

Cristian Robert Munteanu

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/5090167/cristian-robert-munteanu-publications-by-year.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Bioinformatic tools for research in CRC 2022 , 231-247		
110	Applying Artificial Intelligence for Operating System Fingerprinting. <i>Engineering Proceedings</i> , 2021 , 7, 51	0.5	
109	Molecular docking, SAR analysis and biophysical approaches in the study of the antibacterial activity of ceramides isolated from <i>Cissus incisa</i> . <i>Bioorganic Chemistry</i> , 2021 , 109, 104745	5.1	3
108	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. <i>Frontiers in Pharmacology</i> , 2021 , 12, 598925	5.6	7
107	Perturbation-Theory Machine Learning (PTML) Multilabel Model of the ChEMBL Dataset of Preclinical Assays for Antisarcoma Compounds. <i>ACS Omega</i> , 2020 , 5, 27211-27220	3.9	
106	OncoOmics approaches to reveal essential genes in breast cancer: a panoramic view from pathogenesis to precision medicine. <i>Scientific Reports</i> , 2020 , 10, 5285	4.9	17
105	Molecular docking and machine learning analysis of Abemaciclib in colon cancer. <i>BMC Molecular and Cell Biology</i> , 2020 , 21, 52	2.7	7
104	Gene Prioritization through Consensus Strategy, Enrichment Methodologies Analysis, and Networking for Osteosarcoma Pathogenesis. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	6
103	Net-Net AutoML Selection of Artificial Neural Network Topology for Brain Connectome Prediction. <i>Applied Sciences (Switzerland)</i> , 2020 , 10, 1308	2.6	0
102	MCDCalc: Markov Chain Molecular Descriptors Calculator for Medicinal Chemistry. <i>Current Topics in Medicinal Chemistry</i> , 2020 , 20, 305-317	3	0
101	PTML Multi-Label Algorithms: Models, Software, and Applications. <i>Current Topics in Medicinal Chemistry</i> , 2020 , 20, 2326-2337	3	3
100	Prediction of breast cancer proteins involved in immunotherapy, metastasis, and RNA-binding using molecular descriptors and artificial neural networks. <i>Scientific Reports</i> , 2020 , 10, 8515	4.9	12
99	Discovery of novel immunopharmacological ligands targeting the IL-17 inflammatory pathway. <i>International Immunopharmacology</i> , 2020 , 89, 107026	5.8	1
98	Drugs Repurposing Using QSAR, Docking and Molecular Dynamics for Possible Inhibitors of the SARS-CoV-2 M Protease. <i>Molecules</i> , 2020 , 25,	4.8	23
97	A Multi-Objective Approach for Anti-Osteosarcoma Cancer Agents Discovery through Drug Repurposing. <i>Pharmaceuticals</i> , 2020 , 13,	5.2	4
96	Prediction of Antimalarial Drug-Decorated Nanoparticle Delivery Systems with Random Forest Models. <i>Biology</i> , 2020 , 9,	4.9	10
95	Design and Implementation of a Physical Bitcoin Coin. <i>Proceedings (mdpi)</i> , 2020 , 54, 21	0.3	

