Cristian Robert Munteanu

List of Publications by Citations

111 papers	1,819 citations	24 h-index	37 g-index
121 ext. papers	2,073 ext. citations	3.6 avg, IF	4.62 L-index

#	Paper	IF	Citations
111	Automatic feature extraction using genetic programming: An application to epileptic EEG classification. *Expert Systems With Applications*, **2011**, 38, 10425-10436	7.8	183
110	The eNanoMapper database for nanomaterial safety information. *Beilstein Journal of Nanotechnology*, **2015**, 6, 1609-34	3	64
109	MIND-BEST: Web server for drugs and target discovery; design, synthesis, and assay of MAO-B inhibitors and theoretical-experimental study of G3PDH protein from Trichomonas gallinae. *Journal of Proteome Research*, **2011**, 10, 1698-718	5.6	60
108	Enzymes/non-enzymes classification model complexity based on composition, sequence, 3D and topological indices. *Journal of Theoretical Biology*, **2008**, 254, 476-82	2.3	57
107	Multi-target QPDR classification model for human breast and colon cancer-related proteins using star graph topological indices. *Journal of Theoretical Biology*, **2009**, 257, 303-11	2.3	56
106	eNanoMapper: harnessing ontologies to enable data integration for nanomaterial risk assessment. *Journal of Biomedical Semantics*, **2015**, 6, 10	2.2	48
105	Trypano-PPI: a web server for prediction of unique targets in trypanosome proteome by using electrostatic parameters of protein-protein interactions. *Journal of Proteome Research*, **2010**, 9, 1182-90	5.6	44
104	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, 744-55	6.1	42
103	Artificial intelligence techniques for colorectal cancer drug metabolism: ontology and complex network. *Current Drug Metabolism*, **2010**, 11, 347-68	3.5	42
102	Drug discovery and design for complex diseases through QSAR computational methods. *Current Pharmaceutical Design*, **2010**, 16, 2640-55	3.3	37
101	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, 1784-94	4	37
100	Random Forest classification based on star graph topological indices for antioxidant proteins. *Journal of Theoretical Biology*, **2013**, 317, 331-7	2.3	36
99	Complex network spectral moments for ATCUN motif DNA cleavage: first predictive study on proteins of human pathogen parasites. *Journal of Proteome Research*, **2009**, 8, 5219-28	5.6	36
98	Ontologies of drug discovery and design for neurology, cardiology and oncology. *Current Pharmaceutical Design*, **2010**, 16, 2724-36	3.3	31
97	Perturbation Theory/Machine Learning Model of ChEMBL Data for Dopamine Targets: Docking, Synthesis, and Assay of New l-Prolyl-l-leucyl-glycinamide Peptidomimetics. *ACS Chemical Neuroscience*, **2018**, 9, 2572-2587	5.7	31
96	New Markov-Shannon Entropy models to assess connectivity quality in complex networks: from molecular to cellular pathway, Parasite-Host, Neural, Industry, and Legal-Social networks. *Journal of Theoretical Biology*, **2012**, 293, 174-88	2.3	30
95	RRegrs: an R package for computer-aided model selection with multiple regression models. *Journal of Cheminformatics*, **2015**, 7, 46	8.6	30

