Isabel Rocha

List of Publications by Year in Descending Order

143 papers	2,803 citations	28 h-index	49 g-index
156 ext. papers	3,443 ext. citations	4.8 avg, IF	5.22 L-index

#	Paper	IF	Citations
143	Inclusion of maintenance energy improves the intracellular flux predictions of CHO. *PLoS Computational Biology*, **2021**, 17, e1009022	5	0
142	Enhancing acetic acid and 5-hydroxymethyl furfural tolerance of C. saccharoperbutylacetonicum through adaptive laboratory evolution. *Process Biochemistry*, **2021**, 101, 179-189	4.8	4
141	Model-guided development of an evolutionarily stable yeast chassis. *Molecular Systems Biology*, **2021**, 17, e10253	12.2	3
140	Metabolic engineering strategies for butanol production in Escherichia coli. *Biotechnology and Bioengineering*, **2020**, 117, 2571-2587	4.9	5
139	Key Challenges in Designing CHO Chassis Platforms. *Processes*, **2020**, 8, 643	2.9	5
138	MEMOTE for standardized genome-scale metabolic model testing. *Nature Biotechnology*, **2020**, 38, 272-276	44.5	121
137	A review of methods for the reconstruction and analysis of integrated genome-scale models of metabolism and regulation. *Biochemical Society Transactions*, **2020**, 48, 1889-1903	5.1	6
136	Genome-Scale Metabolic Model of the Human Pathogen : A Promising Platform for Drug Target Prediction. *Journal of Fungi (Basel, Switzerland)*, **2020**, 6,	5.6	6
135	SamPler - a novel method for selecting parameters for gene functional annotation routines. *BMC Bioinformatics*, **2019**, 20, 454	3.6	3
134	Modulation of the central carbon metabolism of Corynebacterium glutamicum improves malonyl-CoA availability and increases plant polyphenol synthesis. *Biotechnology and Bioengineering*, **2019**, 116, 1380-1391	4.9	22
133	Turnover Dependent Phenotypic Simulation: A Quantitative Constraint-Based Simulation Method That Accommodates All Main Strain Design Strategies. *ACS Synthetic Biology*, **2019**, 8, 976-988	5.7	
132	Comparison of pathway analysis and constraint-based methods for cell factory design. *BMC Bioinformatics*, **2019**, 20, 350	3.6	1
131	iDS372, a Phenotypically Reconciled Model for the Metabolism of Strain R6. *Frontiers in Microbiology*, **2019**, 10, 1283	5.7	6
130	Genome-wide sequencing and metabolic annotation of Pythium irregulare CBS 494.86: understanding Eicosapentaenoic acid production. *BMC Biotechnology*, **2019**, 19, 41	3.5	4
129	Discovery and implementation of a novel pathway for -butanol production via 2-oxoglutarate. *Biotechnology for Biofuels*, **2019**, 12, 230	7.8	9
128	Microbial Hosts as a Promising Platform for Polyphenol Production **2019**, 71-103		2
127	Identification and Microbial Production of the Raspberry Phenol Salidroside that Is Active against Huntington's Disease. *Plant Physiology*, **2019**, 179, 969-985	6.6	17

126	Mapping Salmonella typhimurium pathways using C metabolic flux analysis. *Metabolic Engineering*, **2019**, 52, 303-314	9.7	1
125	Metabolite secretion in microorganisms: the theory of metabolic overflow put to the test. *Metabolomics*, **2018**, 14, 43	4.7	29
124	BacHBerry: BACterial Hosts for production of Bioactive phenolics from bERRY fruits. *Phytochemistry Reviews*, **2018**, 17, 291-326	7.7	12
123	Quantitative physiology and elemental composition of Kluyveromyces lactis CBS 2359 during growth on glucose at different specific growth rates. *Antonie Van Leeuwenhoek*, **2018**, 111, 183-195	2.1	2
122	Methods for automated genome-scale metabolic model reconstruction. *Biochemical Society Transactions*, **2018**, 46, 931-936	5.1	33
121	Heterologous production of resveratrol in bacterial hosts: current status and perspectives. *World Journal of Microbiology and Biotechnology*, **2018**, 34, 122	4.4	23
