Miguel P Rocha

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/1648167/miguel-p-rocha-publications-by-year.pdf
Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Recurrent Deep Neural Networks for Enzyme Functional Annotation. *Lecture Notes in Networks and Systems*, **2022**, 62-73	0.5	1
194	Combinatorial Optimization of Succinate Production in Escherichia coli. *Lecture Notes in Networks and Systems*, **2022**, 155-164	0.5	
193	Computational Tools for the Analysis of 2D-Nuclear Magnetic Resonance Data. *Lecture Notes in Networks and Systems*, **2022**, 52-61	0.5	
192	BioTMPy: A Deep Learning-Based Tool to Classify Biomedical Literature. *Lecture Notes in Networks and Systems*, **2022**, 115-125	0.5	1
191	Computational Methods for the Identification of Genetic Variants in Complex Diseases. *Lecture Notes in Networks and Systems*, **2022**, 1-10	0.5	
190	A Comparison of Different Compound Representations for Drug Sensitivity Prediction. *Lecture Notes in Networks and Systems*, **2022**, 145-154	0.5	0
189	UPIMAPI, reCOGnizer and KEGGCharter: Bioinformatics tools for functional annotation and visualization of (meta)-omics datasets.. *Computational and Structural Biotechnology Journal*, **2022**, 20, 1798-1810	6.8	2
188	Exploring synergies between plant metabolic modelling and machine learning.. *Computational and Structural Biotechnology Journal*, **2022**, 20, 1885-1900	6.8	1
187	Reconstruction of tissue-specific genome-scale metabolic models for human cancer stem cells.. *Computers in Biology and Medicine*, **2021**, 142, 105177	7	2
186	Generative Deep Learning for Targeted Compound Design. *Journal of Chemical Information and Modeling*, **2021**, 61, 5343-5361	6.1	7
185	Reconciliation of Regulatory Data: The Regulatory Networks of Escherichia coli and Bacillus subtilis. *Advances in Intelligent Systems and Computing*, **2021**, 155-165	0.4	
184	Deep learning for drug response prediction in cancer. *Briefings in Bioinformatics*, **2021**, 22, 360-379	13.4	39
183	ProPythia: A Python Automated Platform for the Classification of Proteins Using Machine Learning. *Advances in Intelligent Systems and Computing*, **2021**, 32-41	0.4	1
182	Combining Multi-objective Evolutionary Algorithms with Deep Generative Models Towards Focused Molecular Design. *Lecture Notes in Computer Science*, **2021**, 81-96	0.9	1
181	MEWpy: A Computational Strain Optimization Workbench in Python. *Bioinformatics*, **2021**,	7.2	2
180	NMRFinder: a novel method for 1D H-NMR metabolite annotation. *Metabolomics*, **2021**, 17, 21	4.7	
179	Model-guided development of an evolutionarily stable yeast chassis. *Molecular Systems Biology*, **2021**, 17, e10253	12.2	3

178	Going virtual and going wide: comparing Team-Based Learning in-class online and across disciplines. *Education and Information Technologies*, **2021**, 1-19	3.6	3
177	Causal integration of multi-omics data with prior knowledge to generate mechanistic hypotheses. *Molecular Systems Biology*, **2021**, 17, e9730	12.2	20
176	A comparison of multi-objective optimization algorithms for weight setting problems in traffic engineering. *Natural Computing*, **2020**, 1	1.3	
175	Traffic Engineering With Three-Segments Routing. *IEEE Transactions on Network and Service Management*, **2020**, 17, 1896-1909	4.8	5
174	Botanical source investigation and evaluation of the effect of seasonality on Brazilian propolis from Apis mellifera L.. *Scientia Agricola*, **2020**, 77,	2.5	1
173	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
172	Predicting Promoters in Phage Genomes Using Machine Learning Models. *Advances in Intelligent Systems and Computing*, **2020**, 105-112	0.4	1
171	Towards the Reconstruction of Integrated Genome-Scale Models of Metabolism and Gene Expression. *Advances in Intelligent Systems and Computing*, **2020**, 173-181	0.4	
170	Troppo - A Python Framework for the Reconstruction of Context-Specific Metabolic Models. *Advances in Intelligent Systems and Computing*, **2020**, 146-153	0.4	2
169	Artificial Intelligence in Biological Activity Prediction. *Advances in Intelligent Systems and Computing* , **2020**, 164-172	0.4	2
168	SamPler - a novel method for selecting parameters for gene functional annotation routines. *BMC Bioinformatics*, **2019**, 20, 454	3.6	3
167	Deep Neural Networks for Network Routing **2019**,		7
166	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. *Nature Communications*, **2019**, 10, 2674	17.4	119
165	Machine Learning-Enhanced T Cell Neoepitope Discovery for Immunotherapy Design. *Cancer Informatics*, **2019**, 18, 1176935119852081	2.4	8
164	Selected Extended Papers of the 12th International Conference on Practical Applications of Computational Biology and Bioinformatics (PACBB). *Journal of Integrative Bioinformatics*, **2019**, 16,	3.8	78
163	DNA Microarrays: Fundamentals, Data Integration and Applications **2019**, 349-362		
162	In Silico Predictions for Fucoxanthin Production by the Diatom Phaeodactylum Tricornutum. *Advances in Intelligent Systems and Computing*, **2019**, 139-148	0.4	
161	MOSCA: An Automated Pipeline for Integrated Metagenomics and Metatranscriptomics Data Analysis. *Advances in Intelligent Systems and Computing*, **2019**, 183-191	0.4	2

