

# Miguel P Rocha

## List of Publications by Citations

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195  
papers

2,372  
citations

26  
h-index

44  
g-index

222  
ext. papers

3,013  
ext. citations

3.6  
avg, IF

5.47  
L-index

#	Paper	IF	Citations
195	OptFlux: an open-source software platform for in silico metabolic engineering. <i>BMC Systems Biology</i> , <b>2010</b> , 4, 45	3.5	258
194	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. <i>Nature Communications</i> , <b>2019</b> , 10, 2674	17.4	119
193	Modeling formalisms in Systems Biology. <i>AMB Express</i> , <b>2011</b> , 1, 45	4.1	107
192	Prediction of overall survival for patients with metastatic castration-resistant prostate cancer: development of a prognostic model through a crowdsourced challenge with open clinical trial data. <i>Lancet Oncology</i> , <b>2017</b> , 18, 132-142	21.7	90
191	Reconstructing genome-scale metabolic models with merlin. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 3899-910	20.1	82
190	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
189	Selected Extended Papers of the 12th International Conference on Practical Applications of Computational Biology and Bioinformatics (PACBB). <i>Journal of Integrative Bioinformatics</i> , <b>2019</b> , 16,	3.8	78
188	Selected Extended Papers of the 11th International Conference on Practical Applications of Computational Biology and Bioinformatics (PACBB). <i>Journal of Integrative Bioinformatics</i> , <b>2017</b> , 14,	3.8	78
187	Metabolomics combined with chemometric tools (PCA, HCA, PLS-DA and SVM) for screening cassava ( <i>Manihot esculenta</i> Crantz) roots during postharvest physiological deterioration. <i>Food Chemistry</i> , <b>2014</b> , 161, 67-78	8.5	77
186	Natural computation meta-heuristics for the in silico optimization of microbial strains. <i>BMC Bioinformatics</i> , <b>2008</b> , 9, 499	3.6	75
185	Evolution of neural networks for classification and regression. <i>Neurocomputing</i> , <b>2007</b> , 70, 2809-2816	5.4	66
184	Bridging the layers: towards integration of signal transduction, regulation and metabolism into mathematical models. <i>Molecular BioSystems</i> , <b>2013</b> , 9, 1576-83		65
183	Transcript level and sequence determinants of protein abundance and noise in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 4791-9	20.1	57
182	Evolving Time Series Forecasting ARMA Models. <i>Journal of Heuristics</i> , <b>2004</b> , 10, 415-429	1.9	55
181	The role of ascorbate peroxidase, guaiacol peroxidase, and polysaccharides in cassava ( <i>Manihot esculenta</i> Crantz) roots under postharvest physiological deterioration. <i>Food Chemistry</i> , <b>2016</b> , 197, 737-46	8.5	43
180	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
179	Deep learning for drug response prediction in cancer. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22, 360-379	13.4	39

