

# Isabel Rocha

## List of Publications by Citations

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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	Evolutionary programming as a platform for in silico metabolic engineering. <i>BMC Bioinformatics</i> , <b>2005</b> , 6, 308	3.6	312
142	OptFlux: an open-source software platform for in silico metabolic engineering. <i>BMC Systems Biology</i> , <b>2010</b> , 4, 45	3.5	258
141	Galacto-oligosaccharides production during lactose hydrolysis by free <i>Aspergillus oryzae</i> galactosidase and immobilized on magnetic polysiloxane-polyvinyl alcohol. <i>Food Chemistry</i> , <b>2009</b> , 115, 92-99	8.5	148
140	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 272-276	14.5	121
139	Modeling formalisms in Systems Biology. <i>AMB Express</i> , <b>2011</b> , 1, 45	4.1	107
138	Reconstructing genome-scale metabolic models with merlin. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 3899-910	20.1	82
137	In Silico Constraint-Based Strain Optimization Methods: the Quest for Optimal Cell Factories. <i>Microbiology and Molecular Biology Reviews</i> , <b>2016</b> , 80, 45-67	13.2	81
136	Natural computation meta-heuristics for the in silico optimization of microbial strains. <i>BMC Bioinformatics</i> , <b>2008</b> , 9, 499	3.6	75
135	New improved method for fructooligosaccharides production by <i>Aureobasidium pullulans</i> . <i>Carbohydrate Polymers</i> , <b>2012</b> , 89, 1174-9	10.3	60
134	Metabolic responses to recombinant bioprocesses in <i>Escherichia coli</i> . <i>Journal of Biotechnology</i> , <b>2013</b> , 164, 396-408	3.7	59
133	Random sampling of elementary flux modes in large-scale metabolic networks. <i>Bioinformatics</i> , <b>2012</b> , 28, i515-i521	7.2	53
132	Integration of Biomass Formulations of Genome-Scale Metabolic Models with Experimental Data Reveals Universally Essential Cofactors in Prokaryotes. <i>Metabolic Engineering</i> , <b>2017</b> , 39, 200-208	9.7	51
131	Comparison of adsorption equilibrium of fructose, glucose and sucrose on potassium gel-type and macroporous sodium ion-exchange resins. <i>Analytica Chimica Acta</i> , <b>2009</b> , 654, 71-6	6.6	49
130	Monitoring of fed-batch <i>E. coli</i> fermentations with software sensors. <i>Bioprocess and Biosystems Engineering</i> , <b>2009</b> , 32, 381-8	3.7	43
129	Systems biology perspectives on minimal and simpler cells. <i>Microbiology and Molecular Biology Reviews</i> , <b>2014</b> , 78, 487-509	13.2	42
128	Hybrid dynamic modeling of <i>Escherichia coli</i> central metabolic network combining Michaelis-Menten and approximate kinetic equations. <i>BioSystems</i> , <b>2010</b> , 100, 150-7	1.9	40
127	Design and application of genome-scale reconstructed metabolic models. <i>Methods in Molecular Biology</i> , <b>2008</b> , 416, 409-31	1.4	40

126	On-line simultaneous monitoring of glucose and acetate with FIA during high cell density fermentation of recombinant E. coli. <i>Analytica Chimica Acta</i> , <b>2002</b> , 462, 293-304	6.6	40
125	Optimization of fed-batch fermentation processes with bio-inspired algorithms. <i>Expert Systems With Applications</i> , <b>2014</b> , 41, 2186-2195	7.8	39
124	Virtual laboratories in (bio)chemical engineering education. <i>Education for Chemical Engineers</i> , <b>2010</b> , 5, e22-e27	2.4	38
123	Rhodococcus opacus B4: a promising bacterium for production of biofuels and biobased chemicals. <i>AMB Express</i> , <b>2016</b> , 6, 35	4.1	35
122	Methods for automated genome-scale metabolic model reconstruction. <i>Biochemical Society Transactions</i> , <b>2018</b> , 46, 931-936	5.1	33
121	Genome-scale modeling of yeast: chronology, applications and critical perspectives. <i>FEMS Yeast Research</i> , <b>2017</b> , 17,	3.1	33
120	Improving the flux distributions simulated with genome-scale metabolic models of. <i>Metabolic Engineering Communications</i> , <b>2016</b> , 3, 153-163	6.5	32
