Cristian Robert Munteanu

List of Publications by Year
in descending order

113	2,535	186209	254106
papers	citations	28 h-index	43 g-index

121	121	121	2405
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Automatic feature extraction using genetic programming: An application to epileptic EEG classification. Expert Systems With Applications, 2011, 38, 10425-10436.	4.4	222
2	The eNanoMapper database for nanomaterial safety information. Beilstein Journal of Nanotechnology, 2015, 6, 1609-1634.	1.5	92
3	MIND-BEST: Web Server for Drugs and Target Discovery; Design, Synthesis, and Assay of MAO-B Inhibitors and Theoreticalâ^'Experimental Study of G3PDH Protein fromTrichomonas gallinae. Journal of Proteome Research, 2011, 10, 1698-1718.	1.8	75
4	Multi-target QPDR classification model for human breast and colon cancer-related proteins using star graph topological indices. Journal of Theoretical Biology, 2009, 257, 303-311.	0.8	72
5	Automatic assessment of Alzheimerâ€™s disease diagnosis based on deep learning techniques. Computers in Biology and Medicine, 2020, 120, 103764.	3.9	71
6	Enzymes/non-enzymes classification model complexity based on composition, sequence, 3D and topological indices. Journal of Theoretical Biology, 2008, 254, 476-482.	0.8	63
7	eNanoMapper: harnessing ontologies to enable data integration for nanomaterial risk assessment. Journal of Biomedical Semantics, 2015, 6, 10.	0.9	63
8	Trypano-PPI: A Web Server for Prediction of Unique Targets in Trypanosome Proteome by using Electrostatic Parameters of Proteinâ^'protein Interactions. Journal of Proteome Research, 2010, 9, 1182-1190.	1.8	61
9	Artificial Intelligence Techniques for Colorectal Cancer Drug Metabolism: Ontologies and Complex Networks. Current Drug Metabolism, 2010, 11, 347-368.	0.7	59
10	ANN Multiscale Model of Anti-HIV Drugs Activity vs AIDS Prevalence in the US at County Level Based on Information Indices of Molecular Graphs and Social Networks. Journal of Chemical Information and Modeling, 2014, 54, 744-755.	2.5	58
11	3D entropy and moments prediction of enzyme classes and experimental-theoretic study of peptide fingerprints in Leishmania parasites. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2009, 1794, 1784-1794.	1.1	52
12	Drug Discovery and Design for Complex Diseases through QSAR Computational Methods. Current Pharmaceutical Design, 2010, 16, 2640-2655.	0.9	50
13	Random Forest classification based on star graph topological indices for antioxidant proteins. Journal of Theoretical Biology, 2013, 317, 331-337.	0.8	45
14	NL MIND-BEST: A web server for ligands and proteins discoveryâ€"Theoretic-experimental study of proteins of Giardia lamblia and new compounds active against Plasmodium falciparum. Journal of Theoretical Biology, 2011, 276, 229-249.	0.8	43
15	RRegrs: an R package for computer-aided model selection with multiple regression models. Journal of Cheminformatics, 2015, 7, 46.	2.8	43
16	Complex Network Spectral Moments for ATCUN Motif DNA Cleavage: First Predictive Study on Proteins of Human Pathogen Parasites. Journal of Proteome Research, 2009, 8, 5219-5228.	1.8	42
17	Drugs Repurposing Using QSAR, Docking and Molecular Dynamics for Possible Inhibitors of the SARS-CoV-2 Mpro Protease. Molecules, 2020, 25, 5172.	1.7	42
18	Ontologies of Drug Discovery and Design for Neurology, Cardiology and Oncology. Current Pharmaceutical Design, 2010, 16, 2724-2736.	0.9	42