178	A Review of Dynamic Modeling Approaches and Their Application in Computational Strain Optimization for Metabolic Engineering. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 1690	5.7	37
177	AlBench: a rapid application development framework for translational research in biomedicine. <i>Computer Methods and Programs in Biomedicine</i> , <b>2010</b> , 98, 191-203	6.9	37
176	Preventing Premature Convergence to Local Optima in Genetic Algorithms via Random Offspring Generation. <i>Lecture Notes in Computer Science</i> , <b>1999</b> , 127-136	0.9	36
175	A transcriptomic signature mediated by HOXA9 promotes human glioblastoma initiation, aggressiveness and resistance to temozolomide. <i>Oncotarget</i> , <b>2015</b> , 6, 7657-74	3.3	34
174	Methods for automated genome-scale metabolic model reconstruction. <i>Biochemical Society Transactions</i> , <b>2018</b> , 46, 931-936	5.1	33
173	Data-driven reverse engineering of signaling pathways using ensembles of dynamic models. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005379	5	31
172	An R package for the integrated analysis of metabolomics and spectral data. <i>Computer Methods and Programs in Biomedicine</i> , <b>2016</b> , 129, 117-24	6.9	29
171	@Note: a workbench for biomedical text mining. <i>Journal of Biomedical Informatics</i> , <b>2009</b> , 42, 710-20	10.2	28
170	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
169	D-Tailor: automated analysis and design of DNA sequences. <i>Bioinformatics</i> , <b>2014</b> , 30, 1087-1094	7.2	23
168	Metabolic Profiling and Classification of Propolis Samples from Southern Brazil: An NMR-Based Platform Coupled with Machine Learning. <i>Journal of Natural Products</i> , <b>2016</b> , 79, 13-23	4.9	22
167	Causal integration of multi-omics data with prior knowledge to generate mechanistic hypotheses. <i>Molecular Systems Biology</i> , <b>2021</b> , 17, e9730	12.2	20
166	Quality of Service constrained routing optimization using Evolutionary Computation. <i>Applied Soft Computing Journal</i> , <b>2011</b> , 11, 356-364	7.5	19
165	Symbiotic filtering for spam email detection. <i>Expert Systems With Applications</i> , <b>2011</b> , 38, 9365-9372	7.8	17
164	The long non-coding RNA is transcriptionally activated by HOXA9 and is an independent prognostic marker in patients with malignant glioma. <i>Oncotarget</i> , <b>2018</b> , 9, 15740-15756	3.3	17
163	Reverse engineering of logic-based differential equation models using a mixed-integer dynamic optimization approach. <i>Bioinformatics</i> , <b>2015</b> , 31, 2999-3007	7.2	16
162	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
161	Evolutionary Neural Network Learning. <i>Lecture Notes in Computer Science</i> , <b>2003</b> , 24-28	0.9	15

160	Predicting promoters in phage genomes using PhagePromoter. <i>Bioinformatics</i> , <b>2019</b> , 35, 5301-5302	7.2	14
159	In vitro exposure of <i>Ulva lactuca</i> Linnaeus (Chlorophyta) to gasoline - Biochemical and morphological alterations. <i>Chemosphere</i> , <b>2016</b> , 156, 428-437	8.4	14
158	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
157	A Lamarckian Approach for Neural Network Training. <i>Neural Processing Letters</i> , <b>2002</b> , 15, 105-116	2.4	13
156	Metabolomics of <i>Ulva lactuca</i> Linnaeus (Chlorophyta) exposed to oil fuels: Fourier transform infrared spectroscopy and multivariate analysis as tools for metabolic fingerprint. <i>Marine Pollution Bulletin</i> , <b>2017</b> , 114, 831-836	6.7	12
155	Time Series Forecasting by Evolutionary Neural Networks <b>2006</b> , 47-70		12
154	WebSpecmine: A Website for Metabolomics Data Analysis and Mining. <i>Metabolites</i> , <b>2019</b> , 9,	5.6	11
153	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
152	Multi-scale Internet traffic forecasting using neural networks and time series methods. <i>Expert Systems</i> , <b>2010</b> , 29, no-no	2.1	11
151	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
150	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
149	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
148	Reconstructing High-Quality Large-Scale Metabolic Models with merlin. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1716, 1-36	1.4	10
147	Discrimination of Brazilian propolis according to the seasoning using chemometrics and machine learning based on UV-Vis scanning data. <i>Journal of Integrative Bioinformatics</i> , <b>2015</b> , 12, 15-26	3.8	9
146	BioDR: Semantic indexing networks for biomedical document retrieval. <i>Expert Systems With Applications</i> , <b>2010</b> , 37, 3444-3453	7.8	9
145	Simultaneous Evolution of Neural Network Topologies and Weights for Classification and Regression. <i>Lecture Notes in Computer Science</i> , <b>2005</b> , 59-66	0.9	9
144	Toward better understanding of postharvest deterioration: biochemical changes in stored cassava ( <i>Manihot esculenta</i> Crantz) roots. <i>Food Science and Nutrition</i> , <b>2016</b> , 4, 409-22	3.2	9
143	Machine Learning-Enhanced T Cell Neopeptide Discovery for Immunotherapy Design. <i>Cancer Informatics</i> , <b>2019</b> , 18, 1176935119852081	2.4	8