119	UV spectrophotometry method for the monitoring of galacto-oligosaccharides production. <i>Food Chemistry</i> , <b>2009</b> , 113, 246-252	8.5	32
118	iOD907, the first genome-scale metabolic model for the milk yeast <i>Kluyveromyces lactis</i> . <i>Biotechnology Journal</i> , <b>2014</b> , 9, 776-90	5.6	31
117	Current state and challenges for dynamic metabolic modeling. <i>Current Opinion in Microbiology</i> , <b>2016</b> , 33, 97-104	7.9	30
116	Metabolite secretion in microorganisms: the theory of metabolic overflow put to the test. <i>Metabolomics</i> , <b>2018</b> , 14, 43	4.7	29
115	@Note: a workbench for biomedical text mining. <i>Journal of Biomedical Informatics</i> , <b>2009</b> , 42, 710-20	10.2	28
114	Metabolic footprint analysis of recombinant <i>Escherichia coli</i> strains during fed-batch fermentations. <i>Molecular BioSystems</i> , <b>2011</b> , 7, 899-910		27
113	Stoichiometric Representation of Gene-Protein-Reaction Associations Leverages Constraint-Based Analysis from Reaction to Gene-Level Phenotype Prediction. <i>PLoS Computational Biology</i> , <b>2016</b> , 12, e1005140	5.140	27
112	Genome-scale bacterial transcriptional regulatory networks: reconstruction and integrated analysis with metabolic models. <i>Briefings in Bioinformatics</i> , <b>2014</b> , 15, 592-611	13.4	26
111	Exploring the gap between dynamic and constraint-based models of metabolism. <i>Metabolic Engineering</i> , <b>2012</b> , 14, 112-9	9.7	26
110	Memote: A community driven effort towards a standardized genome-scale metabolic model test suite		26
109	Impact of the cultivation strategy on resveratrol production from glucose in engineered <i>Corynebacterium glutamicum</i> . <i>Journal of Biotechnology</i> , <b>2018</b> , 265, 70-75	3.7	24

108	Heterologous production of resveratrol in bacterial hosts: current status and perspectives. <i>World Journal of Microbiology and Biotechnology</i> , <b>2018</b> , 34, 122	4.4	23
107	Modulation of the central carbon metabolism of <i>Corynebacterium glutamicum</i> improves malonyl-CoA availability and increases plant polyphenol synthesis. <i>Biotechnology and Bioengineering</i> , <b>2019</b> , 116, 1380-1391	4.9	22
106	Yeast metabolic chassis designs for diverse biotechnological products. <i>Scientific Reports</i> , <b>2016</b> , 6, 29694	4.9	22
105	Modeling the Contribution of Allosteric Regulation for Flux Control in the Central Carbon Metabolism of <i>E. coli</i> . <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2015</b> , 3, 154	5.8	21
104	Estimation of multiple biomass growth rates and biomass concentration in a class of bioprocesses. <i>Bioprocess and Biosystems Engineering</i> , <b>2003</b> , 25, 395-406	3.7	19
103	Critical perspective on the consequences of the limited availability of kinetic data in metabolic dynamic modelling. <i>IET Systems Biology</i> , <b>2011</b> , 5, 157-63	1.4	17
102	Identification and Microbial Production of the Raspberry Phenol Salidroside that Is Active against Huntington's Disease. <i>Plant Physiology</i> , <b>2019</b> , 179, 969-985	6.6	17
101	Identification of metabolic engineering targets through analysis of optimal and sub-optimal routes. <i>PLoS ONE</i> , <b>2013</b> , 8, e61648	3.7	15
100	A computational tool for the simulation and optimization of microbial strains accounting integrated metabolic/regulatory information. <i>BioSystems</i> , <b>2011</b> , 103, 435-41	1.9	15
99	Optimization approaches for the in silico discovery of optimal targets for gene over/underexpression. <i>Journal of Computational Biology</i> , <b>2012</b> , 19, 102-14	1.7	13
98	Selection of Elementary Modes for Bioprocess Control. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , <b>2010</b> , 43, 156-161		13
97	A Comparison of Algorithms for the Optimization of Fermentation Processes		13