160	Metabolite Integration Pipeline for the Improvement of Human Metabolic Models. *Advances in Intelligent Systems and Computing*, **2019**, 192-199	0.4	
159	A Review on Metabolomics Data Analysis for Cancer Applications. *Advances in Intelligent Systems and Computing*, **2019**, 157-165	0.4	
158	Comparison of pathway analysis and constraint-based methods for cell factory design. *BMC Bioinformatics*, **2019**, 20, 350	3.6	1
157	Predicting promoters in phage genomes using PhagePromoter. *Bioinformatics*, **2019**, 35, 5301-5302	7.2	14
156	CoBAMP: a Python framework for metabolic pathway analysis in constraint-based models. *Bioinformatics*, **2019**, 35, 5361-5362	7.2	3
155	WebSpecmine: A Website for Metabolomics Data Analysis and Mining. *Metabolites*, **2019**, 9,	5.6	11
154	17□Ethinylestradiol Analysis of Endo- and Exometabolome of Ulva lactuca (Chlorophyta) by 1H-NMR Spectroscopy and Bioinformatics Tools. *Advances in Intelligent Systems and Computing*, **2019**, 216-223	0.4	0
153	Triptych: Multi-objective Optimisation of Service Deployment Costs, Application Delay and Bandwidth Usage **2019**,		1
152	In vitro fucoxanthin production by the Phaeodactylum tricornutum diatom. *Studies in Natural Products Chemistry*, **2019**, 63, 211-242	1.5	6
151	Utilitarian Placement of Composite Services. *IEEE Transactions on Network and Service Management* , **2018**, 15, 638-649	4.8	5
150	Development of an information retrieval tool for biomedical patents. *Computer Methods and Programs in Biomedicine*, **2018**, 159, 125-134	6.9	5
149	Methods for automated genome-scale metabolic model reconstruction. *Biochemical Society Transactions*, **2018**, 46, 931-936	5.1	33
148	A Review of Dynamic Modeling Approaches and Their Application in Computational Strain Optimization for Metabolic Engineering. *Frontiers in Microbiology*, **2018**, 9, 1690	5.7	37
147	Graphs and Biological Networks **2018**, 289-311		
146	Automating the Extraction of Essential Genes from Literature. *Lecture Notes in Computer Science*, **2018**, 75-87	0.9	
145	Reconstructing High-Quality Large-Scale Metabolic Models with merlin. *Methods in Molecular Biology*, **2018**, 1716, 1-36	1.4	10
144	Analyzing and Designing Cell Factories with OptFlux. *Methods in Molecular Biology*, **2018**, 1716, 37-76	1.4	3
143	A Model Integration Pipeline for the Improvement of Human Genome-Scale Metabolic Reconstructions. *Journal of Integrative Bioinformatics*, **2018**, 16,	3.8	2