142	UV-Vis and CIELAB Based Chemometric Characterization of Manihot esculenta Carotenoid Contents. <i>Journal of Integrative Bioinformatics</i> , <b>2017</b> , 14,	3.8	8
141	Transcriptional profiling of HOXA9-regulated genes in human glioblastoma cell models. <i>Genomics Data</i> , <b>2015</b> , 5, 54-8		8
140	Evaluating evolutionary multiobjective algorithms for the in silico optimization of mutant strains <b>2008</b> ,		8
139	Deep Neural Networks for Network Routing <b>2019</b> ,		7
138	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
137	Generative Deep Learning for Targeted Compound Design. <i>Journal of Chemical Information and Modeling</i> , <b>2021</b> , 61, 5343-5361	6.1	7
136	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
135	Computing and Applying Atomic Regulons to Understand Gene Expression and Regulation. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 1819	5.7	7
134	Efficient OSPF Weight Allocation for Intra-domain QoS Optimization. <i>Lecture Notes in Computer Science</i> , <b>2006</b> , 37-48	0.9	7
133	Analysing Algorithms and Data Sources for the Tissue-Specific Reconstruction of Liver Healthy and Cancer Cells. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , <b>2017</b> , 9, 36-45	3.5	6
132	Parallel evolutionary computation in bioinformatics applications. <i>Computer Methods and Programs in Biomedicine</i> , <b>2013</b> , 110, 183-91	6.9	6
131	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
130	An integrated network visualization framework towards metabolic engineering applications. <i>BMC Bioinformatics</i> , <b>2014</b> , 15, 420	3.6	6
129	EMAIL SPAM DETECTION: A SYMBIOTIC FEATURE SELECTION APPROACH FOSTERED BY EVOLUTIONARY COMPUTATION. <i>International Journal of Information Technology and Decision Making</i> , <b>2013</b> , 12, 863-884	2.8	6
128	Implementing Metaheuristic Optimization Algorithms with JEColi <b>2009</b> ,		6
127	Evolutionary Design of Neural Networks for Classification and Regression <b>2005</b> , 304-307		6
126	Evolutionary Algorithms for Static and Dynamic Optimization of Fed-batch Fermentation Processes <b>2005</b> , 288-291		6
125	Discrimination of Brazilian propolis according to the seasoning using chemometrics and machine learning based on UV-Vis scanning data. <i>Journal of Integrative Bioinformatics</i> , <b>2015</b> , 12, 279	3.8	6

124	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
123	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
122	In vitro fucoxanthin production by the <i>Phaeodactylum tricornutum</i> diatom. <i>Studies in Natural Products Chemistry</i> , <b>2019</b> , 63, 211-242	1.5	6
121	A Critical Evaluation of Methods for the Reconstruction of Tissue-Specific Models. <i>Lecture Notes in Computer Science</i> , <b>2015</b> , 340-352	0.9	5
120	Traffic Engineering With Three-Segments Routing. <i>IEEE Transactions on Network and Service Management</i> , <b>2020</b> , 17, 1896-1909	4.8	5
119	Utilitarian Placement of Composite Services. <i>IEEE Transactions on Network and Service Management</i> , <b>2018</b> , 15, 638-649	4.8	5
118	Development of an information retrieval tool for biomedical patents. <i>Computer Methods and Programs in Biomedicine</i> , <b>2018</b> , 159, 125-134	6.9	5
117	Semantic annotation of biological concepts interplaying microbial cellular responses. <i>BMC Bioinformatics</i> , <b>2011</b> , 12, 460	3.6	5
116	Symbiotic Data Mining for Personalized Spam Filtering <b>2009</b> ,		5
115	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
114	Spam Email Filtering Using Network-Level Properties. <i>Lecture Notes in Computer Science</i> , <b>2010</b> , 476-489	0.9	5
113	A Collaborative Approach for Spam Detection <b>2010</b> ,		4
112	Challenges in integrating <i>Escherichia coli</i> molecular biology data. <i>Briefings in Bioinformatics</i> , <b>2011</b> , 12, 91-103	13.4	4
111	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
110	Topology Aware Internet Traffic Forecasting Using Neural Networks. <i>Lecture Notes in Computer Science</i> , <b>2007</b> , 445-454	0.9	4
109	Evaluating Evolutionary Algorithms and Differential Evolution for the Online Optimization of Fermentation Processes <b>2007</b> , 236-246		4
108	SamPler - a novel method for selecting parameters for gene functional annotation routines. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 454	3.6	3
107	CoBAMP: a Python framework for metabolic pathway analysis in constraint-based models. <i>Bioinformatics</i> , <b>2019</b> , 35, 5361-5362	7.2	3