94	Web Server and R Library for the Calculation of Markov Chains Molecular Descriptors. <i>Proceedings (mdpi)</i> , 2020 , 54, 28	0.3	
93	Automatic assessment of Alzheimer's disease diagnosis based on deep learning techniques. <i>Computers in Biology and Medicine</i> , 2020 , 120, 103764	7	20
92	System for Automatic Assessment of Alzheimer's Disease Diagnosis Based on Deep Learning Techniques. <i>Proceedings (mdpi)</i> , 2019 , 21, 28	0.3	
91	Improvement of Epitope Prediction Using Peptide Sequence Descriptors and Machine Learning. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	3
90	Identification of coenzyme-binding proteins with machine learning algorithms. <i>Computational Biology and Chemistry</i> , 2019 , 79, 185-192	3.6	1
89	Translational Bioinformatics: Informatics, Medicine, and -Omics 2019 , 507-514		
88	PTML Model of Enzyme Subclasses for Mining the Proteome of Biofuel Producing Microorganisms. <i>Journal of Proteome Research</i> , 2019 , 18, 2735-2746	5.6	18
87	Perturbation Theory Machine Learning Modeling of Immunotoxicity for Drugs Targeting Inflammatory Cytokines and Study of the Antimicrobial G1 Using Cytometric Bead Arrays. <i>Chemical Research in Toxicology</i> , 2019 , 32, 1811-1823	4	3
86	Evaluation as a Continuous Improvement Process in the Learning of Programming Languages. <i>Advances in Intelligent Systems and Computing</i> , 2019 , 521-529	0.4	
85	Machine Learning in Biomedical Informatics 2019 , 389-399		
84	Net-Net Auto Machine Learning (AutoML) Prediction of Complex Ecosystems. <i>Scientific Reports</i> , 2018 , 8, 12340	4.9	7
83	Gene prioritization, communality analysis, networking and metabolic integrated pathway to better understand breast cancer pathogenesis. <i>Scientific Reports</i> , 2018 , 8, 16679	4.9	19
82	Perturbation Theory/Machine Learning Model of ChEMBL Data for Dopamine Targets: Docking, Synthesis, and Assay of New l-Prolyl-l-leucyl-glycinamide Peptidomimetics. <i>ACS Chemical Neuroscience</i> , 2018 , 9, 2572-2587	5.7	31
81	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. <i>Journal of Chemical Information and Modeling</i> , 2017 , 57, 1029-1044	6.1	26
80	Decrypting Strong and Weak Single-Walled Carbon Nanotubes Interactions with Mitochondrial Voltage-Dependent Anion Channels Using Molecular Docking and Perturbation Theory. <i>Scientific Reports</i> , 2017 , 7, 13271	4.9	15
79	SNOMED2HL7: A tool to normalize and bind SNOMED CT concepts to the HL7 Reference Information Model. <i>Computer Methods and Programs in Biomedicine</i> , 2017 , 149, 1-9	6.9	2
78	Experimental study and Random Forest prediction model of microbiome cell surface hydrophobicity. <i>Expert Systems With Applications</i> , 2017 , 72, 306-316	7.8	17
77	Carbon Nanotubes' Effect on Mitochondrial Oxygen Flux Dynamics: Polarography Experimental Study and Machine Learning Models using Star Graph Trace Invariants of Raman Spectra. <i>Nanomaterials</i> , 2017 , 7,	5.4	10

76	Experimental Study and ANN Dual-Time Scale Perturbation Model of Electrokinetic Properties of Microbiota. <i>Frontiers in Microbiology</i> , 2017 , 8, 1216	5.7	1
75	General Machine Learning Model, Review, and Experimental-Theoretic Study of Magnolol Activity in Enterotoxigenic Induced Oxidative Stress. <i>Current Topics in Medicinal Chemistry</i> , 2017 , 17, 2977-2988	3	6
74	A methodology for the design of experiments in computational intelligence with multiple regression models. <i>PeerJ</i> , 2016 , 4, e2721	3.1	20
73	Gastrointestinal Spatiotemporal mRNA Expression of Ghrelin vs Growth Hormone Receptor and New Growth Yield Machine Learning Model Based on Perturbation Theory. <i>Scientific Reports</i> , 2016 , 6, 30174	4.9	7
72	Experimental and computational studies of fatty acid distribution networks. <i>Molecular BioSystems</i> , 2015 , 11, 2964-77		5
71	eNanoMapper: harnessing ontologies to enable data integration for nanomaterial risk assessment. <i>Journal of Biomedical Semantics</i> , 2015 , 6, 10	2.2	48
70	Classification of mild cognitive impairment and Alzheimer's Disease with machine-learning techniques using 1H Magnetic Resonance Spectroscopy data. <i>Expert Systems With Applications</i> , 2015 , 42, 6205-6214	7.8	24
69	Solvent accessible surface area-based hot-spot detection methods for protein-protein and protein-nucleic acid interfaces. <i>Journal of Chemical Information and Modeling</i> , 2015 , 55, 1077-86	6.1	21
68	Classification of signaling proteins based on molecular star graph descriptors using Machine Learning models. <i>Journal of Theoretical Biology</i> , 2015 , 384, 50-8	2.3	19
67	RRegrs: an R package for computer-aided model selection with multiple regression models. <i>Journal of Cheminformatics</i> , 2015 , 7, 46	8.6	30
66	Prediction of Nucleotide Binding Peptides Using Star Graph Topological Indices. <i>Molecular Informatics</i> , 2015 , 34, 736-41	3.8	4
65	The eNanoMapper database for nanomaterial safety information. <i>Beilstein Journal of Nanotechnology</i> , 2015 , 6, 1609-34	3	64
64	Bio-AIMS Collection of Chemoinformatics Web Tools based on Molecular Graph Information and Artificial Intelligence Models. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2015 , 18, 735-50	1.3	3
63	Graph-Based Processing of Macromolecular Information. <i>Current Bioinformatics</i> , 2015 , 10, 606-631	4.7	3
62	Markov mean properties for cell death-related protein classification. <i>Journal of Theoretical Biology</i> , 2014 , 349, 12-21	2.3	9
61	Modeling complex metabolic reactions, ecological systems, and financial and legal networks with MIANN models based on Markov-Wiener node descriptors. <i>Journal of Chemical Information and Modeling</i> , 2014 , 54, 16-29	6.1	19
60	Improving enzyme regulatory protein classification by means of SVM-RFE feature selection. <i>Molecular BioSystems</i> , 2014 , 10, 1063-71		19
59	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. <i>Journal of Chemical Information and Modeling</i> , 2014 , 54, 744-55	6.1	42

