

Rui Alves

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

2,150
citations

257101

24
h-index

243296

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. <i>Nature Biotechnology</i> , 2006, 24, 667-672. | 9.4 | 180 |
| 2 | The ChEMBL corpus of chemicals and drugs and its annotation principles. <i>Journal of Cheminformatics</i> , 2015, 7, S2. | 2.8 | 166 |
| 3 | Revisiting Trade-offs between Rubisco Kinetic Parameters. <i>Biochemistry</i> , 2019, 58, 3365-3376. | 1.2 | 142 |
| 4 | <i>Saccharomyces cerevisiae</i> as a Model Organism: A Comparative Study. <i>PLoS ONE</i> , 2011, 6, e16015. | 1.1 | 130 |
| 5 | Lipid peroxidation in mitochondrial inner membranes. I. An integrative kinetic model. <i>Free Radical Biology and Medicine</i> , 1996, 21, 917-943. | 1.3 | 128 |
| 6 | 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. | 1.2 | 85 |
| 7 | Relative Amino Acid Composition Signatures of Organisms and Environments. <i>PLoS ONE</i> , 2013, 8, e77319. | 1.1 | 82 |
| 8 | Extending the method of mathematically controlled comparison to include numerical comparisons. <i>Bioinformatics</i> , 2000, 16, 786-798. | 1.8 | 78 |
| 9 | Evolution of Enzymes in Metabolism: A Network Perspective. <i>Journal of Molecular Biology</i> , 2002, 320, 751-770. | 2.0 | 73 |
| 10 | Evaluating multi-locus phylogenies for species boundaries determination in the genus <i>Diaporthe</i> . <i>PeerJ</i> , 2017, 5, e3120. | 0.9 | 72 |
| 11 | An <i>in vitro</i> system for the rapid functional characterization of genes involved in carotenoid biosynthesis and accumulation. <i>Plant Journal</i> , 2014, 77, 464-475. | 2.8 | 63 |
| 12 | Hysteretic and graded responses in bacterial two-component signal transduction. <i>Molecular Microbiology</i> , 2008, 68, 1196-1215. | 1.2 | 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. <i>Biotechnology and Bioengineering</i> , 2007, 97, 1259-1277. | 1.7 | 55 |
| 15 | Comparing systemic properties of ensembles of biological networks by graphical and statistical methods. <i>Bioinformatics</i> , 2000, 16, 527-533. | 1.8 | 50 |
| 16 | Effect of Overall Feedback Inhibition in Unbranched Biosynthetic Pathways. <i>Biophysical Journal</i> , 2000, 79, 2290-2304. | 0.2 | 49 |
| 17 | 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 |
| 18 | Evolution based on domain combinations: the case of glutaredoxins. <i>BMC Evolutionary Biology</i> , 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. <i>Molecular Microbiology</i> , 2005, 56, 1017-1034. | 1.2 | 34 |
| 20 | 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. | 1.5 | 32 |
| 21 | Optimization and evolution in metabolic pathways: Global optimization techniques in Generalized Mass Action models. <i>Journal of Biotechnology</i> , 2010, 149, 141-153. | 1.9 | 32 |
| 22 | 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. | 1.2 | 30 |
| 23 | Mathematical formalisms based on approximated kinetic representations for modeling genetic and metabolic pathways. <i>Biotechnology and Genetic Engineering Reviews</i> , 2008, 25, 1-40. | 2.4 | 29 |
| 24 | Targeted transcriptomic and metabolic profiling reveals temporal bottlenecks in the maize carotenoid pathway that may be addressed by multigene engineering. <i>Plant Journal</i> , 2013, 75, 441-455. | 2.8 | 27 |
| 25 | Minimization of Biosynthetic Costs in Adaptive Gene Expression Responses of Yeast to Environmental Changes. <i>PLoS Computational Biology</i> , 2010, 6, e1000674. | 1.5 | 25 |
| 26 | 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. | 1.5 | 24 |
| 27 | Computer-assisted initial diagnosis of rare diseases. <i>PeerJ</i> , 2016, 4, e2211. | 0.9 | 24 |
| 28 | 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 |
| 29 | Identification of regulatory structure and kinetic parameters of biochemical networks via mixed-integer dynamic optimization. <i>BMC Systems Biology</i> , 2013, 7, 113. | 3.0 | 21 |
| 30 | Global optimization of hybrid kinetic/FBA models via outer-approximation. <i>Computers and Chemical Engineering</i> , 2015, 72, 325-333. | 2.0 | 21 |
| 31 | Heuristics for the early/tardy scheduling problem with release dates. <i>International Journal of Production Economics</i> , 2007, 106, 261-274. | 5.1 | 20 |
| 32 | Quantitative Operating Principles of Yeast Metabolism during Adaptation to Heat Stress. <i>Cell Reports</i> , 2018, 22, 2421-2430. | 2.9 | 19 |
| 33 | Regulation of the Na ⁺ /K ⁺ -ATPase Ena1 Expression by Calcineurin/Crz1 under High pH Stress: A Quantitative Study. <i>PLoS ONE</i> , 2016, 11, e0158424. | 1.1 | 19 |
| 34 | Irreversibility in Unbranched Pathways: Preferred Positions Based on Regulatory Considerations. <i>Biophysical Journal</i> , 2001, 80, 1174-1185. | 0.2 | 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. <i>PeerJ</i> , 2015, 3, e1183. | 0.9 | 16 |
| 36 | CheNER: chemical named entity recognizer. <i>Bioinformatics</i> , 2014, 30, 1039-1040. | 1.8 | 15 |