96	BachBerry: BACTERIAL Hosts for production of Bioactive phenolics from bERRY fruits. <i>Phytochemistry Reviews</i> , <b>2018</b> , 17, 291-326	7.7	12
95	Reconstruction of a genome-scale metabolic model for <i>Actinobacillus succinogenes</i> 130Z. <i>BMC Systems Biology</i> , <b>2018</b> , 12, 61	3.5	12
94	Genome-wide metabolic (re-) annotation of <i>Kluyveromyces lactis</i> . <i>BMC Genomics</i> , <b>2012</b> , 13, 517	4.5	12
93	Metabolic models and gene essentiality data reveal essential and conserved metabolism in prokaryotes. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1006556	5	12
92	Genome-wide metabolic re-annotation of <i>Ashbya gossypii</i> : new insights into its metabolism through a comparative analysis with <i>Saccharomyces cerevisiae</i> and <i>Kluyveromyces lactis</i> . <i>BMC Genomics</i> , <b>2014</b> , 15, 810	4.5	11
91	State and specific growth estimation in heterologous protein production by <i>Pichia pastoris</i> . <i>AICHE Journal</i> , <b>2012</b> , 58, 2966-2979	3.6	11

90	Re-annotation of the genome sequence of <i>Helicobacter pylori</i> 26695. <i>Journal of Integrative Bioinformatics</i> , <b>2013</b> , 10, 66-78	3.8	11
89	IMPLEMENTATION OF A SPECIFIC RATE CONTROLLER IN A FED-BATCH E. COLI FERMENTATION. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , <b>2008</b> , 41, 15565-15570		11
88	Genome-Wide Semi-Automated Annotation of Transporter Systems. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2017</b> , 14, 443-456	3	10
87	Dietary Sugars Analysis: Quantification of Fructooligosaccharides during Fermentation by HPLC-RI Method. <i>Frontiers in Nutrition</i> , <b>2014</b> , 1, 11	6.2	10
86	<i>Salmonella typhimurium</i> and <i>Escherichia coli</i> dissimilarity: Closely related bacteria with distinct metabolic profiles. <i>Biotechnology Progress</i> , <b>2015</b> , 31, 1217-25	2.8	10
85	Assessment of physiological conditions in <i>E. coli</i> fermentations by epifluorescent microscopy and image analysis. <i>Biotechnology Progress</i> , <b>2009</b> , 25, 882-91	2.8	10
84	Evolutionary Algorithms for Optimal Control in Fed-Batch Fermentation Processes. <i>Lecture Notes in Computer Science</i> , <b>2004</b> , 84-93	0.9	10
83	Re-annotation of the genome sequence of <i>Helicobacter pylori</i> 26695. <i>Journal of Integrative Bioinformatics</i> , <b>2013</b> , 10, 233	3.8	10
82	Reconstructing High-Quality Large-Scale Metabolic Models with merlin. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1716, 1-36	1.4	10
81	An adsorptive bioprocess for production and recovery of resveratrol with <i>Corynebacterium glutamicum</i> . <i>Journal of Chemical Technology and Biotechnology</i> , <b>2018</b> , 93, 1661-1668	3.5	10
80	Discovery and implementation of a novel pathway for $\gamma$ -butanol production via 2-oxoglutarate. <i>Biotechnology for Biofuels</i> , <b>2019</b> , 12, 230	7.8	9
79	Stringent response of <i>Escherichia coli</i> : revisiting the bibliome using literature mining. <i>Microbial Informatics and Experimentation</i> , <b>2011</b> , 1, 14		9
78	BioDR: Semantic indexing networks for biomedical document retrieval. <i>Expert Systems With Applications</i> , <b>2010</b> , 37, 3444-3453	7.8	9
77	Influence of the RelA Activity on <i>E. coli</i> Metabolism by Metabolite Profiling of Glucose-Limited Chemostat Cultures. <i>Metabolites</i> , <b>2012</b> , 2, 717-32	5.6	8
76	Evaluating evolutionary multiobjective algorithms for the in silico optimization of mutant strains <b>2008</b> ,		8
75	Development and application of efficient pathway enumeration algorithms for metabolic engineering applications. <i>Computer Methods and Programs in Biomedicine</i> , <b>2015</b> , 118, 134-46	6.9	7
74	A kinetic model for curcumin production in <i>Escherichia coli</i> . <i>BioSystems</i> , <b>2014</b> , 125, 16-21	1.9	7