120	Reconstruction of a genome-scale metabolic model for Actinobacillus succinogenes 130Z. *BMC Systems Biology*, **2018**, 12, 61	3.5	12
119	Reconstructing High-Quality Large-Scale Metabolic Models with merlin. *Methods in Molecular Biology*, **2018**, 1716, 1-36	1.4	10
118	Analyzing and Designing Cell Factories with OptFlux. *Methods in Molecular Biology*, **2018**, 1716, 37-76	1.4	3
117	An adsorptive bioprocess for production and recovery of resveratrol with Corynebacterium glutamicum. *Journal of Chemical Technology and Biotechnology*, **2018**, 93, 1661-1668	3.5	10
116	Impact of the cultivation strategy on resveratrol production from glucose in engineered Corynebacterium glutamicum. *Journal of Biotechnology*, **2018**, 265, 70-75	3.7	24
115	Production of mannosylglycerate in Saccharomyces cerevisiae by metabolic engineering and bioprocess optimization. *Microbial Cell Factories*, **2018**, 17, 178	6.4	6
114	Metabolic models and gene essentiality data reveal essential and conserved metabolism in prokaryotes. *PLoS Computational Biology*, **2018**, 14, e1006556	5	12
113	Genome-Wide Semi-Automated Annotation of Transporter Systems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2017**, 14, 443-456	3	10
112	Development of a Framework for Metabolic Pathway Analysis-Driven Strain Optimization Methods. *Interdisciplinary Sciences, Computational Life Sciences*, **2017**, 9, 46-55	3.5	1
111	Integration of Biomass Formulations of Genome-Scale Metabolic Models with Experimental Data Reveals Universally Essential Cofactors in Prokaryotes. *Metabolic Engineering*, **2017**, 39, 200-208	9.7	51
110	Identification of robust strain designs via tandem pFBA/LMOMA phenotype prediction **2017**,		1
109	Genome-scale modeling of yeast: chronology, applications and critical perspectives. *FEMS Yeast Research*, **2017**, 17,	3.1	33

108	Yeast metabolic chassis designs for diverse biotechnological products. *Scientific Reports*, **2016**, 6, 29694	4.9	22
107	Rhodococcus opacus B4: a promising bacterium for production of biofuels and biobased chemicals. *AMB Express*, **2016**, 6, 35	4.1	35
106	A Computation Tool for the Estimation of Biomass Composition from Genomic and Transcriptomic Information. *Advances in Intelligent Systems and Computing*, **2016**, 161-169	0.4	2
105	Development of an Integrated Framework for Minimal Cut Set Enumeration in Constraint-Based Models. *Advances in Intelligent Systems and Computing*, **2016**, 193-201	0.4	1
104	Improving the flux distributions simulated with genome-scale metabolic models of. *Metabolic Engineering Communications*, **2016**, 3, 153-163	6.5	32
103	In Silico Constraint-Based Strain Optimization Methods: the Quest for Optimal Cell Factories. *Microbiology and Molecular Biology Reviews*, **2016**, 80, 45-67	13.2	81
102	Estimation of biomass composition from genomic and transcriptomic information. *Journal of Integrative Bioinformatics*, **2016**, 13, 285	3.8	4
101	Estimation of biomass composition from genomic and transcriptomic information. *Journal of Integrative Bioinformatics*, **2016**, 13, 1-14	3.8	3
100	A Comparative Proteome Analysis of Δ Mutant Cells. *Frontiers in Bioengineering and Biotechnology*, **2016**, 4, 78	5.8	3
99	Reconstruction of the Regulatory Network for Bacillus subtilis and Reconciliation with Gene Expression Data. *Frontiers in Microbiology*, **2016**, 7, 275	5.7	7
98	Computing and Applying Atomic Regulons to Understand Gene Expression and Regulation. *Frontiers in Microbiology*, **2016**, 7, 1819	5.7	7