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|----|--|-----|-----------|
| 37 | In silico pathway reconstruction: Iron-sulfur cluster biogenesis in <i>Saccharomyces cerevisiae</i> . <i>BMC Systems Biology</i> , 2007, 1, 10. | 3.0 | 13 |
| 38 | Methods for and results from the study of design principles in molecular systems. <i>Mathematical Biosciences</i> , 2011, 231, 3-18. | 0.9 | 13 |
| 39 | Special issue on biological design principles. <i>Mathematical Biosciences</i> , 2011, 231, 1-2. | 0.9 | 12 |
| 40 | 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. | 0.7 | 11 |
| 41 | Biblio-MetReS: A bibliometric network reconstruction application and server. <i>BMC Bioinformatics</i> , 2011, 12, 387. | 1.2 | 11 |
| 42 | S-PC: An e-treatment application for management of smoke-quitting patients. <i>Computer Methods and Programs in Biomedicine</i> , 2014, 115, 33-45. | 2.6 | 11 |
| 43 | Rare Disease Discovery: An Optimized Disease Ranking System. <i>IEEE Transactions on Industrial Informatics</i> , 2017, 13, 1184-1192. | 7.2 | 11 |
| 44 | TControl: A mobile app to follow up tobacco-quitting patients. <i>Computer Methods and Programs in Biomedicine</i> , 2017, 142, 81-89. | 2.6 | 10 |
| 45 | CheNER: a tool for the identification of chemical entities and their classes in biomedical literature. <i>Journal of Cheminformatics</i> , 2015, 7, S15. | 2.8 | 9 |
| 46 | 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. | 2.8 | 9 |
| 47 | Two Component Systems: Physiological Effect of a Third Component. <i>PLoS ONE</i> , 2012, 7, e31095. | 1.1 | 9 |
| 48 | Non-invasive imaging techniques and assessment of carotid vasa vasorum neovascularization: Promises and pitfalls. <i>Trends in Cardiovascular Medicine</i> , 2019, 29, 71-80. | 2.3 | 8 |
| 49 | Avaliação de sistema de tratamento de dejetos suínos instalado no estado de Santa Catarina. <i>Revista Brasileira De Engenharia Agrícola E Ambiental</i> , 2012, 16, 745-753. | 0.4 | 6 |
| 50 | Multi-level Optimization Framework Applied to the Systematic Evaluation of Metabolic Objective Functions. <i>Computer Aided Chemical Engineering</i> , 2014, 33, 961-966. | 0.3 | 6 |
| 51 | Lipid fraction quality of milk produced by Minhota (Portuguese autochthonous breed) compared to Holstein Friesian cow's. <i>Journal of the Science of Food and Agriculture</i> , 2012, 92, 2994-3001. | 1.7 | 4 |
| 52 | Biblio-MetReS for user-friendly mining of genes and biological processes in scientific documents. <i>PeerJ</i> , 2014, 2, e276. | 0.9 | 4 |
| 53 | Multilevel interactions between native and ectopic isoprenoid pathways affect global metabolism in rice. <i>Transgenic Research</i> , 2022, 31, 249-268. | 1.3 | 4 |
| 54 | Teaching systems biology. <i>IET Systems Biology</i> , 2011, 5, 131-136. | 0.8 | 3 |

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|----|---|-----|-----------|
| 55 | CAM Models: Lessons and Implications for CAM Evolution. <i>Frontiers in Plant Science</i> , 0, 13, . | 1.7 | 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. <i>Ultrasound in Medicine and Biology</i> , 2018, 44, 2780-2792. | 0.7 | 2 |
| 58 | Maximization of information transmission influences selection of native phosphorelay architectures. <i>PeerJ</i> , 2021, 9, e11558. | 0.9 | 2 |
| 59 | Database Constraints Applied to Metabolic Pathway Reconstruction Tools. <i>Scientific World Journal</i> , The, 2014, 2014, 1-12. | 0.8 | 1 |
| 60 | MetReS, an Efficient Database for Genomic Applications. <i>Journal of Computational Biology</i> , 2018, 25, 200-213. | 0.8 | 1 |
| 61 | EasyModel: user-friendly tool for building and analysis of simple mathematical models in systems biology. <i>Bioinformatics</i> , 2019, 36, 976-977. | 1.8 | 1 |
| 62 | MetReS: A Metabolic Reconstruction Database for Cloud Computing. , 2014, , . | | 0 |
| 63 | Editorial: Foundations of Theoretical Approaches in Systems Biology. <i>Frontiers in Genetics</i> , 2018, 9, 290. | 1.1 | 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 |