94	Alignment-free prediction of mycobacterial DNA promoters based on pseudo-folding lattice network or star-graph topological indices. *Journal of Theoretical Biology*, **2009**, 256, 458-66	2.3	30
93	Generalized lattice graphs for 2D-visualization of biological information. *Journal of Theoretical Biology*, **2009**, 261, 136-47	2.3	30
92	Natural/random protein classification models based on star network topological indices. *Journal of Theoretical Biology*, **2008**, 254, 775-83	2.3	30
91	NL MIND-BEST: a web server for ligands and proteins discovery--theoretic-experimental study of proteins of Giardia lamblia and new compounds active against Plasmodium falciparum. *Journal of Theoretical Biology*, **2011**, 276, 229-49	2.3	29
90	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, 927-60	3	27
89	Experimental-Computational Study of Carbon Nanotube Effects on Mitochondrial Respiration: In Silico Nano-QSPR Machine Learning Models Based on New Raman Spectra Transform with Markov-Shannon Entropy Invariants. *Journal of Chemical Information and Modeling*, **2017**, 57, 1029-1044	6.1	26
88	Accurate intermolecular ground-state potential-energy surfaces of the HCCH-He, Ne, and Ar van der Waals complexes. *Journal of Chemical Physics*, **2005**, 123, 014309	3.9	26
87	Classification of mild cognitive impairment and Alzheimer Disease with machine-learning techniques using 1H Magnetic Resonance Spectroscopy data. *Expert Systems With Applications*, **2015**, 42, 6205-6214	7.8	24
86	Drugs Repurposing Using QSAR, Docking and Molecular Dynamics for Possible Inhibitors of the SARS-CoV-2 M Protease. *Molecules*, **2020**, 25,	4.8	23
85	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	3.9	22
84	Evolutionary computation and QSAR research. *Current Computer-Aided Drug Design*, **2013**, 9, 206-25	1.4	22
83	Solvent accessible surface area-based hot-spot detection methods for protein-protein and protein-nucleic acid interfaces. *Journal of Chemical Information and Modeling*, **2015**, 55, 1077-86	6.1	21
82	MIANN models in medicinal, physical and organic chemistry. *Current Topics in Medicinal Chemistry*, **2013**, 13, 619-41	3	21
81	Naïve Bayes QSDR classification based on spiral-graph Shannon entropies for protein biomarkers in human colon cancer. *Molecular BioSystems*, **2012**, 8, 1716-22		20
80	The chlorobenzene-argon ground state intermolecular potential energy surface. *Journal of Chemical Physics*, **2004**, 121, 1390-6	3.9	20
79	Improving Ontology Alignment through Genetic Algorithms **2010**, 240-259		20
78	A methodology for the design of experiments in computational intelligence with multiple regression models. *PeerJ*, **2016**, 4, e2721	3.1	20
77	Automatic assessment of Alzheimer's disease diagnosis based on deep learning techniques. *Computers in Biology and Medicine*, **2020**, 120, 103764	7	20

76	Classification of signaling proteins based on molecular star graph descriptors using Machine Learning models. *Journal of Theoretical Biology*, **2015**, 384, 50-8	2.3	19
75	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	6.1	19
74	Improving enzyme regulatory protein classification by means of SVM-RFE feature selection. *Molecular BioSystems*, **2014**, 10, 1063-71		19
73	QSAR and complex network study of the chiral HMGR inhibitor structural diversity. *Bioorganic and Medicinal Chemistry*, **2009**, 17, 165-75	3.4	19
72	Gene prioritization, communality analysis, networking and metabolic integrated pathway to better understand breast cancer pathogenesis. *Scientific Reports*, **2018**, 8, 16679	4.9	19
71	PTML Model of Enzyme Subclasses for Mining the Proteome of Biofuel Producing Microorganisms. *Journal of Proteome Research*, **2019**, 18, 2735-2746	5.6	18
70	Plasmod-PPI: A web-server predicting complex biopolymer targets in plasmodium with entropy measures of protein□protein interactions. *Polymer*, **2010**, 51, 264-273	3.9	18
69	OncoOmics approaches to reveal essential genes in breast cancer: a panoramic view from pathogenesis to precision medicine. *Scientific Reports*, **2020**, 10, 5285	4.9	17
68	Experimental study and Random Forest prediction model of microbiome cell surface hydrophobicity. *Expert Systems With Applications*, **2017**, 72, 306-316	7.8	17
67	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	4.9	15
66	Star Graphs of Protein Sequences and Proteome Mass Spectra in Cancer Prediction. *Current Proteomics*, **2009**, 6, 275-288	0.7	15
65	Accurate intermolecular ground state potential of the Ar-N2 van der Waals complex. *Journal of Chemical Physics*, **2004**, 121, 10419-25	3.9	15
64	Accurate intermolecular ground state potential of the Ne-N2 van der Waals complex. *Journal of Chemical Physics*, **2004**, 120, 9104-12	3.9	14
63	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, 851-62		13
62	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	4.7	13
61	Quantitative Proteome-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, 9684-93	3.4	13
60	Kernel-based feature selection techniques for transport proteins based on star graph topological indices. *Current Topics in Medicinal Chemistry*, **2013**, 13, 1681-91	3	13
59	Nanoinformatics: developing new computing applications for nanomedicine. *Computing (Vienna/New York)*, **2012**, 94, 521-539	2.2	12