97	Stoichiometric Representation of Gene-Protein-Reaction Associations Leverages Constraint-Based Analysis from Reaction to Gene-Level Phenotype Prediction. *PLoS Computational Biology*, **2016**, 12, e1005140	5	27
96	A Comparative Analysis of Dynamic Models of the Central Carbon Metabolism of Escherichia coli. *IFAC-PapersOnLine*, **2016**, 49, 270-276	0.7	2
95	Current state and challenges for dynamic metabolic modeling. *Current Opinion in Microbiology*, **2016**, 33, 97-104	7.9	30
94	A Text Mining Approach for the Extraction of Kinetic Information from Literature. *Advances in Intelligent Systems and Computing*, **2015**, 89-98	0.4	
93	Reconstructing genome-scale metabolic models with merlin. *Nucleic Acids Research*, **2015**, 43, 3899-910	20.1	82
92	Development and application of efficient pathway enumeration algorithms for metabolic engineering applications. *Computer Methods and Programs in Biomedicine*, **2015**, 118, 134-46	6.9	7
91	Salmonella typhimurium and Escherichia coli dissimilarity: Closely related bacteria with distinct metabolic profiles. *Biotechnology Progress*, **2015**, 31, 1217-25	2.8	10

90	Modeling the Contribution of Allosteric Regulation for Flux Control in the Central Carbon Metabolism of E. coli. *Frontiers in Bioengineering and Biotechnology*, **2015**, 3, 154	5.8	21
89	Extracting kinetic information from literature with KineticRE. *Journal of Integrative Bioinformatics*, **2015**, 12, 56-68	3.8	
88	Optimization of fed-batch fermentation processes with bio-inspired algorithms. *Expert Systems With Applications*, **2014**, 41, 2186-2195	7.8	39
87	A kinetic model for curcumin production in Escherichia coli. *BioSystems*, **2014**, 125, 16-21	1.9	7
86	Systems biology perspectives on minimal and simpler cells. *Microbiology and Molecular Biology Reviews*, **2014**, 78, 487-509	13.2	42
85	iOD907, the first genome-scale metabolic model for the milk yeast Kluyveromyces lactis. *Biotechnology Journal*, **2014**, 9, 776-90	5.6	31
84	Genome-scale bacterial transcriptional regulatory networks: reconstruction and integrated analysis with metabolic models. *Briefings in Bioinformatics*, **2014**, 15, 592-611	13.4	26
83	Dietary Sugars Analysis: Quantification of Fructooligossacharides during Fermentation by HPLC-RI Method. *Frontiers in Nutrition*, **2014**, 1, 11	6.2	10
82	CBFA: phenotype prediction integrating metabolic models with constraints derived from experimental data. *BMC Systems Biology*, **2014**, 8, 123	3.5	6
81	Genome-wide metabolic re-annotation of Ashbya gossypii: new insights into its metabolism through a comparative analysis with Saccharomyces cerevisiae and Kluyveromyces lactis. *BMC Genomics*, **2014**, 15, 810	4.5	11
80	Evaluating Pathway Enumeration Algorithms in Metabolic Engineering Case Studies. *Advances in Intelligent Systems and Computing*, **2014**, 215-223	0.4	
79	Yeast metabolomics: sample preparation for a GC/MS-based analysis. *Methods in Molecular Biology*, **2014**, 1152, 197-207	1.4	2
78	TNA4OptFlux--a software tool for the analysis of strain optimization strategies. *BMC Research Notes*, **2013**, 6, 175	2.3	1
77	Assignment of Novel Functions to Helicobacter pylori 26695 Genome. *Advances in Intelligent Systems and Computing*, **2013**, 29-36	0.4	
76	Evolutionary computation for predicting optimal reaction knockouts and enzyme modulation strategies **2013**,		1
75	An integrated framework for strain optimization **2013**,		3
74	Metabolic responses to recombinant bioprocesses in Escherichia coli. *Journal of Biotechnology*, **2013**, 164, 396-408	3.7	59
73	Genome scale metabolic network reconstruction of the pathogen Enterococcus faecalis. *IFAC Postprint Volumes IPPV / International Federation of Automatic Control*, **2013**, 46, 131-136		1