#	Article	IF	Citations
19	Generalized lattice graphs for 2D-visualization of biological information. Journal of Theoretical Biology, 2009, 261, 136-147.	0.8	41
20	Natural/random protein classification models based on star network topological indices. Journal of Theoretical Biology, 2008, 254, 775-783.	0.8	39
21	New Markovâ€“Shannon Entropy models to assess connectivity quality in complex networks: From molecular to cellular pathway, Parasiteâ€“Host, Neural, Industry, and Legalâ€“Social networks. Journal of Theoretical Biology, 2012, 293, 174-188.	0.8	39
22	Perturbation Theory/Machine Learning Model of ChEMBL Data for Dopamine Targets: Docking, Synthesis, and Assay of New <scp>l</scp>-Prolyl-<scp>l</scp>-leucyl-glycinamide Peptidomimetics. ACS Chemical Neuroscience, 2018, 9, 2572-2587.	1.7	38
23	Alignment-free prediction of mycobacterial DNA promoters based on pseudo-folding lattice network or star-graph topological indices. Journal of Theoretical Biology, 2009, 256, 458-466.	0.8	36
24	OncoOmics approaches to reveal essential genes in breast cancer: a panoramic view from pathogenesis to precision medicine. Scientific Reports, 2020, 10, 5285.	1.6	36
25	From QSAR models of Drugs to Complex Networks: State-of-Art Review and Introduction of New Markov-Spectral Moments Indices. Current Topics in Medicinal Chemistry, 2012, 12, 927-960.	1.0	35
26	Solvent Accessible Surface Area-Based Hot-Spot Detection Methods for Proteinâ€“Protein and Proteinâ€“Nucleic Acid Interfaces. Journal of Chemical Information and Modeling, 2015, 55, 1077-1086.	2.5	33
27	Classification of mild cognitive impairment and Alzheimerâ€™s Disease with machine-learning techniques using 1H Magnetic Resonance Spectroscopy data. Expert Systems With Applications, 2015, 42, 6205-6214.	4.4	32
28	Experimentalâ€“Computational Study of Carbon Nanotube Effects on Mitochondrial Respiration: In Silico Nano-QSPR Machine Learning Models Based on New Raman Spectra Transform with Markovâ€“Shannon Entropy Invariants. Journal of Chemical Information and Modeling, 2017, 57, 1029-1044.	2.5	32
29	Gene prioritization, communality analysis, networking and metabolic integrated pathway to better understand breast cancer pathogenesis. Scientific Reports, 2018, 8, 16679.	1.6	29
30	PTML Model of Enzyme Subclasses for Mining the Proteome of Biofuel Producing Microorganisms. Journal of Proteome Research, 2019, 18, 2735-2746.	1.8	29
31	Prediction of breast cancer proteins involved in immunotherapy, metastasis, and RNA-binding using molecular descriptors and artificial neural networks. Scientific Reports, 2020, 10, 8515.	1.6	29
32	Accurate intermolecular ground-state potential-energy surfaces of the HCCHâ€“He, Ne, and Ar van der Waals complexes. Journal of Chemical Physics, 2005, 123, 014309.	1.2	28
33	Evolutionary Computation and QSAR Research. Current Computer-Aided Drug Design, 2013, 9, 206-225.	0.8	28
34	Stochastic molecular descriptors for polymers. 4. Study of complex mixtures with topological indices of mass spectra spiral and star networks: The blood proteome case. Polymer, 2008, 49, 5575-5587.	1.8	27
35	NaÃ¯ve Bayes QSDR classification based on spiral-graph Shannon entropies for protein biomarkers in human colon cancer. Molecular BioSystems, 2012, 8, 1716.	2.9	26
36	Improving Ontology Alignment through Genetic Algorithms. , 2010, , 240-259.		26