73	A Study of the Short and Long-term Regulation of <i>E. coli</i> Metabolic Pathways. <i>Journal of Integrative Bioinformatics</i> , <b>2011</b> , 8, 195-209	3.8	7

72	Identification of minimal metabolic pathway models consistent with phenotypic data. <i>Journal of Process Control</i> , <b>2011</b> , 21, 1483-1492	3.9	7
71	A Dynamical Model for the Fermentative Production of Fructooligosaccharides. <i>Computer Aided Chemical Engineering</i> , <b>2009</b> , 1827-1832	0.6	7
70	Reconstruction of the Regulatory Network for Bacillus subtilis and Reconciliation with Gene Expression Data. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 275	5.7	7
69	Computing and Applying Atomic Regulons to Understand Gene Expression and Regulation. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 1819	5.7	7
68	iDS372, a Phenotypically Reconciled Model for the Metabolism of Strain R6. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 1283	5.7	6
67	CBFA: phenotype prediction integrating metabolic models with constraints derived from experimental data. <i>BMC Systems Biology</i> , <b>2014</b> , 8, 123	3.5	6
66	Evolutionary Algorithms for Static and Dynamic Optimization of Fed-batch Fermentation Processes <b>2005</b> , 288-291		6
65	Metaheuristics for Strain Optimization Using Transcriptional Information Enriched Metabolic Models. <i>Lecture Notes in Computer Science</i> , <b>2010</b> , 205-216	0.9	6
64	A review of methods for the reconstruction and analysis of integrated genome-scale models of metabolism and regulation. <i>Biochemical Society Transactions</i> , <b>2020</b> , 48, 1889-1903	5.1	6
63	Genome-Scale Metabolic Model of the Human Pathogen : A Promising Platform for Drug Target Prediction. <i>Journal of Fungi (Basel, Switzerland)</i> , <b>2020</b> , 6,	5.6	6
62	Production of mannosylglycerate in Saccharomyces cerevisiae by metabolic engineering and bioprocess optimization. <i>Microbial Cell Factories</i> , <b>2018</b> , 17, 178	6.4	6
61	Metabolic engineering strategies for butanol production in Escherichia coli. <i>Biotechnology and Bioengineering</i> , <b>2020</b> , 117, 2571-2587	4.9	5
60	Key Challenges in Designing CHO Chassis Platforms. <i>Processes</i> , <b>2020</b> , 8, 643	2.9	5
59	Semantic annotation of biological concepts interplaying microbial cellular responses. <i>BMC Bioinformatics</i> , <b>2011</b> , 12, 460	3.6	5
58	Differential Evolution for the Offline and Online Optimization of Fed-Batch Fermentation Processes. <i>Studies in Computational Intelligence</i> , <b>2008</b> , 299-317	0.8	5
57	Genome-wide sequencing and metabolic annotation of Pythium irregulare CBS 494.86: understanding Eicosapentaenoic acid production. <i>BMC Biotechnology</i> , <b>2019</b> , 19, 41	3.5	4
56	Challenges in integrating Escherichia coli molecular biology data. <i>Briefings in Bioinformatics</i> , <b>2011</b> , 12, 91-103	13.4	4
55	An integrated computational environment for elementary modes analysis of biochemical networks. <i>International Journal of Data Mining and Bioinformatics</i> , <b>2012</b> , 6, 382-95	0.5	4

54	Estimation of biomass composition from genomic and transcriptomic information. <i>Journal of Integrative Bioinformatics</i> , <b>2016</b> , 13, 285	3.8	4
53	Evaluating Evolutionary Algorithms and Differential Evolution for the Online Optimization of Fermentation Processes <b>2007</b> , 236-246		4
52	Enhancing acetic acid and 5-hydroxymethyl furfural tolerance of <i>C. saccharoperbutylacetonicum</i> through adaptive laboratory evolution. <i>Process Biochemistry</i> , <b>2021</b> , 101, 179-189	4.8	4
51	SamPler - a novel method for selecting parameters for gene functional annotation routines. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 454	3.6	3
50	An integrated framework for strain optimization <b>2013</b> ,		3
49	Merlin: Metabolic Models Reconstruction using Genome-Scale Information*. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , <b>2010</b> , 43, 120-125		3