72	Re-annotation of the genome sequence of Helicobacter pylori 26695. *Journal of Integrative Bioinformatics*, **2013**, 10, 66-78	3.8	11
71	Identification of metabolic engineering targets through analysis of optimal and sub-optimal routes. *PLoS ONE*, **2013**, 8, e61648	3.7	15
70	Re-annotation of the genome sequence of Helicobacter pylori 26695. *Journal of Integrative Bioinformatics*, **2013**, 10, 233	3.8	10
69	Exploring the gap between dynamic and constraint-based models of metabolism. *Metabolic Engineering*, **2012**, 14, 112-9	9.7	26
68	Optimization approaches for the in silico discovery of optimal targets for gene over/underexpression. *Journal of Computational Biology*, **2012**, 19, 102-14	1.7	13
67	New improved method for fructooligosaccharides production by Aureobasidium pullulans. *Carbohydrate Polymers*, **2012**, 89, 1174-9	10.3	60
66	Influence of the RelA Activity on E. coli Metabolism by Metabolite Profiling of Glucose-Limited Chemostat Cultures. *Metabolites*, **2012**, 2, 717-32	5.6	8
65	State and specific growth estimation in heterologous protein production by Pichia pastoris. *AICHE Journal*, **2012**, 58, 2966-2979	3.6	11
64	Random sampling of elementary flux modes in large-scale metabolic networks. *Bioinformatics*, **2012**, 28, i515-i521	7.2	53
63	Genome-wide metabolic (re-) annotation of Kluyveromyces lactis. *BMC Genomics*, **2012**, 13, 517	4.5	12
62	Optimization of culture conditions to improve Helicobacter pylori growth in Ham's F-12 medium by response surface methodology. *International Journal of Immunopathology and Pharmacology*, **2012**, 25, 901-9	3	1
61	An integrated computational environment for elementary modes analysis of biochemical networks. *International Journal of Data Mining and Bioinformatics*, **2012**, 6, 382-95	0.5	4
60	Computational Tools for Strain Optimization by Tuning the Optimal Level of Gene Expression. *Advances in Intelligent and Soft Computing*, **2012**, 251-258		1
59	Metabolic footprint analysis of recombinant Escherichia coli strains during fed-batch fermentations. *Molecular BioSystems*, **2011**, 7, 899-910		27
58	A Study of the Short and Long-term Regulation of E. coli Metabolic Pathways. *Journal of Integrative Bioinformatics*, **2011**, 8, 195-209	3.8	7
57	Identification of minimal metabolic pathway models consistent with phenotypic data. *Journal of Process Control*, **2011**, 21, 1483-1492	3.9	7
56	Critical perspective on the consequences of the limited availability of kinetic data in metabolic dynamic modelling. *IET Systems Biology*, **2011**, 5, 157-63	1.4	17
55	Stringent response of Escherichia coli: revisiting the bibliome using literature mining. *Microbial Informatics and Experimentation*, **2011**, 1, 14		9

54	Modeling formalisms in Systems Biology. *AMB Express*, **2011**, 1, 45	4.1	107
53	A Systematic Modeling Approach to Elucidate the Triggering of the Stringent Response in Recombinant E. coli Systems. *Advances in Intelligent and Soft Computing*, **2011**, 313-320		1
52	Semantic annotation of biological concepts interplaying microbial cellular responses. *BMC Bioinformatics*, **2011**, 12, 460	3.6	5
51	A computational tool for the simulation and optimization of microbial strains accounting integrated metabolic/regulatory information. *BioSystems*, **2011**, 103, 435-41	1.9	15
50	Challenges in integrating Escherichia coli molecular biology data. *Briefings in Bioinformatics*, **2011**, 12, 91-103	13.4	4
49	Highlighting Metabolic Strategies Using Network Analysis over Strain Optimization Results. *Lecture Notes in Computer Science*, **2011**, 109-120	0.9	