106	An integrated framework for strain optimization <b>2013</b> ,		3
105	Comparison of Single and Multi-objective Evolutionary Algorithms for Robust Link-State Routing. <i>Lecture Notes in Computer Science</i> , <b>2015</b> , 573-587	0.9	3
104	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
103	A platform for the selection of genes in DNA microarraydata using evolutionary algorithms <b>2007</b> ,		3
102	A Study of Order Based Genetic and Evolutionary Algorithms in Combinatorial Optimization Problems. <i>Lecture Notes in Computer Science</i> , <b>2000</b> , 601-611	0.9	3
101	Modelling Fed-Batch Fermentation Processes: An Approach Based on Artificial Neural Networks. <i>Advances in Soft Computing</i> , <b>2009</b> , 30-39		3
100	merlinv4.0: an updated platform for the reconstruction of high-quality genome-scale metabolic models		3
99	Analyzing and Designing Cell Factories with OptFlux. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1716, 37-76	1.4	3
98	Model-guided development of an evolutionarily stable yeast chassis. <i>Molecular Systems Biology</i> , <b>2021</b> , 17, e10253	12.2	3
97	Going virtual and going wide: comparing Team-Based Learning in-class online and across disciplines. <i>Education and Information Technologies</i> , <b>2021</b> , 1-19	3.6	3
96	Transcript-based reannotation for microarray probesets <b>2015</b> ,		2
95	Development of a Machine Learning Framework for Biomedical Text Mining. <i>Advances in Intelligent Systems and Computing</i> , <b>2016</b> , 41-49	0.4	2
94	Data supporting the role of enzymes and polysaccharides during cassava postharvest physiological deterioration. <i>Data in Brief</i> , <b>2016</b> , 6, 503-6	1.2	2
93	MOSCA: An Automated Pipeline for Integrated Metagenomics and Metatranscriptomics Data Analysis. <i>Advances in Intelligent Systems and Computing</i> , <b>2019</b> , 183-191	0.4	2
92	Optimizing Segment Routing using Evolutionary Computation. <i>Procedia Computer Science</i> , <b>2017</b> , 110, 312-319	1.6	2
91	A Chemometrics Approach for Nuclear Magnetic Resonance Data to Characterize the Partial Metabolome Banana Peels from Southern Brazil. <i>Journal of Integrative Bioinformatics</i> , <b>2017</b> , 14,	3.8	2
90	Traffic Engineering Approaches Using Multicriteria Optimization Techniques. <i>Lecture Notes in Computer Science</i> , <b>2011</b> , 104-115	0.9	2
89	Reconstruction of tissue-specific genome-scale metabolic models for human cancer stem cells.. <i>Computers in Biology and Medicine</i> , <b>2021</b> , 142, 105177	7	2