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37	Classification of signaling proteins based on molecular star graph descriptors using Machine Learning models. Journal of Theoretical Biology, 2015, 384, 50-58.	0.8	25
38	A methodology for the design of experiments in computational intelligence with multiple regression models. PeerJ, 2016, 4, e2721.	0.9	25
39	MIANN Models in Medicinal, Physical and Organic Chemistry. Current Topics in Medicinal Chemistry, 2013, 13, 619-641.	1.0	25
40	Star Graphs of Protein Sequences and Proteome Mass Spectra in Cancer Prediction. Current Proteomics, 2009, 6, 275-288.	0.1	24
41	QSAR and complex network study of the chiral HMGR inhibitor structural diversity. Bioorganic and Medicinal Chemistry, 2009, 17, 165-175.	1.4	24
42	Plasmod-PPI: A web-server predicting complex biopolymer targets in plasmodium with entropy measures of proteinâ€“protein interactions. Polymer, 2010, 51, 264-273.	1.8	24
43	Modeling Complex Metabolic Reactions, Ecological Systems, and Financial and Legal Networks with MIANN Models Based on Markov-Wiener Node Descriptors. Journal of Chemical Information and Modeling, 2014, 54, 16-29.	2.5	22
44	Experimental study and Random Forest prediction model of microbiome cell surface hydrophobicity. Expert Systems With Applications, 2017, 72, 306-316.	4.4	22
45	Decrypting Strong and Weak Single-Walled Carbon Nanotubes Interactions with Mitochondrial Voltage-Dependent Anion Channels Using Molecular Docking and Perturbation Theory. Scientific Reports, 2017, 7, 13271.	1.6	22
46	Prediction of Antimalarial Drug-Decorated Nanoparticle Delivery Systems with Random Forest Models. Biology, 2020, 9, 198.	1.3	22
47	The chlorobenzene-argon ground state intermolecular potential energy surface. Journal of Chemical Physics, 2004, 121, 1390-1396.	1.2	21
48	MISS-Prot: web server for self/non-self discrimination of protein residue networks in parasites; theory and experiments in Fasciola peptides and Anisakis allergens. Molecular BioSystems, 2011, 7, 1938.	2.9	20
49	Improving enzyme regulatory protein classification by means of SVM-RFE feature selection. Molecular BioSystems, 2014, 10, 1063.	2.9	20
50	Molecular docking and machine learning analysis of Abemaciclib in colon cancer. BMC Molecular and Cell Biology, 2020, 21, 52.	1.0	20
51	LIBP-Pred: web server for lipid binding proteins using structural network parameters; PDB mining of human cancer biomarkers and drug targets in parasites and bacteria. Molecular BioSystems, 2012, 8, 851.	2.9	19
52	Quantitative Proteomeâ€“Property Relationships (QPPRs). Part 1: Finding biomarkers of organic drugs with mean Markov connectivity indices of spiral networks of blood mass spectra. Bioorganic and Medicinal Chemistry, 2008, 16, 9684-9693.	1.4	18
53	Machine Learning Techniques for Single Nucleotide Polymorphismâ€”Disease Classification Models in Schizophrenia. Molecules, 2010, 15, 4875-4889.	1.7	17
54	Definition of Markov-Harary Invariants and Review of Classic Topological Indices and Databases in Biology, Parasitology, Technology,and Social-Legal Networks. Current Bioinformatics, 2011, 6, 94-121.	0.7	17

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55	S2SNet: A Tool for Transforming Characters and Numeric Sequences into Star Network Topological Indices in Chemoinformatics, Bioinformatics, Biomedical, and Social-Legal Sciences. Current Bioinformatics, 2013, 8, 429-437.	0.7	17
56	In silico Analyses of Immune System Protein Interactome Network, Single-Cell RNA Sequencing of Human Tissues, and Artificial Neural Networks Reveal Potential Therapeutic Targets for Drug Repurposing Against COVID-19. Frontiers in Pharmacology, 2021, 12, 598925.	1.6	16
57	Kernel-Based Feature Selection Techniques for Transport Proteins Based on Star Graph Topological Indices. Current Topics in Medicinal Chemistry, 2013, 13, 1681-1691.	1.0	16
58	Accurate intermolecular ground state potential of the Ar-N2 van der Waals complex. Journal of Chemical Physics, 2004, 121, 10419-10425.	1.2	15
59	Nanoinformatics: developing new computing applications for nanomedicine. Computing (Vienna/New) Tj ETQq1 1 0.784314 rgBT /Ov	3.2	15
60	Accurate intermolecular ground state potential of the Neâ€“N2 van der Waals complex. Journal of Chemical Physics, 2004, 120, 9104-9112.	1.2	14
61	Carbon Nanotubesâ€™ Effect on Mitochondrial Oxygen Flux Dynamics: Polarography Experimental Study and Machine Learning Models using Star Graph Trace Invariants of Raman Spectra. Nanomaterials, 2017, 7, 386.	1.9	14
62	Automatic seizure detection based on star graph topological indices. Journal of Neuroscience Methods, 2012, 209, 410-419.	1.3	13
63	Markov mean properties for cell death-related protein classification. Journal of Theoretical Biology, 2014, 349, 12-21.	0.8	13
64	Gene Prioritization through Consensus Strategy, Enrichment Methodologies Analysis, and Networking for Osteosarcoma Pathogenesis. International Journal of Molecular Sciences, 2020, 21, 1053.	1.8	13
65	The RÃ¼ckerâ€“Markov invariants of complex Bio-Systems: Applications in Parasitology and Neuroinformatics. BioSystems, 2013, 111, 199-207.	0.9	12
66	General Machine Learning Model, Review, and Experimental-Theoretic Study of Magnolol Activity in Enterotoxigenic Induced Oxidative Stress. Current Topics in Medicinal Chemistry, 2017, 17, 2977-2988.	1.0	11
67	From Chemical Graphs in Computer-Aided Drug Design to General Markov-Galvez Indices of Drug-Target, Proteome, Drug-Parasitic Disease, Technological, and Social-Legal Networks. Current Computer-Aided Drug Design, 2011, 7, 315-337.	0.8	10
68	LECTINPred: web Server that Uses Complex Networks of Protein Structure for Prediction of Lectins with Potential Use as Cancer Biomarkers or in Parasite Vaccine Design. Molecular Informatics, 2014, 33, 276-285.	1.4	10
69	Amino acid pair- and triplet-wise groupings in the interior of Î±-helical segments in proteins. Journal of Theoretical Biology, 2011, 271, 136-144.	0.8	9
70	Gastrointestinal Spatiotemporal mRNA Expression of Ghrelin vs Growth Hormone Receptor and New Growth Yield Machine Learning Model Based on Perturbation Theory. Scientific Reports, 2016, 6, 30174.	1.6	9
71	Net-Net Auto Machine Learning (AutoML) Prediction of Complex Ecosystems. Scientific Reports, 2018, 8, 12340.	1.6	9
72	Perturbation Theory Machine Learning Modeling of Immunotoxicity for Drugs Targeting Inflammatory Cytokines and Study of the Antimicrobial G1 Using Cytometric Bead Arrays. Chemical Research in Toxicology, 2019, 32, 1811-1823.	1.7	9

