

Rui Alves

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

2,150
citations

257450

24
h-index

243625

44
g-index

74
all docs

74
docs citations

74
times ranked

2692
citing authors

#	ARTICLE	IF	CITATIONS
1	Multilevel interactions between native and ectopic isoprenoid pathways affect global metabolism in rice. <i>Transgenic Research</i> , 2022, 31, 249-268.	2.4	4
2	Maximization of information transmission influences selection of native phosphorelay architectures. <i>PeerJ</i> , 2021, 9, e11558.	2.0	2
3	EasyModel 1.1: User-friendly Stochastic and Deterministic Simulations for Systems Biology Models. , 2020, , .		0
4	Non-invasive imaging techniques and assessment of carotid vasa vasorum neovascularization: Promises and pitfalls. <i>Trends in Cardiovascular Medicine</i> , 2019, 29, 71-80.	4.9	8
5	Revisiting Trade-offs between Rubisco Kinetic Parameters. <i>Biochemistry</i> , 2019, 58, 3365-3376.	2.5	142
6	EasyModel: user-friendly tool for building and analysis of simple mathematical models in systems biology. <i>Bioinformatics</i> , 2019, 36, 976-977.	4.1	1
7	Quantitative Operating Principles of Yeast Metabolism during Adaptation to Heat Stress. <i>Cell Reports</i> , 2018, 22, 2421-2430.	6.4	19
8	MetReS, an Efficient Database for Genomic Applications. <i>Journal of Computational Biology</i> , 2018, 25, 200-213.	1.6	1
9	Automatic Methods for Carotid Contrast-Enhanced Ultrasound Imaging Quantification of Adventitial Vasa Vasorum. <i>Ultrasound in Medicine and Biology</i> , 2018, 44, 2780-2792.	1.5	2
10	Editorial: Foundations of Theoretical Approaches in Systems Biology. <i>Frontiers in Genetics</i> , 2018, 9, 290.	2.3	0
11	Rare Disease Discovery: An Optimized Disease Ranking System. <i>IEEE Transactions on Industrial Informatics</i> , 2017, 13, 1184-1192.	11.3	11
12	TControl: A mobile app to follow up tobacco-quitting patients. <i>Computer Methods and Programs in Biomedicine</i> , 2017, 142, 81-89.	4.7	10
13	Evaluating multi-locus phylogenies for species boundaries determination in the genus <i>Diaporthe</i> . <i>PeerJ</i> , 2017, 5, e3120.	2.0	72
14	Identification of line-specific strategies for improving carotenoid production in synthetic maize through data-driven mathematical modeling. <i>Plant Journal</i> , 2016, 87, 455-471.	5.7	9
15	Regulation of the Na ⁺ /K ⁺ -ATPase <i>Ena1</i> Expression by Calcineurin/ <i>Crz1</i> under High pH Stress: A Quantitative Study. <i>PLoS ONE</i> , 2016, 11, e0158424.	2.5	19
16	Computer-assisted initial diagnosis of rare diseases. <i>PeerJ</i> , 2016, 4, e2211.	2.0	24
17	CheNER: a tool for the identification of chemical entities and their classes in biomedical literature. <i>Journal of Cheminformatics</i> , 2015, 7, S15.	6.1	9
18	The CHEMDNER corpus of chemicals and drugs and its annotation principles. <i>Journal of Cheminformatics</i> , 2015, 7, S2.	6.1	166

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19	A survey of HK, HPt, and RR domains and their organization in two-component systems and phosphorelay proteins of organisms with fully sequenced genomes. PeerJ, 2015, 3, e1183.	2.0	16
20	Gobal optimization of hybrid kinetic/FBA models via outer-approximation. Computers and Chemical Engineering, 2015, 72, 325-333.	3.8	21
21	Database Constraints Applied to Metabolic Pathway Reconstruction Tools. Scientific World Journal, The, 2014, 2014, 1-12.	2.1	1
22	Multi-level Optimization Framework Applied to the Systematic Evaluation of Metabolic Objective Functions. Computer Aided Chemical Engineering, 2014, 33, 961-966.	0.5	6
23	CheNER: chemical named entity recognizer. Bioinformatics, 2014, 30, 1039-1040.	4.1	15
24	MetReS: A Metabolic Reconstruction Database for Cloud Computing. , 2014, , .		0
25	An <i>in vitro</i> system for the rapid functional characterization of genes involved in carotenoid biosynthesis and accumulation. Plant Journal, 2014, 77, 464-475.	5.7	63
26	S-PC: An e-treatment application for management of smoke-quitting patients. Computer Methods and Programs in Biomedicine, 2014, 115, 33-45.	4.7	11
27	Biblio-MetReS for user-friendly mining of genes and biological processes in scientific documents. PeerJ, 2014, 2, e276.	2.0	4
28	Differential Evolutionary Particle Swarm Optimization (DEEPSO): A Successful Hybrid. , 2013, , .		60
29	Targeted transcriptomic and metabolic profiling reveals temporal bottlenecks in the maize carotenoid pathway that may be addressed by multigene engineering. Plant Journal, 2013, 75, 441-455.	5.7	27
30	Identification of regulatory structure and kinetic parameters of biochemical networks via mixed-integer dynamic optimization. BMC Systems Biology, 2013, 7, 113.	3.0	21
31	Relative Amino Acid Composition Signatures of Organisms and Environments. PLoS ONE, 2013, 8, e77319.	2.5	82
32	Avaliaço de sistema de tratamento de dejetos sunos instalado no estado de Santa Catarina. Revista Brasileira De Engenharia Agrícola E Ambiental, 2012, 16, 745-753.	1.1	6
33	Lipid fraction quality of milk produced by Minhota (Portuguese autochthonous breed) compared to Holstein Friesian cow's. Journal of the Science of Food and Agriculture, 2012, 92, 2994-3001.	3.5	4
34	Two Component Systems: Physiological Effect of a Third Component. PLoS ONE, 2012, 7, e31095.	2.5	9
35	Saccharomyces cerevisiae as a Model Organism: A Comparative Study. PLoS ONE, 2011, 6, e16015.	2.5	130
36	Methods for and results from the study of design principles in molecular systems. Mathematical Biosciences, 2011, 231, 3-18.	1.9	13