88	A Critical Evaluation of Automatic Atom Mapping Algorithms and Tools. <i>Advances in Intelligent Systems and Computing</i> , <b>2017</b> , 257-264	0.4	2
87	Development of Text Mining Tools for Information Retrieval from Patents. <i>Advances in Intelligent Systems and Computing</i> , <b>2017</b> , 66-73	0.4	2
86	Class-Based OSPF Traffic Engineering Inspired on Evolutionary Computation <b>2007</b> , 141-152		2
85	A Framework for Robust Traffic Engineering Using Evolutionary Computation. <i>Lecture Notes in Computer Science</i> , <b>2013</b> , 1-12	0.9	2
84	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
83	iEC7871 Quercus suber model: the first multi-tissue diel cycle genome-scale metabolic model of a woody tree		2
82	Troppo - A Python Framework for the Reconstruction of Context-Specific Metabolic Models. <i>Advances in Intelligent Systems and Computing</i> , <b>2020</b> , 146-153	0.4	2
81	Artificial Intelligence in Biological Activity Prediction. <i>Advances in Intelligent Systems and Computing</i> , <b>2020</b> , 164-172	0.4	2
80	MEWpy: A Computational Strain Optimization Workbench in Python. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	2
79	A Model Integration Pipeline for the Improvement of Human Genome-Scale Metabolic Reconstructions. <i>Journal of Integrative Bioinformatics</i> , <b>2018</b> , 16,	3.8	2
78	UPIAPI, reCOGNizer and KEGGCharter: Bioinformatics tools for functional annotation and visualization of (meta)-omics datasets.. <i>Computational and Structural Biotechnology Journal</i> , <b>2022</b> , 20, 1798-1810	6.8	2
77	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
76	Identification of robust strain designs via tandem pFBA/LMOMA phenotype prediction <b>2017</b> ,		1
75	Carotenoid Analysis of Cassava Genotypes Roots (Manihot Esculenta Crantz) Cultivated in Southern Brazil Using Chemometric Tools. <i>Advances in Intelligent Systems and Computing</i> , <b>2015</b> , 11-18	0.4	1
74	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
73	Comparison of pathway analysis and constraint-based methods for cell factory design. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 350	3.6	1
72	TNA4OptFlux--a software tool for the analysis of strain optimization strategies. <i>BMC Research Notes</i> , <b>2013</b> , 6, 175	2.3	1
71	Evolutionary computation for predicting optimal reaction knockouts and enzyme modulation strategies <b>2013</b> ,		1



70	UV-visible scanning spectrophotometry and chemometric analysis as tools for carotenoids analysis in cassava genotypes ( <i>Manihot esculenta</i> Crantz). <i>Journal of Integrative Bioinformatics</i> , <b>2015</b> , 12, 27-38	3.8	1
69	An Integrated Computational Platform for Metabolomics Data Analysis. <i>Advances in Intelligent Systems and Computing</i> , <b>2015</b> , 37-47	0.4	1
68	Microarray Gene Expression Data Integration: An Application to Brain Tumor Grade Determination. <i>Advances in Intelligent Systems and Computing</i> , <b>2015</b> , 127-135	0.4	1
67	A Machine Learning and Chemometrics Assisted Interpretation of Spectroscopic Data IIA NMR-Based Metabolomics Platform for the Assessment of Brazilian Propolis. <i>Lecture Notes in Computer Science</i> , <b>2012</b> , 129-140	0.9	1
66	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
65	Optimization of Bacterial Strains with Variable-Sized Evolutionary Algorithms <b>2007</b> ,		1
64	Botanical source investigation and evaluation of the effect of seasonality on Brazilian propolis from <i>Apis mellifera</i> L.. <i>Scientia Agricola</i> , <b>2020</b> , 77,	2.5	1
63	Evolutionary Computation for Quality of Service Internet Routing Optimization <b>2007</b> , 71-80		1
62	Evaluating Simulated Annealing Algorithms in the Optimization of Bacterial Strains <b>2007</b> , 473-484		1
61	getALife - An Artificial Life Environment for the Evaluation of Agent-Based Systems and Evolutionary Algorithms for Reinforcement Learning. <i>Studies in Computational Intelligence</i> , <b>2008</b> , 35-44	0.8	1
60	Viewing Scheduling Problems through Genetic and Evolutionary Algorithms. <i>Lecture Notes in Computer Science</i> , <b>2000</b> , 612-619	0.9	1
59	Classification Tools for Carotenoid Content Estimation in <i>Manihot esculenta</i> via Metabolomics and Machine Learning. <i>Advances in Intelligent Systems and Computing</i> , <b>2017</b> , 280-288	0.4	1
58	Characterization of the Chemical Composition of Banana Peels from Southern Brazil Across the Seasons Using Nuclear Magnetic Resonance and Chemometrics. <i>Advances in Intelligent Systems and Computing</i> , <b>2017</b> , 321-328	0.4	1
57	Data Integration Issues in the Reconstruction of the Genome-Scale Metabolic Model of <i>Zymomonas Mobilis</i> . <i>Advances in Soft Computing</i> , <b>2009</b> , 92-101		1
56	Multiconstrained Optimization of Networks with Multicast and Unicast Traffic. <i>Lecture Notes in Computer Science</i> , <b>2008</b> , 139-150	0.9	1
55	Analysis of the Effect of Reversibility Constraints on the Predictions of Genome-Scale Metabolic Models. <i>Advances in Intelligent and Soft Computing</i> , <b>2010</b> , 209-215		1
54	An Algorithm to Assemble Gene-Protein-Reaction Associations for Genome-Scale Metabolic Model Reconstruction. <i>Lecture Notes in Computer Science</i> , <b>2012</b> , 118-128	0.9	1
53	Reconstruction of consensus tissue-specific metabolic models		1

