577.	1.8	3
47	Exploring the high selectivity of 3-D protein structures using distributed memetic algorithms. Journal of Computational Science, 2020, 41, 101087.	1.5	3
48	Multi-Agent Systems in Three-Dimensional Protein Structure Prediction. Advances in Computational Intelligence and Robotics Book Series, 2017, , 241-278.	0.4	3
49	Parallel Verified Linear System Solver for Uncertain Input Data. , 2008, , .		2
50	Hardware implementation of GMDH-type artificial neural networks and its use to predict approximate three-dimensional structures of proteins. , 2012, , .		2
51	A molecular dynamics and knowledge-based computational strategy to predict native-like structures of polypeptides. Expert Systems With Applications, 2013, 40, 698-706.	4.4	2
52	A Memetic Algorithm for Protein Structure Prediction based on Conformational Preferences of Aminoacid Residues. , 2015, , .		2
53	An evolutionary multi-agent algorithm to explore the high degree of selectivity in three-dimensional protein structures. , 2017, , .		2
54	Microarray Classification and Gene Selection with FS-NEAT. , 2018, , .		2

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55	A Knowledge-Based Artificial Bee Colony Algorithm for the 3-D Protein Structure Prediction Problem. , 2018, , .		2
56	A Genetic Algorithm Based on Restricted Tournament Selection for the 3D-PSP Problem. , 2018, , .		2
57	Multi-Objective Differential Evolution Algorithms for the Protein Structure Prediction Problem. , 2020, , .		2
58	Modifying the catalytic preference of alphaâ€amylase toward nâ€alkanes for bioremediation purposes using in silico strategies. Journal of Computational Chemistry, 2021, 42, 1540-1551.	1.5	2
59	An interval-based algorithm to represent conformational states of experimentally determined polypeptide templates and fast prediction of approximated 3D protein structures. International Journal of Bioinformatics Research and Applications, 2013, 9, 462.	0.1	1
60	Evaluation of a combined energy fitness function for a distributed memetic algorithm to tackle the 3D protein structure prediction problem. , 2016, , .		1
61	Improving protein tertiary structure prediction with conformational propensities of amino acid residues. , 2016, , .		1
62	Using local search strategies to improve the performance of NSGA-II for the Multi-Criteria Minimum Spanning Tree problem. , 2017, , .		1
63	A Biased Random Key Genetic Algorithm with Local Search Chains for Molecular Docking. Lecture Notes in Computer Science, 2019, , 360-376.	1.0	1
64	Rosetta Ligand-Protein Docking with Self-Adaptive Differential Evolution. , 2019, , .		1
65	Differential Evolution Multi-Objective for Tertiary Protein Structure Prediction. Lecture Notes in Computer Science, 2020, , 165-180.	1.0	1
66	A dynamic evolutionary multi-agent system to predict the 3D structure of proteins. , 2020, , .		1
67	Predicting protein structural features with NeuroEvolution of Augmenting Topologies. , 2016, , .		0
68	Determining the Conformational Flexibility of Disaccharides with an Adaptive Differential Evolution Approach. , 2020, , .		0
69	Evaluating the Success-History Based Adaptive Differential Evolution in the Protein Structure Prediction Problem. Lecture Notes in Computer Science, 2021, , 194-209.	1.0	0
70	Gene Expression Variation Analysis (GEVA): A new R package to evaluate variations in differential expression in multiple biological conditions. Journal of Biomedical Informatics, 2022, 129, 104053.	2.5	0