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37	Special issue on biological design principles. <i>Mathematical Biosciences</i> , 2011, 231, 1-2.	1.9	12
38	Teaching systems biology. <i>IET Systems Biology</i> , 2011, 5, 131-136.	1.5	3
39	Steady-state global optimization of metabolic non-linear dynamic models through recasting into power-law canonical models. <i>BMC Systems Biology</i> , 2011, 5, 137.	3.0	21
40	Biblio-MetReS: A bibliometric network reconstruction application and server. <i>BMC Bioinformatics</i> , 2011, 12, 387.	2.6	11
41	Optimization and evolution in metabolic pathways: Global optimization techniques in Generalized Mass Action models. <i>Journal of Biotechnology</i> , 2010, 149, 141-153.	3.8	32
42	Minimization of Biosynthetic Costs in Adaptive Gene Expression Responses of Yeast to Environmental Changes. <i>PLoS Computational Biology</i> , 2010, 6, e1000674.	3.2	25
43	Evolution based on domain combinations: the case of glutaredoxins. <i>BMC Evolutionary Biology</i> , 2009, 9, 66.	3.2	35
44	Hysteretic and graded responses in bacterial two-component signal transduction. <i>Molecular Microbiology</i> , 2008, 68, 1196-1215.	2.5	60
45	Mathematical formalisms based on approximated kinetic representations for modeling genetic and metabolic pathways. <i>Biotechnology and Genetic Engineering Reviews</i> , 2008, 25, 1-40.	6.2	29
46	Integrating Bioinformatics and Computational Biology: Perspectives and Possibilities for In Silico Network Reconstruction in Molecular Systems Biology. <i>Current Bioinformatics</i> , 2008, 3, 98-129.	1.5	11
47	Cooperativity and saturation in biochemical networks: A saturable formalism using Taylor series approximations. <i>Biotechnology and Bioengineering</i> , 2007, 97, 1259-1277.	3.3	55
48	Heuristics for the early/tardy scheduling problem with release dates. <i>International Journal of Production Economics</i> , 2007, 106, 261-274.	8.9	20
49	In silico pathway reconstruction: Iron-sulfur cluster biogenesis in <i>Saccharomyces cerevisiae</i> . <i>BMC Systems Biology</i> , 2007, 1, 10.	3.0	13
50	Tools for kinetic modeling of biochemical networks. <i>Nature Biotechnology</i> , 2006, 24, 667-672.	17.5	180
51	Use of physiological constraints to identify quantitative design principles for gene expression in yeast adaptation to heat shock. <i>BMC Bioinformatics</i> , 2006, 7, 184.	2.6	30
52	Evidence of selection for low cognate amino acid bias in amino acid biosynthetic enzymes. <i>Molecular Microbiology</i> , 2005, 56, 1017-1034.	2.5	34
53	Predictive reconstruction of the mitochondrial iron-sulfur cluster assembly metabolism: I. The role of the protein pair ferredoxin-ferredoxin reductase (Yah1-Arh1). <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 56, 354-366.	2.6	24
54	Predictive reconstruction of the mitochondrial iron-sulfur cluster assembly metabolism. II. Role of glutaredoxin Grx5. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 481-492.	2.6	32

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55	Evolution and Cellular Function of Monothiol Glutaredoxins: Involvement in Iron-Sulphur Cluster Assembly. <i>Comparative and Functional Genomics</i> , 2004, 5, 328-341.	2.0	47
56	Comparative analysis of prototype two-component systems with either bifunctional or monofunctional sensors: differences in molecular structure and physiological function. <i>Molecular Microbiology</i> , 2003, 48, 25-51.	2.5	85
57	Evolution of Enzymes in Metabolism: A Network Perspective. <i>Journal of Molecular Biology</i> , 2002, 320, 751-770.	4.2	73
58	Irreversibility in Unbranched Pathways: Preferred Positions Based on Regulatory Considerations. <i>Biophysical Journal</i> , 2001, 80, 1174-1185.	0.5	17
59	Comparing systemic properties of ensembles of biological networks by graphical and statistical methods. <i>Bioinformatics</i> , 2000, 16, 527-533.	4.1	50
60	Extending the method of mathematically controlled comparison to include numerical comparisons. <i>Bioinformatics</i> , 2000, 16, 786-798.	4.1	78
61	Effect of Overall Feedback Inhibition in Unbranched Biosynthetic Pathways. <i>Biophysical Journal</i> , 2000, 79, 2290-2304.	0.5	49
62	Lipid peroxidation in mitochondrial inner membranes. I. An integrative kinetic model. <i>Free Radical Biology and Medicine</i> , 1996, 21, 917-943.	2.9	128
63	TCM coding of PPM based modulations for Infrared WLAN's impaired by ISI. , 0, , .		2
64	MATHEMATICAL FORMALISMS BASED ON APPROXIMATED KINETIC REPRESENTATIONS FOR MODELING GENETIC AND METABOLIC PATHWAYS. , 0, , 1-40.		0
65	CAM Models: Lessons and Implications for CAM Evolution. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	3