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73	Biomedical Data Integration in Computational Drug Design and Bioinformatics. Current Computer-Aided Drug Design, 2013, 9, 108-117.	0.8	8
74	PTML Multi-Label Algorithms: Models, Software, and Applications. Current Topics in Medicinal Chemistry, 2020, 20, 2326-2337.	1.0	8
75	Experimental and computational studies of fatty acid distribution networks. Molecular BioSystems, 2015, 11, 2964-2977.	2.9	6
76	A Multi-Objective Approach for Anti-Osteosarcoma Cancer Agents Discovery through Drug Repurposing. Pharmaceuticals, 2020, 13, 409.	1.7	6
77	Data Mining in Complex Diseases Using Evolutionary Computation. Lecture Notes in Computer Science, 2009, , 917-924.	1.0	6
78	The first eNanoMapper prototype: A substance database to support safe-by-design. , 2014, , .		5
79	Prediction of Nucleotide Binding Peptides Using Star Graph Topological Indices. Molecular Informatics, 2015, 34, 736-741.	1.4	5
80	SNOMED2HL7: A tool to normalize and bind SNOMED CT concepts to the HL7 Reference Information Model. Computer Methods and Programs in Biomedicine, 2017, 149, 1-9.	2.6	5
81	Improvement of Epitope Prediction Using Peptide Sequence Descriptors and Machine Learning. International Journal of Molecular Sciences, 2019, 20, 4362.	1.8	5
82	Molecular docking, SAR analysis and biophysical approaches in the study of the antibacterial activity of ceramides isolated from Cissus incisa. Bioorganic Chemistry, 2021, 109, 104745.	2.0	5
83	Bio-AIMS Collection of Chemoinformatics Web Tools based on Molecular Graph Information and Artificial Intelligence Models. Combinatorial Chemistry and High Throughput Screening, 2015, 18, 735-750.	0.6	5
84	Markov-Randic Indices for QSPR Re-Evaluation of Metabolic, Parasite- Host, Fasciolosis Spreading, Brain Cortex and Legal-Social Complex Networks. Current Bioinformatics, 2013, 8, 401-415.	0.7	5
85	Prediction of Anti-Glioblastoma Drug-Decorated Nanoparticle Delivery Systems Using Molecular Descriptors and Machine Learning. International Journal of Molecular Sciences, 2021, 22, 11519.	1.8	5
86	Prot-2S: a new python web tool for protein secondary structure studies. International Journal of Bioinformatics Research and Applications, 2009, 5, 402.	0.1	4
87	Discovery of novel immunopharmacological ligands targeting the IL-17 inflammatory pathway. International Immunopharmacology, 2020, 89, 107026.	1.7	4
88	Perturbation-Theory Machine Learning (PTML) Multilabel Model of the ChEMBL Dataset of Preclinical Assays for Antisarcoma Compounds. ACS Omega, 2020, 5, 27211-27220.	1.6	4
89	Graph-Based Processing of Macromolecular Information. Current Bioinformatics, 2015, 10, 606-631.	0.7	4
90	MCDCalc: Markov Chain Molecular Descriptors Calculator for Medicinal Chemistry. Current Topics in Medicinal Chemistry, 2020, 20, 305-317.	1.0	4

