

Luis M. Rocha

List of Publications by Year in Descending Order

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

50
papers

1,255
citations

17
h-index

34
g-index

61
ext. papers

1,566
ext. citations

4.2
avg, IF

4.59
L-index

#	Paper	IF	Citations
50	Effective connectivity determines the critical dynamics of biochemical networks.. <i>Journal of the Royal Society Interface</i> , 2022 , 19, 20210659	4.1	1
49	Small cohort of patients with epilepsy showed increased activity on Facebook before sudden unexpected death.. <i>Epilepsy and Behavior</i> , 2022 , 128, 108580	3.2	0
48	The effective graph reveals redundancy, canalization, and control pathways in biochemical regulation and signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	11
47	Introduction to the special issue on COMPLEX NETWORKS 2019. <i>Network Science</i> , 2021 , 9, S1-S3	2.9	
46	Mining Social Media Data for Biomedical Signals and Health-Related Behavior. <i>Annual Review of Biomedical Data Science</i> , 2020 , 3, 433-458	5.6	12
45	Translational Knowledge Discovery Between Drug Interactions and Pharmacogenetics. <i>Clinical Pharmacology and Therapeutics</i> , 2020 , 107, 886-902	6.1	6
44	Introduction to the special issue on COMPLEX NETWORKS 2018. <i>Network Science</i> , 2020 , 8, S1-S3	2.9	
43	City-wide electronic health records reveal gender and age biases in administration of known drug-drug interactions. <i>Npj Digital Medicine</i> , 2019 , 2, 74	15.7	2
42	CANA: A Python Package for Quantifying Control and Canalization in Boolean Networks. <i>Frontiers in Physiology</i> , 2018 , 9, 1046	4.6	10
41	Human Sexual Cycles are Driven by Culture and Match Collective Moods. <i>Scientific Reports</i> , 2017 , 7, 17973	4.9	12
40	Control of complex networks requires both structure and dynamics. <i>Scientific Reports</i> , 2016 , 6, 24456	4.9	74
39	MONITORING POTENTIAL DRUG INTERACTIONS AND REACTIONS VIA NETWORK ANALYSIS OF INSTAGRAM USER TIMELINES. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2016 , 21, 492-503	1.3	18
38	Distance closures on complex networks. <i>Network Science</i> , 2015 , 3, 227-268	2.9	23
37	Modularity and the spread of perturbations in complex dynamical systems. <i>Physical Review E</i> , 2015 , 92, 060801	2.4	5
36	Extraction of pharmacokinetic evidence of drug-drug interactions from the literature. <i>PLoS ONE</i> , 2015 , 10, e0122199	3.7	20
35	Computational Fact Checking from Knowledge Networks. <i>PLoS ONE</i> , 2015 , 10, e0128193	3.7	135
34	Multi-scale integration and predictability in resting state brain activity. <i>Frontiers in Neuroinformatics</i> , 2014 , 8, 66	3.9	10

