Rui Alves

List of Publications by Year
in descending order

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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	Tools for kinetic modeling of biochemical networks. Nature Biotechnology, 2006, 24, 667-672.	17.5	180
2	The CHEMDNER corpus of chemicals and drugs and its annotation principles. Journal of Cheminformatics, 2015, 7, S2.	6.1	166
3	Revisiting Trade-offs between Rubisco Kinetic Parameters. Biochemistry, 2019, 58, 3365-3376.	2.5	142
4	Saccharomyces cerevisiae as a Model Organism: A Comparative Study. PLoS ONE, 2011, 6, e16015.	2.5	130
5	Lipid peroxidation in mitochondrial inner membranes. I. An integrative kinetic model. Free Radical Biology and Medicine, 1996, 21, 917-943.	2.9	128
6	Comparative analysis of prototype two-component systems with either bifunctional or monofunctional sensors: differences in molecular structure and physiological function. Molecular Microbiology, 2003, 48, 25-51.	2.5	85
7	Relative Amino Acid Composition Signatures of Organisms and Environments. PLoS ONE, 2013, 8, e77319.	2.5	82
8	Extending the method of mathematically controlled comparison to include numerical comparisons. Bioinformatics, 2000, 16, 786-798.	4.1	78
9	Evolution of Enzymes in Metabolism: A Network Perspective. Journal of Molecular Biology, 2002, 320, 751-770.	4.2	73
10	Evaluating multi-locus phylogenies for species boundaries determination in the genus<i>Diaporthe</i>. PeerJ, 2017, 5, e3120.	2.0	72
11	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
12	Hysteretic and graded responses in bacterial two-component signal transduction. Molecular Microbiology, 2008, 68, 1196-1215.	2.5	60
13	Differential Evolutionary Particle Swarm Optimization (DEEPSO): A Successful Hybrid. , 2013, , .		60
14	Cooperativity and saturation in biochemical networks: A saturable formalism using Taylor series approximations. Biotechnology and Bioengineering, 2007, 97, 1259-1277.	3.3	55
15	Comparing systemic properties of ensembles of biological networks by graphical and statistical methods. Bioinformatics, 2000, 16, 527-533.	4.1	50
16	Effect of Overall Feedback Inhibition in Unbranched Biosynthetic Pathways. Biophysical Journal, 2000, 79, 2290-2304.	0.5	49
17	Evolution and Cellular Function of Monothiol Glutaredoxins: Involvement in Iron-Sulphur Cluster Assembly. Comparative and Functional Genomics, 2004, 5, 328-341.	2.0	47
18	Evolution based on domain combinations: the case of glutaredoxins. BMC Evolutionary Biology, 2009, 9, 66.	3.2	35

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19	Evidence of selection for low cognate amino acid bias in amino acid biosynthetic enzymes. Molecular Microbiology, 2005, 56, 1017-1034.	2.5	34
20	Predictive reconstruction of the mitochondrial iron-sulfur cluster assembly metabolism. II. Role of glutaredoxin Grx5. Proteins: Structure, Function and Bioinformatics, 2004, 57, 481-492.	2.6	32
21	Optimization and evolution in metabolic pathways: Global optimization techniques in Generalized Mass Action models. Journal of Biotechnology, 2010, 149, 141-153.	3.8	32
22	Use of physiological constraints to identify quantitative design principles for gene expression in yeast adaptation to heat shock. BMC Bioinformatics, 2006, 7, 184.	2.6	30
23	Mathematical formalisms based on approximated kinetic representations for modeling genetic and metabolic pathways. Biotechnology and Genetic Engineering Reviews, 2008, 25, 1-40.	6.2	29
24	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
25	Minimization of Biosynthetic Costs in Adaptive Gene Expression Responses of Yeast to Environmental Changes. PLoS Computational Biology, 2010, 6, e1000674.	3.2	25
26	Predictive reconstruction of the mitochondrial iron-sulfur cluster assembly metabolism: I. The role of the protein pair ferredoxin-ferredoxin reductase (Yah1-Arh1). Proteins: Structure, Function and Bioinformatics, 2004, 56, 354-366.	2.6	24
27	Computer-assisted initial diagnosis of rare diseases. PeerJ, 2016, 4, e2211.	2.0	24
28	Steady-state global optimization of metabolic non-linear dynamic models through recasting into power-law canonical models. BMC Systems Biology, 2011, 5, 137.	3.0	21
29	Identification of regulatory structure and kinetic parameters of biochemical networks via mixed-integer dynamic optimization. BMC Systems Biology, 2013, 7, 113.	3.0	21
30	Gobal optimization of hybrid kinetic/FBA models via outer-approximation. Computers and Chemical Engineering, 2015, 72, 325-333.	3.8	21
31	Heuristics for the early/tardy scheduling problem with release dates. International Journal of Production Economics, 2007, 106, 261-274.	8.9	20
32	Quantitative Operating Principles of Yeast Metabolism during Adaptation to Heat Stress. Cell Reports, 2018, 22, 2421-2430.	6.4	19
33	Regulation of the Na+/K+-ATPase Ena1 Expression by Calcineurin/Crz1 under High pH Stress: A Quantitative Study. PLoS ONE, 2016, 11, e0158424.	2.5	19
34	Irreversibility in Unbranched Pathways: Preferred Positions Based on Regulatory Considerations. Biophysical Journal, 2001, 80, 1174-1185.	0.5	17
35	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
36	CheNER: chemical named entity recognizer. Bioinformatics, 2014, 30, 1039-1040.	4.1	15