48	Interpreting the Regulatory Interplay in E. coli Metabolic Pathways. *Advances in Intelligent and Soft Computing*, **2011**, 303-312		
47	A study of the short and long-term regulation of E. coli metabolic pathways. *Journal of Integrative Bioinformatics*, **2011**, 8, 183	3.8	1
46	Selection of Elementary Modes for Bioprocess Control. *IFAC Postprint Volumes IPPV / International Federation of Automatic Control*, **2010**, 43, 156-161		13
45	Evaluating the integration of proteomic data for the prediction of intracellular fluxes after knockout experiments. *IFAC Postprint Volumes IPPV / International Federation of Automatic Control*, **2010**, 43, 114-119		
44	Merlin: Metabolic Models Reconstruction using Genome-Scale Information*. *IFAC Postprint Volumes IPPV / International Federation of Automatic Control*, **2010**, 43, 120-125		3
43	Applying a Metabolic Footprinting Approach to Characterize the Impact of the Recombinant Protein Production in Escherichia coli. *Advances in Intelligent and Soft Computing*, **2010**, 193-200		1
42	OptFlux: an open-source software platform for in silico metabolic engineering. *BMC Systems Biology*, **2010**, 4, 45	3.5	258
41	BioDR: Semantic indexing networks for biomedical document retrieval. *Expert Systems With Applications*, **2010**, 37, 3444-3453	7.8	9
40	Hybrid dynamic modeling of Escherichia coli central metabolic network combining Michaelis-Menten and approximate kinetic equations. *BioSystems*, **2010**, 100, 150-7	1.9	40
39	Virtual laboratories in (bio)chemical engineering education. *Education for Chemical Engineers*, **2010**, 5, e22-e27	2.4	38
38	Metaheuristics for Strain Optimization Using Transcriptional Information Enriched Metabolic Models. *Lecture Notes in Computer Science*, **2010**, 205-216	0.9	6
37	Enhancing Elementary Flux Modes Analysis Using Filtering Techniques in an Integrated Environment. *Advances in Intelligent and Soft Computing*, **2010**, 217-224		

36	A Dynamical Model for the Fermentative Production of Fructooligosaccharides. *Computer Aided Chemical Engineering*, **2009**, 1827-1832	0.6	7
35	A Critical Review on Modelling Formalisms and Simulation Tools in Computational Biosystems. *Lecture Notes in Computer Science*, **2009**, 1063-1070	0.9	1
34	@Note: a workbench for biomedical text mining. *Journal of Biomedical Informatics*, **2009**, 42, 710-20	10.2	28
33	Assessment of physiological conditions in E. coli fermentations by epifluorescent microscopy and image analysis. *Biotechnology Progress*, **2009**, 25, 882-91	2.8	10
32	Monitoring of fed-batch E. coli fermentations with software sensors. *Bioprocess and Biosystems Engineering*, **2009**, 32, 381-8	3.7	43
31	Comparison of adsorption equilibrium of fructose, glucose and sucrose on potassium gel-type and macroporous sodium ion-exchange resins. *Analytica Chimica Acta*, **2009**, 654, 71-6	6.6	49
30	Galacto-oligosaccharides production during lactose hydrolysis by free Aspergillus oryzae β-galactosidase and immobilized on magnetic polysiloxane-polyvinyl alcohol. *Food Chemistry*, **2009**, 115, 92-99	8.5	148
29	UV spectrophotometry method for the monitoring of galacto-oligosaccharides production. *Food Chemistry*, **2009**, 113, 246-252	8.5	32
28	Large Scale Dynamic Model Reconstruction for the Central Carbon Metabolism of Escherichia coli. *Lecture Notes in Computer Science*, **2009**, 1079-1083	0.9	1
27	Data Integration Issues in the Reconstruction of the Genome-Scale Metabolic Model of Zymomonas Mobillis. *Advances in Soft Computing*, **2009**, 92-101		1
26	Modelling Fed-Batch Fermentation Processes: An Approach Based on Artificial Neural Networks. *Advances in Soft Computing*, **2009**, 30-39		3