33	An integrated pharmacokinetics ontology and corpus for text mining. <i>BMC Bioinformatics</i> , 2013 , 14, 35	3.6	32
32	Canalization and control in automata networks: body segmentation in <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2013 , 8, e55946	3.7	25
31	Semi-metric Networks for Recommender Systems 2012 ,		6
30	Correction: A linear classifier based on entity recognition tools and a statistical approach to method extraction in the protein-protein interaction literature. <i>BMC Bioinformatics</i> , 2012 , 13, 180	3.6	78
29	Collective classification of textual documents by guided self-organization in T-Cell cross-regulation dynamics. <i>Evolutionary Intelligence</i> , 2011 , 4, 69-80	1.7	5
28	A linear classifier based on entity recognition tools and a statistical approach to method extraction in the protein-protein interaction literature. <i>BMC Bioinformatics</i> , 2011 , 12 Suppl 8, S12	3.6	7
27	Schema redescription in cellular automata: Revisiting emergence in complex systems 2011 ,		4
26	Classification of protein-protein interaction full-text documents using text and citation network features. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2010 , 7, 400-11	3	18
25	BioDR: Semantic indexing networks for biomedical document retrieval. <i>Expert Systems With Applications</i> , 2010 , 37, 3444-3453	7.8	9
24	Biomedical Article Classification Using an Agent-Based Model of T-Cell Cross-Regulation. <i>Lecture Notes in Computer Science</i> , 2010 , 237-249	0.9	2
23	Literature mining on pharmacokinetics numerical data: a feasibility study. <i>Journal of Biomedical Informatics</i> , 2009 , 42, 726-35	10.2	16
22	Biomedical Text Mining Applied to Document Retrieval and Semantic Indexing. <i>Lecture Notes in Computer Science</i> , 2009 , 954-963	0.9	
21	Uncovering protein interaction in abstracts and text using a novel linear model and word proximity networks. <i>Genome Biology</i> , 2008 , 9 Suppl 2, S11	18.3	21
20	Adaptive Spam Detection Inspired by a Cross-Regulation Model of Immune Dynamics: A Study of Concept Drift. <i>Lecture Notes in Computer Science</i> , 2008 , 36-47	0.9	7
19	Stochastic model for scale-free networks with cutoffs. <i>Physical Review E</i> , 2008 , 78, 066116	2.4	2
18	The Role of Conceptual Structure in Designing Cellular Automata to Perform Collective Computation. <i>Lecture Notes in Computer Science</i> , 2008 , 146-163	0.9	6
17	Agent-based model of genotype editing. <i>Evolutionary Computation</i> , 2007 , 15, 253-89	4.3	6
16	Genotype Editing and the Evolution of Regulation and Memory 2007 , 63-73		3

15	Large-scale testing of bibliome informatics using Pfam protein families. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2006 , 76-87	1.3	3
14	Protein annotation as term categorization in the gene ontology using word proximity networks. <i>BMC Bioinformatics</i> , 2005 , 6 Suppl 1, S20	3.6	20
13	Introduction to the Special Issue: Embodied and Situated Cognition. <i>Artificial Life</i> , 2005 , 11, 5-11	1.4	5
12	Material representations: from the genetic code to the evolution of cellular automata. <i>Artificial Life</i> , 2005 , 11, 189-214	1.4	29
11	Evaluation of the host transcriptional response to human cytomegalovirus infection. <i>Physiological Genomics</i> , 2004 , 18, 51-62	3.6	31
10	Bioinformatics for Geneticists. Michael R. Barnes and Ian C. Gray, editors. Chichester, West Sussex, United Kingdom: John Wiley & Sons Ltd., 2003, 422 pp., \$65.00, softcover. ISBN 0-470-84394-2.. <i>Clinical Chemistry</i> , 2004 , 50, 2471-2472	5.5	1
9	A Systematic Study of Genetic Algorithms with Genotype Editing. <i>Lecture Notes in Computer Science</i> , 2004 , 1233-1245	0.9	4
8	Singular Value Decomposition and Principal Component Analysis 2003 , 91-109		445
7	Evolution with material symbol systems. <i>BioSystems</i> , 2001 , 60, 95-121	1.9	34
6	Adaptive recommendation and open-ended semiosis. <i>Kybernetes</i> , 2001 , 30, 821-854	2	1
5	Syntactic autonomy. Why there is no autonomy without symbols and how self-organizing systems might evolve them. <i>Annals of the New York Academy of Sciences</i> , 2000 , 901, 207-23	6.5	8
4	EVIDENCE SETS: MODELING SUBJECTIVE CATEGORIES. <i>International Journal of General Systems</i> , 1999 , 27, 457-494	2.1	12
3	RELATIVE UNCERTAINTY AND EVIDENCE SETS: A CONSTRUCTIVIST FRAMEWORK. <i>International Journal of General Systems</i> , 1997 , 26, 35-61	2.1	10
2	Eigenbehavior and symbols. <i>Systems Research and Behavioral Science</i> , 1996 , 13, 371-384		26
1	Contextual genetic algorithms: Evolving developmental rules. <i>Lecture Notes in Computer Science</i> , 1995 , 368-382	0.9	8