#	Article	IF	Citations
37	In silico pathway reconstruction: Iron-sulfur cluster biogenesis in Saccharomyces cerevisiae. BMC Systems Biology, 2007, 1, 10.	3.0	13
38	Methods for and results from the study of design principles in molecular systems. Mathematical Biosciences, 2011, 231, 3-18.	1.9	13
39	Special issue on biological design principles. Mathematical Biosciences, 2011, 231, 1-2.	1.9	12
40	Integrating Bioinformatics and Computational Biology: Perspectives and Possibilities for In Silico Network Reconstruction in Molecular Systems Biology. Current Bioinformatics, 2008, 3, 98-129.	1.5	11
41	Biblio-MetReS: A bibliometric network reconstruction application and server. BMC Bioinformatics, 2011, 12, 387.	2.6	11
42	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
43	Rare Disease Discovery: An Optimized Disease Ranking System. IEEE Transactions on Industrial Informatics, 2017, 13, 1184-1192.	11.3	11
44	TControl: A mobile app to follow up tobacco-quitting patients. Computer Methods and Programs in Biomedicine, 2017, 142, 81-89.	4.7	10
45	CheNER: a tool for the identification of chemical entities and their classes in biomedical literature. Journal of Cheminformatics, 2015, 7, S15.	6.1	9
46	Identification of lineâ€specific strategies for improving carotenoid production in synthetic maize through dataâ€driven mathematical modeling. Plant Journal, 2016, 87, 455-471.	5.7	9
47	Two Component Systems: Physiological Effect of a Third Component. PLoS ONE, 2012, 7, e31095.	2.5	9
48	Non-invasive imaging techniques and assessment of carotid vasa vasorum neovascularization: Promises and pitfalls. Trends in Cardiovascular Medicine, 2019, 29, 71-80.	4.9	8
49	AvaliaÃ§Ã£o de sistema de tratamento de dejetos suÃnos instalado no estado de Santa Catarina. Revista Brasileira De Engenharia Agricola E Ambiental, 2012, 16, 745-753.	1.1	6
50	Multi-level Optimization Framework Applied to the Systematic Evaluation of Metabolic Objective Functions. Computer Aided Chemical Engineering, 2014, 33, 961-966.	0.5	6
51	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
52	Biblio-MetReS for user-friendly mining of genes and biological processes in scientific documents. PeerJ, 2014, 2, e276.	2.0	4
53	Multilevel interactions between native and ectopic isoprenoid pathways affect global metabolism in rice. Transgenic Research, 2022, 31, 249-268.	2.4	4
54	Teaching systems biology. IET Systems Biology, 2011, 5, 131-136.	1.5	3

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55	CAM Models: Lessons and Implications for CAM Evolution. Frontiers in Plant Science, 0, 13, .	3.6	3
56	TCM coding of PPM based modulations for Infrared WLAN's impaired by ISI. , 0, , .		2
57	Automatic Methods for Carotid Contrast-Enhanced Ultrasound Imaging Quantification of Adventitial Vasa Vasorum. Ultrasound in Medicine and Biology, 2018, 44, 2780-2792.	1.5	2
58	Maximization of information transmission influences selection of native phosphorelay architectures. PeerJ, 2021, 9, e11558.	2.0	2
59	Database Constraints Applied to Metabolic Pathway Reconstruction Tools. Scientific World Journal, The, 2014, 2014, 1-12.	2.1	1
60	MetReS, an Efficient Database for Genomic Applications. Journal of Computational Biology, 2018, 25, 200-213.	1.6	1
61	EasyModel: user-friendly tool for building and analysis of simple mathematical models in systems biology. Bioinformatics, 2019, 36, 976-977.	4.1	1
62	MetReS: A Metabolic Reconstruction Database for Cloud Computing. , 2014, , .		0
63	Editorial: Foundations of Theoretical Approaches in Systems Biology. Frontiers in Genetics, 2018, 9, 290.	2.3	0
64	EasyModel 1.1: User-friendly Stochastic and Deterministic Simulations for Systems Biology Models. , 2020, , .		0
65	MATHEMATICAL FORMALISMS BASED ON APPROXIMATED KINETIC REPRESENTATIONS FOR MODELING GENETIC AND METABOLIC PATHWAYS. , 0, , 1-40.		0