52	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
51	Network Visualization Tools to Enhance Metabolic Engineering Platforms. <i>Advances in Intelligent Systems and Computing</i> , <b>2013</b> , 137-144	0.4	1
50	Metagenomic Analysis of the Saliva Microbiome with Merlin. <i>Advances in Intelligent Systems and Computing</i> , <b>2014</b> , 191-199	0.4	1
49	Reconstruction of Metabolic Models for Liver Cancer Cells. <i>Advances in Intelligent Systems and Computing</i> , <b>2016</b> , 213-221	0.4	1
48	Triptych: Multi-objective Optimisation of Service Deployment Costs, Application Delay and Bandwidth Usage <b>2019</b> ,		1
47	Predicting Promoters in Phage Genomes Using Machine Learning Models. <i>Advances in Intelligent Systems and Computing</i> , <b>2020</b> , 105-112	0.4	1
46	ProPythia: A Python Automated Platform for the Classification of Proteins Using Machine Learning. <i>Advances in Intelligent Systems and Computing</i> , <b>2021</b> , 32-41	0.4	1
45	Combining Multi-objective Evolutionary Algorithms with Deep Generative Models Towards Focused Molecular Design. <i>Lecture Notes in Computer Science</i> , <b>2021</b> , 81-96	0.9	1
44	Recurrent Deep Neural Networks for Enzyme Functional Annotation. <i>Lecture Notes in Networks and Systems</i> , <b>2022</b> , 62-73	0.5	1
43	BioTMPy: A Deep Learning-Based Tool to Classify Biomedical Literature. <i>Lecture Notes in Networks and Systems</i> , <b>2022</b> , 115-125	0.5	1
42	Exploring synergies between plant metabolic modelling and machine learning.. <i>Computational and Structural Biotechnology Journal</i> , <b>2022</b> , 20, 1885-1900	6.8	1
41	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
40	UV-Visible Spectrophotometry-Based Metabolomic Analysis of Cedrela Fissilis Vellozo (Meliaceae) Calluses - A Screening Tool for Culture Medium Composition and Cell Metabolic Profiles. <i>Advances in Intelligent Systems and Computing</i> , <b>2015</b> , 29-36	0.4	0
39	<sup>17</sup> Ethinylestradiol Analysis of Endo- and Exometabolome of Ulva lactuca (Chlorophyta) by <sup>1</sup> H-NMR Spectroscopy and Bioinformatics Tools. <i>Advances in Intelligent Systems and Computing</i> , <b>2019</b> , 216-223	0.4	0
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