48	Modelling Fed-Batch Fermentation Processes: An Approach Based on Artificial Neural Networks. <i>Advances in Soft Computing</i> , <b>2009</b> , 30-39		3
47	Estimation of biomass composition from genomic and transcriptomic information. <i>Journal of Integrative Bioinformatics</i> , <b>2016</b> , 13, 1-14	3.8	3
46	A Comparative Proteome Analysis of A Mutant Cells. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2016</b> , 4, 78	5.8	3
45	Analyzing and Designing Cell Factories with OptFlux. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1716, 37-76	1.4	3
44	Model-guided development of an evolutionarily stable yeast chassis. <i>Molecular Systems Biology</i> , <b>2021</b> , 17, e10253	12.2	3
43	Quantitative physiology and elemental composition of <i>Kluyveromyces lactis</i> CBS 2359 during growth on glucose at different specific growth rates. <i>Antonie Van Leeuwenhoek</i> , <b>2018</b> , 111, 183-195	2.1	2
42	A Computation Tool for the Estimation of Biomass Composition from Genomic and Transcriptomic Information. <i>Advances in Intelligent Systems and Computing</i> , <b>2016</b> , 161-169	0.4	2
41	A new representation in evolutionary algorithms for the optimization of bioprocesses		2
40	Application of a genome-scale metabolic model to the inference of nutritional requirements and metabolic bottlenecks during recombinant protein production in <i>Escherichia coli</i> . <i>Microbial Cell Factories</i> , <b>2006</b> , 5, P52	6.4	2
39	DESIGN OF ON-LINE STATE ESTIMATORS FOR A RECOMBINANT E. COLI FED-BATCH FERMENTATION. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , <b>2005</b> , 38, 67-72		2
38	Microbial Hosts as a Promising Platform for Polyphenol Production <b>2019</b> , 71-103		2
37	Yeast metabolomics: sample preparation for a GC/MS-based analysis. <i>Methods in Molecular Biology</i> , <b>2014</b> , 1152, 197-207	1.4	2

36	Evolutionary Approaches for Strain Optimization Using Dynamic Models under a Metabolic Engineering Perspective. <i>Lecture Notes in Computer Science</i> , <b>2009</b> , 140-151	0.9	2
35	iEC7871 Quercus suber model: the first multi-tissue diel cycle genome-scale metabolic model of a woody tree		2
34	A Comparative Analysis of Dynamic Models of the Central Carbon Metabolism of Escherichia coli. <i>IFAC-PapersOnLine</i> , <b>2016</b> , 49, 270-276	0.7	2
33	Development of a Framework for Metabolic Pathway Analysis-Driven Strain Optimization Methods. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , <b>2017</b> , 9, 46-55	3.5	1
32	Identification of robust strain designs via tandem pFBA/LMOMA phenotype prediction <b>2017</b> ,		1
31	Development of an Integrated Framework for Minimal Cut Set Enumeration in Constraint-Based Models. <i>Advances in Intelligent Systems and Computing</i> , <b>2016</b> , 193-201	0.4	1
30	Comparison of pathway analysis and constraint-based methods for cell factory design. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 350	3.6	1
29	TNA4OptFlux--a software tool for the analysis of strain optimization strategies. <i>BMC Research Notes</i> , <b>2013</b> , 6, 175	2.3	1
28	Evolutionary computation for predicting optimal reaction knockouts and enzyme modulation strategies <b>2013</b> ,		1
27	Genome scale metabolic network reconstruction of the pathogen Enterococcus faecalis. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , <b>2013</b> , 46, 131-136		1
26	A Systematic Modeling Approach to Elucidate the Triggering of the Stringent Response in Recombinant E. coli Systems. <i>Advances in Intelligent and Soft Computing</i> , <b>2011</b> , 313-320		1
25	A Critical Review on Modelling Formalisms and Simulation Tools in Computational Biosystems. <i>Lecture Notes in Computer Science</i> , <b>2009</b> , 1063-1070	0.9	1
24	Optimization of culture conditions to improve Helicobacter pylori growth in Ham's F-12 medium by response surface methodology. <i>International Journal of Immunopathology and Pharmacology</i> , <b>2012</b> , 25, 901-9	3	1