25	Evolutionary Approaches for Strain Optimization Using Dynamic Models under a Metabolic Engineering Perspective. *Lecture Notes in Computer Science*, **2009**, 140-151	0.9	2
24	A Software Tool for the Simulation and Optimization of Dynamic Metabolic Models. *Lecture Notes in Computer Science*, **2009**, 1071-1078	0.9	
23	Modelling of Biotechnological Processes An Approach Based on Artificial Neural Networks. *Studies in Computational Intelligence*, **2009**, 311-332	0.8	
22	Biomedical Text Mining Applied to Document Retrieval and Semantic Indexing. *Lecture Notes in Computer Science*, **2009**, 954-963	0.9	
21	Natural computation meta-heuristics for the in silico optimization of microbial strains. *BMC Bioinformatics*, **2008**, 9, 499	3.6	75
20	Evaluating evolutionary multiobjective algorithms for the in silico optimization of mutant strains **2008**,		8
19	Design and application of genome-scale reconstructed metabolic models. *Methods in Molecular Biology*, **2008**, 416, 409-31	1.4	40

#	Reference	IF	Citations
18	IMPLEMENTATION OF A SPECIFIC RATE CONTROLLER IN A FED-BATCH E. COLI FERMENTATION. *IFAC Postprint Volumes IPPV / International Federation of Automatic Control*, **2008**, 41, 15565-15570		11
17	Differential Evolution for the Offline and Online Optimization of Fed-Batch Fermentation Processes. *Studies in Computational Intelligence*, **2008**, 299-317	0.8	5
16	Optimization of Bacterial Strains with Variable-Sized Evolutionary Algorithms **2007**,		1
15	Evaluating Simulated Annealing Algorithms in the Optimization of Bacterial Strains **2007**, 473-484		1
14	Evaluating Evolutionary Algorithms and Differential Evolution for the Online Optimization of Fermentation Processes **2007**, 236-246		4
13	Application of a genome-scale metabolic model to the inference of nutritional requirements and metabolic bottlenecks during recombinant protein production in Escherichia coli. *Microbial Cell Factories*, **2006**, 5, P52	6.4	2
12	DESIGN OF ON-LINE STATE ESTIMATORS FOR A RECOMBINANT E. COLI FED-BATCH FERMENTATION. *IFAC Postprint Volumes IPPV / International Federation of Automatic Control*, **2005**, 38, 67-72		2
11	Evolutionary programming as a platform for in silico metabolic engineering. *BMC Bioinformatics*, **2005**, 6, 308	3.6	312
10	Evolutionary Algorithms for Static and Dynamic Optimization of Fed-batch Fermentation Processes **2005**, 288-291		6
9	Evolutionary Algorithms for Optimal Control in Fed-Batch Fermentation Processes. *Lecture Notes in Computer Science*, **2004**, 84-93	0.9	10
8	Identification of Yield Coefficients in an E.coli Model An Optimal Experimental Design Using Genetic Algorithms. *IFAC Postprint Volumes IPPV / International Federation of Automatic Control*, **2004**, 37, 43-48		
7	Estimation of multiple biomass growth rates and biomass concentration in a class of bioprocesses. *Bioprocess and Biosystems Engineering*, **2003**, 25, 395-406	3.7	19
6	On-line simultaneous monitoring of glucose and acetate with FIA during high cell density fermentation of recombinant E. coli. *Analytica Chimica Acta*, **2002**, 462, 293-304	6.6	40
5	An Integrated System for Advanced Monitoring and Control of Fed-Batch Fermevtations of Recombinant E. coli. *IFAC Postprint Volumes IPPV / International Federation of Automatic Control*, **2001**, 34, 349-354		
4	A Comparison of Algorithms for the Optimization of Fermentation Processes		13
3	A new representation in evolutionary algorithms for the optimization of bioprocesses		2
2	Memote: A community driven effort towards a standardized genome-scale metabolic model test suite		26
1	iEC7871 Quercus suber model: the first multi-tissue diel cycle genome-scale metabolic model of a woody tree		2