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91	Experimental Study and ANN Dual-Time Scale Perturbation Model of Electrokinetic Properties of Microbiota. Frontiers in Microbiology, 2017, 8, 1216.	1.5	3
92	Applied Computational Techniques on Schizophrenia Using Genetic Mutations. Current Topics in Medicinal Chemistry, 2013, 13, 675-684.	1.0	3
93	Biomedical Data Integration in Computational Drug Design and Bioinformatics. Current Computer-Aided Drug Design, 2013, 9, 108-117.	0.8	2
94	Net-Net AutoML Selection of Artificial Neural Network Topology for Brain Connectome Prediction. Applied Sciences (Switzerland), 2020, 10, 1308.	1.3	2
95	A Hybrid Evolutionary System for Automated Artificial Neural Networks Generation and Simplification in Biomedical Applications. Current Bioinformatics, 2015, 10, 672-691.	0.7	2
96	The Ability of MEAs Containing Cultured Neuroglial Networks to Process Information. Current Bioinformatics, 2011, 6, 199-214.	0.7	2
97	Heâ€“, Neâ€“, and Arâ€“Phosgene Intermolecular Potential Energy Surfaces. Journal of Physical Chemistry A, 2013, 117, 3835-3843.	1.1	1
98	Regulatory affairs issues and legal ontologies in drug development. Frontiers in Bioscience - Elite, 2013, E5, 446-460.	0.9	1
99	Identification of coenzyme-binding proteins with machine learning algorithms. Computational Biology and Chemistry, 2019, 79, 185-192.	1.1	1
100	Protein Graphs in Cancer Prediction. , 2010, , 125-140.		1
101	SNP-Schizo: A Web Tool for Schizophrenia SNP Sequence Classification. Lecture Notes in Computer Science, 2011, , 252-259.	1.0	1
102	Editorial (Hot Topic: Artificial Intelligence Techniques in Medicinal Chemistry). Current Topics in Medicinal Chemistry, 2013, 13, 525-525.	1.0	0
103	System for Automatic Assessment of Alzheimerâ€™s Disease Diagnosis Based on Deep Learning Techniques. Proceedings (mdpi), 2019, 21, 28.	0.2	0
104	Translational Bioinformatics: Informatics, Medicine, and -Omics. , 2019, , 507-514.		0
105	Design and Implementation of a Physical Bitcoin Coin. Proceedings (mdpi), 2020, 54, 21.	0.2	0
106	Web Server and R Library for the Calculation of Markov Chains Molecular Descriptors. Proceedings (mdpi), 2020, 54, 28.	0.2	0
107	Editorial [Hot Topic: Convergence of Bioinformatics with Nanotechnology and Artificial Intelligence Technologies (Guest Editor: Cristian Robert Munteanu)]. Current Bioinformatics, 2011, 6, 144-144.	0.7	0
108	Editorial (Thematic Issue: Soft Computing, Content-Based Retrieval and Reconstruction in Medical) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.4	0

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109	Bio-AIMS Chemoinformatics Web tools for proteins. , 0, , .		0
110	Evaluation as a Continuous Improvement Process in the Learning of Programming Languages. Advances in Intelligent Systems and Computing, 2019, , 521-529.	0.5	0
111	Machine Learning in Biomedical Informatics. , 2019, , 389-399.		0
112	Applying Artificial Intelligence for Operating System Fingerprinting. Engineering Proceedings, 2021, 7, .	0.4	0
113	Bioinformatic tools for research in CRC. , 2022, , 231-247.		0