58	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	4.7	12
57	Prediction of breast cancer proteins involved in immunotherapy, metastasis, and RNA-binding using molecular descriptors and artificial neural networks. *Scientific Reports*, **2020**, 10, 8515	4.9	12
56	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, 1938-55		11
55	Machine learning techniques for single nucleotide polymorphism--disease classification models in schizophrenia. *Molecules*, **2010**, 15, 4875-89	4.8	11
54	Carbon Nanotubes' Effect on Mitochondrial Oxygen Flux Dynamics: Polarography Experimental Study and Machine Learning Models using Star Graph Trace Invariants of Raman Spectra. *Nanomaterials*, **2017**, 7,	5.4	10
53	Automatic seizure detection based on star graph topological indices. *Journal of Neuroscience Methods*, **2012**, 209, 410-9	3	10
52	Prediction of Antimalarial Drug-Decorated Nanoparticle Delivery Systems with Random Forest Models. *Biology*, **2020**, 9,	4.9	10
51	Markov mean properties for cell death-related protein classification. *Journal of Theoretical Biology*, **2014**, 349, 12-21	2.3	9
50	Molecular docking and machine learning analysis of Abemaciclib in colon cancer. *BMC Molecular and Cell Biology*, **2020**, 21, 52	2.7	7
49	Net-Net Auto Machine Learning (AutoML) Prediction of Complex Ecosystems. *Scientific Reports*, **2018**, 8, 12340	4.9	7
48	The R□ker-Markov invariants of complex Bio-Systems: applications in Parasitology and Neuroinformatics. *BioSystems*, **2013**, 111, 199-207	1.9	7
47	Biomedical Data Integration in Computational Drug Design and Bioinformatics. *Current Computer-Aided Drug Design*, **2013**, 9, 108-117	1.4	7
46	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, 315-37	1.4	7
45	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	4.9	7
44	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	5.6	7
43	Gene Prioritization through Consensus Strategy, Enrichment Methodologies Analysis, and Networking for Osteosarcoma Pathogenesis. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	6
42	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, 276-85	3.8	6
41	Amino acid pair- and triplet-wise groupings in the interior of □helical segments in proteins. *Journal of Theoretical Biology*, **2011**, 271, 136-44	2.3	6

40	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	3	6
39	An Approach for the Automatic Recommendation of Ontologies Using Collaborative Knowledge. *Lecture Notes in Computer Science*, **2010**, 74-81	0.9	6
38	Experimental and computational studies of fatty acid distribution networks. *Molecular BioSystems*, **2015**, 11, 2964-77		5
37	Data Mining in Complex Diseases Using Evolutionary Computation. *Lecture Notes in Computer Science*, **2009**, 917-924	0.9	5
36	Prediction of Nucleotide Binding Peptides Using Star Graph Topological Indices. *Molecular Informatics*, **2015**, 34, 736-41	3.8	4
35	The first eNanoMapper prototype: A substance database to support safe-by-design **2014**,		4
34	Prediction of druggable proteins using machine learning and functional enrichment analysis: a focus on cancer-related proteins and RNA-binding proteins		4
33	A Multi-Objective Approach for Anti-Osteosarcoma Cancer Agents Discovery through Drug Repurposing. *Pharmaceuticals*, **2020**, 13,	5.2	4
32	Improvement of Epitope Prediction Using Peptide Sequence Descriptors and Machine Learning. *International Journal of Molecular Sciences*, **2019**, 20,	6.3	3
31	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	4	3
30	Bio-AIMS Collection of Chemoinformatics Web Tools based on Molecular Graph Information and Artificial Intelligence Models. *Combinatorial Chemistry and High Throughput Screening*, **2015**, 18, 735-50	1.3	3
29	Applied computational techniques on schizophrenia using genetic mutations. *Current Topics in Medicinal Chemistry*, **2013**, 13, 675-84	3	3
28	PTML Multi-Label Algorithms: Models, Software, and Applications. *Current Topics in Medicinal Chemistry*, **2020**, 20, 2326-2337	3	3
27	Graph-Based Processing of Macromolecular Information. *Current Bioinformatics*, **2015**, 10, 606-631	4.7	3
26	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	4.7	3
25	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		3
24	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	5.1	3
23	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	6.9	2