23	Large Scale Dynamic Model Reconstruction for the Central Carbon Metabolism of Escherichia coli. <i>Lecture Notes in Computer Science</i> , <b>2009</b> , 1079-1083	0.9	1
22	Applying a Metabolic Footprinting Approach to Characterize the Impact of the Recombinant Protein Production in Escherichia coli. <i>Advances in Intelligent and Soft Computing</i> , <b>2010</b> , 193-200		1
21	Optimization of Bacterial Strains with Variable-Sized Evolutionary Algorithms <b>2007</b> ,		1
20	Evaluating Simulated Annealing Algorithms in the Optimization of Bacterial Strains <b>2007</b> , 473-484		1
19	Data Integration Issues in the Reconstruction of the Genome-Scale Metabolic Model of Zymomonas Mobilis. <i>Advances in Soft Computing</i> , <b>2009</b> , 92-101		1



18	Computational Tools for Strain Optimization by Tuning the Optimal Level of Gene Expression. <i>Advances in Intelligent and Soft Computing</i> , <b>2012</b> , 251-258		1
17	Mapping Salmonella typhimurium pathways using C metabolic flux analysis. <i>Metabolic Engineering</i> , <b>2019</b> , 52, 303-314	9.7	1
16	A study of the short and long-term regulation of E. coli metabolic pathways. <i>Journal of Integrative Bioinformatics</i> , <b>2011</b> , 8, 183	3.8	1
15	Inclusion of maintenance energy improves the intracellular flux predictions of CHO. <i>PLoS Computational Biology</i> , <b>2021</b> , 17, e1009022	5	0
14	Turnover Dependent Phenotypic Simulation: A Quantitative Constraint-Based Simulation Method That Accommodates All Main Strain Design Strategies. <i>ACS Synthetic Biology</i> , <b>2019</b> , 8, 976-988	5.7	
13	A Text Mining Approach for the Extraction of Kinetic Information from Literature. <i>Advances in Intelligent Systems and Computing</i> , <b>2015</b> , 89-98	0.4	
12	Assignment of Novel Functions to Helicobacter pylori 26695B Genome. <i>Advances in Intelligent Systems and Computing</i> , <b>2013</b> , 29-36	0.4	
11	Extracting kinetic information from literature with KineticRE. <i>Journal of Integrative Bioinformatics</i> , <b>2015</b> , 12, 56-68	3.8	
10	Evaluating Pathway Enumeration Algorithms in Metabolic Engineering Case Studies. <i>Advances in Intelligent Systems and Computing</i> , <b>2014</b> , 215-223	0.4	
9	Evaluating the integration of proteomic data for the prediction of intracellular fluxes after knockout experiments. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , <b>2010</b> , 43, 114-119		
8	Identification of Yield Coefficients in an E.coli Model – An Optimal Experimental Design Using Genetic Algorithms. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , <b>2004</b> , 37, 43-48		
7	An Integrated System for Advanced Monitoring and Control of Fed-Batch Fermentations of Recombinant E. coli. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , <b>2001</b> , 34, 349-354		
6	A Software Tool for the Simulation and Optimization of Dynamic Metabolic Models. <i>Lecture Notes in Computer Science</i> , <b>2009</b> , 1071-1078	0.9	
5	Modelling of Biotechnological Processes – An Approach Based on Artificial Neural Networks. <i>Studies in Computational Intelligence</i> , <b>2009</b> , 311-332	0.8	
4	Biomedical Text Mining Applied to Document Retrieval and Semantic Indexing. <i>Lecture Notes in Computer Science</i> , <b>2009</b> , 954-963	0.9	
3	Enhancing Elementary Flux Modes Analysis Using Filtering Techniques in an Integrated Environment. <i>Advances in Intelligent and Soft Computing</i> , <b>2010</b> , 217-224		
2	Highlighting Metabolic Strategies Using Network Analysis over Strain Optimization Results. <i>Lecture Notes in Computer Science</i> , <b>2011</b> , 109-120	0.9	
1	Interpreting the Regulatory Interplay in E. coli Metabolic Pathways. <i>Advances in Intelligent and Soft Computing</i> , <b>2011</b> , 303-312		