58	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. <i>Molecular Informatics</i> , 2014 , 33, 276-85	3.8	6
57	The first eNanoMapper prototype: A substance database to support safe-by-design 2014 ,		4
56	Random Forest classification based on star graph topological indices for antioxidant proteins. <i>Journal of Theoretical Biology</i> , 2013 , 317, 331-7	2.3	36
55	The R�rker-Markov invariants of complex Bio-Systems: applications in Parasitology and Neuroinformatics. <i>BioSystems</i> , 2013 , 111, 199-207	1.9	7
54	Biomedical Data Integration in Computational Drug Design and Bioinformatics. <i>Current Computer-Aided Drug Design</i> , 2013 , 9, 108-117	1.4	7
53	Regulatory affairs issues and legal ontologies in drug development. <i>Frontiers in Bioscience - Elite</i> , 2013 , 5, 446-60	1.6	1
52	He-, Ne-, and Ar-phosgene intermolecular potential energy surfaces. <i>Journal of Physical Chemistry A</i> , 2013 , 117, 3835-43	2.8	1
51	Biomedical Data Integration in Computational Drug Design and Bioinformatics. <i>Current Computer-Aided Drug Design</i> , 2013 , 9, 108-117	1.4	1
50	S2SNet: A Tool for Transforming Characters and Numeric Sequences into Star Network Topological Indices in Chemoinformatics, Bioinformatics, Biomedical, and Social-Legal Sciences. <i>Current Bioinformatics</i> , 2013 , 8, 429-437	4.7	13
49	MIANN models in medicinal, physical and organic chemistry. <i>Current Topics in Medicinal Chemistry</i> , 2013 , 13, 619-41	3	21
48	Applied computational techniques on schizophrenia using genetic mutations. <i>Current Topics in Medicinal Chemistry</i> , 2013 , 13, 675-84	3	3
47	Kernel-based feature selection techniques for transport proteins based on star graph topological indices. <i>Current Topics in Medicinal Chemistry</i> , 2013 , 13, 1681-91	3	13
46	Evolutionary computation and QSAR research. <i>Current Computer-Aided Drug Design</i> , 2013 , 9, 206-25	1.4	22
45	Markov-Randic Indices for QSPR Re-Evaluation of Metabolic, Parasite- Host, Fasciolosis Spreading, Brain Cortex and Legal-Social Complex Networks. <i>Current Bioinformatics</i> , 2013 , 8, 401-415	4.7	3
44	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. <i>Journal of Theoretical Biology</i> , 2012 , 293, 174-88	2.3	30
43	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. <i>Molecular BioSystems</i> , 2012 , 8, 851-62		13
42	Na�ve Bayes QSDR classification based on spiral-graph Shannon entropies for protein biomarkers in human colon cancer. <i>Molecular BioSystems</i> , 2012 , 8, 1716-22		20
41	Automatic seizure detection based on star graph topological indices. <i>Journal of Neuroscience Methods</i> , 2012 , 209, 410-9	3	10