22	Prot-2S: a new python web tool for protein secondary structure studies. *International Journal of Bioinformatics Research and Applications*, **2009**, 5, 402-16	0.9	2
21	OncoOmics approaches to reveal essential genes in breast cancer: a panoramic view from pathogenesis to precision medicine		2
20	Prediction of breast cancer proteins using molecular descriptors and artificial neural networks: a focus on cancer immunotherapy proteins, metastasis driver proteins, and RNA-binding proteins		2
19	Identification of coenzyme-binding proteins with machine learning algorithms. *Computational Biology and Chemistry*, **2019**, 79, 185-192	3.6	1
18	Experimental Study and ANN Dual-Time Scale Perturbation Model of Electrokinetic Properties of Microbiota. *Frontiers in Microbiology*, **2017**, 8, 1216	5.7	1
17	Regulatory affairs issues and legal ontologies in drug development. *Frontiers in Bioscience - Elite*, **2013**, 5, 446-60	1.6	1
16	He-, Ne-, and Ar-phosgene intermolecular potential energy surfaces. *Journal of Physical Chemistry A* , **2013**, 117, 3835-43	2.8	1
15	Biomedical Data Integration in Computational Drug Design and Bioinformatics. *Current Computer-Aided Drug Design*, **2013**, 9, 108-117	1.4	1
14	Discovery of novel immunopharmacological ligands targeting the IL-17 inflammatory pathway. *International Immunopharmacology*, **2020**, 89, 107026	5.8	1
13	Net-Net AutoML Selection of Artificial Neural Network Topology for Brain Connectome Prediction. *Applied Sciences (Switzerland)*, **2020**, 10, 1308	2.6	0
12	MCDCalc: Markov Chain Molecular Descriptors Calculator for Medicinal Chemistry. *Current Topics in Medicinal Chemistry*, **2020**, 20, 305-317	3	0
11	System for Automatic Assessment of Alzheimer Disease Diagnosis Based on Deep Learning Techniques. *Proceedings (mdpi)*, **2019**, 21, 28	0.3	
10	Translational Bioinformatics: Informatics, Medicine, and -Omics **2019**, 507-514		
9	Perturbation-Theory Machine Learning (PTML) Multilabel Model of the ChEMBL Dataset of Preclinical Assays for Antisarcoma Compounds. *ACS Omega*, **2020**, 5, 27211-27220	3.9	
8	Evaluation as a Continuous Improvement Process in the Learning of Programming Languages. *Advances in Intelligent Systems and Computing*, **2019**, 521-529	0.4	
7	Machine Learning in Biomedical Informatics **2019**, 389-399		
6	Applying Artificial Intelligence for Operating System Fingerprinting. *Engineering Proceedings*, **2021**, 7, 51	0.5	
5	Bioinformatic tools for research in CRC **2022**, 231-247		

4	Protein Graphs in Cancer Prediction **2010**, 125-140	
3	SNP-Schizo: A Web Tool for Schizophrenia SNP Sequence Classification. *Lecture Notes in Computer Science*, **2011**, 252-259	0.9
2	Design and Implementation of a Physical Bitcoin Coin. *Proceedings (mdpi)*, **2020**, 54, 21	0.3
1	Web Server and R Library for the Calculation of Markov Chains Molecular Descriptors. *Proceedings (mdpi)*, **2020**, 54, 28	0.3