40	Nanoinformatics: developing new computing applications for nanomedicine. <i>Computing (Vienna/New York)</i> , 2012 , 94, 521-539	2.2	12
39	From QSAR models of drugs to complex networks: state-of-art review and introduction of new Markov-spectral moments indices. <i>Current Topics in Medicinal Chemistry</i> , 2012 , 12, 927-60	3	27
38	MISS-Prot: web server for self/non-self discrimination of protein residue networks in parasites; theory and experiments in Fasciola peptides and Anisakis allergens. <i>Molecular BioSystems</i> , 2011 , 7, 1938-55		11
37	Automatic feature extraction using genetic programming: An application to epileptic EEG classification. <i>Expert Systems With Applications</i> , 2011 , 38, 10425-10436	7.8	183
36	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. <i>Journal of Proteome Research</i> , 2011 , 10, 1698-718	5.6	60
35	Amino acid pair- and triplet-wise groupings in the interior of helical segments in proteins. <i>Journal of Theoretical Biology</i> , 2011 , 271, 136-44	2.3	6
34	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. <i>Journal of Theoretical Biology</i> , 2011 , 276, 229-49	2.3	29
33	Definition of Markov-Harary Invariants and Review of Classic Topological Indices and Databases in Biology, Parasitology, Technology, and Social-Legal Networks. <i>Current Bioinformatics</i> , 2011 , 6, 94-121	4.7	12
32	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. <i>Current Computer-Aided Drug Design</i> , 2011 , 7, 315-37	1.4	7
31	SNP-Schizo: A Web Tool for Schizophrenia SNP Sequence Classification. <i>Lecture Notes in Computer Science</i> , 2011 , 252-259	0.9	
30	Machine learning techniques for single nucleotide polymorphism--disease classification models in schizophrenia. <i>Molecules</i> , 2010 , 15, 4875-89	4.8	11
29	Drug discovery and design for complex diseases through QSAR computational methods. <i>Current Pharmaceutical Design</i> , 2010 , 16, 2640-55	3.3	37
28	Trypano-PPI: a web server for prediction of unique targets in trypanosome proteome by using electrostatic parameters of protein-protein interactions. <i>Journal of Proteome Research</i> , 2010 , 9, 1182-90	5.6	44
27	Artificial intelligence techniques for colorectal cancer drug metabolism: ontology and complex network. <i>Current Drug Metabolism</i> , 2010 , 11, 347-68	3.5	42
26	Plasmod-PPI: A web-server predicting complex biopolymer targets in plasmodium with entropy measures of protein-protein interactions. <i>Polymer</i> , 2010 , 51, 264-273	3.9	18
25	Ontologies of drug discovery and design for neurology, cardiology and oncology. <i>Current Pharmaceutical Design</i> , 2010 , 16, 2724-36	3.3	31
24	Improving Ontology Alignment through Genetic Algorithms 2010 , 240-259		20
23	An Approach for the Automatic Recommendation of Ontologies Using Collaborative Knowledge. <i>Lecture Notes in Computer Science</i> , 2010 , 74-81	0.9	6

22 Protein Graphs in Cancer Prediction **2010**, 125-140

21 Star Graphs of Protein Sequences and Proteome Mass Spectra in Cancer Prediction. *Current Proteomics*, **2009**, 6, 275-288 0.7 15

20 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

19 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

18 Generalized lattice graphs for 2D-visualization of biological information. *Journal of Theoretical Biology*, **2009**, 261, 136-47 2.3 30

17 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

16 QSAR and complex network study of the chiral HMGR inhibitor structural diversity. *Bioorganic and Medicinal Chemistry*, **2009**, 17, 165-75 3.4 19

15 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

14 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

13 Data Mining in Complex Diseases Using Evolutionary Computation. *Lecture Notes in Computer Science*, **2009**, 917-924 0.9 5

12 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

11 Natural/random protein classification models based on star network topological indices. *Journal of Theoretical Biology*, **2008**, 254, 775-83 2.3 30

10 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

9 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

8 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

7 The chlorobenzene-argon ground state intermolecular potential energy surface. *Journal of Chemical Physics*, **2004**, 121, 1390-6 3.9 20

6 Accurate intermolecular ground state potential of the Ne-N₂ van der Waals complex. *Journal of Chemical Physics*, **2004**, 120, 9104-12 3.9 14

5 Accurate intermolecular ground state potential of the Ar-N₂ van der Waals complex. *Journal of Chemical Physics*, **2004**, 121, 10419-25 3.9 15

4	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
3	OncoOmics approaches to reveal essential genes in breast cancer: a panoramic view from pathogenesis to precision medicine	2
2	Prediction of druggable proteins using machine learning and functional enrichment analysis: a focus on cancer-related proteins and RNA-binding proteins	4
1	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