142	Advanced Practical Applications of Computational Biology & Bioinformatics: PACBB’15. *Current Bioinformatics*, **2018**, 13, 565-565	4.7	
141	The long non-coding RNA is transcriptionally activated by HOXA9 and is an independent prognostic marker in patients with malignant glioma. *Oncotarget*, **2018**, 9, 15740-15756	3.3	17
140	Genome-Wide Semi-Automated Annotation of Transporter Systems. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2017**, 14, 443-456	3	10
139	Analysing Algorithms and Data Sources for the Tissue-Specific Reconstruction of Liver Healthy and Cancer Cells. *Interdisciplinary Sciences, Computational Life Sciences*, **2017**, 9, 36-45	3.5	6
138	Development of a Framework for Metabolic Pathway Analysis-Driven Strain Optimization Methods. *Interdisciplinary Sciences, Computational Life Sciences*, **2017**, 9, 46-55	3.5	1
137	Mixed-Integer Programming Model for Profiling Disease Biomarkers from Gene Expression Studies. *Lecture Notes in Computer Science*, **2017**, 50-61	0.9	
136	Metabolomics of Ulva lactuca Linnaeus (Chlorophyta) exposed to oil fuels: Fourier transform infrared spectroscopy and multivariate analysis as tools for metabolic fingerprint. *Marine Pollution Bulletin*, **2017**, 114, 831-836	6.7	12
135	Identification of robust strain designs via tandem pFBA/LMOMA phenotype prediction **2017**,		1
134	Data-driven reverse engineering of signaling pathways using ensembles of dynamic models. *PLoS Computational Biology*, **2017**, 13, e1005379	5	31
133	Optimizing Segment Routing using Evolutionary Computation. *Procedia Computer Science*, **2017**, 110, 312-319	1.6	2
132	Selected Extended Papers of the 11th International Conference on Practical Applications of Computational Biology and Bioinformatics (PACBB). *Journal of Integrative Bioinformatics*, **2017**, 14,	3.8	78
131	UV-Vis and CIELAB Based Chemometric Characterization of Manihot esculenta Carotenoid Contents. *Journal of Integrative Bioinformatics*, **2017**, 14,	3.8	8
130	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. *Lancet Oncology, The*, **2017**, 18, 132-142	21.7	90
129	A Chemometrics Approach for Nuclear Magnetic Resonance Data to Characterize the Partial Metabolome Banana Peels from Southern Brazil. *Journal of Integrative Bioinformatics*, **2017**, 14,	3.8	2
128	A Critical Evaluation of Automatic Atom Mapping Algorithms and Tools. *Advances in Intelligent Systems and Computing*, **2017**, 257-264	0.4	2
127	Classification Tools for Carotenoid Content Estimation in Manihot esculenta via Metabolomics and Machine Learning. *Advances in Intelligent Systems and Computing*, **2017**, 280-288	0.4	1
126	Characterization of the Chemical Composition of Banana Peels from Southern Brazil Across the Seasons Using Nuclear Magnetic Resonance and Chemometrics. *Advances in Intelligent Systems and Computing*, **2017**, 321-328	0.4	1
125	Development of Text Mining Tools for Information Retrieval from Patents. *Advances in Intelligent Systems and Computing*, **2017**, 66-73	0.4	2

124	UV-Vis Spectrophotometry and Chemometrics as Tools for Recognition of the Biochemical Profiles of Organic Banana Peels (Musa sp.) According to the Seasonality in Southern Brazil. *Advances in Intelligent Systems and Computing*, **2017**, 289-296	0.4	
123	Influence of Solar Radiation on the Production of Secondary Metabolites in Three Rice (Oryza sativa) Cultivars. *Advances in Intelligent Systems and Computing*, **2017**, 297-304	0.4	
122	Development of a Machine Learning Framework for Biomedical Text Mining. *Advances in Intelligent Systems and Computing*, **2016**, 41-49	0.4	2
121	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
120	An R package for the integrated analysis of metabolomics and spectral data. *Computer Methods and Programs in Biomedicine*, **2016**, 129, 117-24	6.9	29
119	Data supporting the role of enzymes and polysaccharides during cassava postharvest physiological deterioration. *Data in Brief*, **2016**, 6, 503-6	1.2	2
118	The role of ascorbate peroxidase, guaiacol peroxidase, and polysaccharides in cassava (Manihot esculenta Crantz) roots under postharvest physiological deterioration. *Food Chemistry*, **2016**, 197, 737-46	8.5	43
117	Metabolic Profiling and Classification of Propolis Samples from Southern Brazil: An NMR-Based Platform Coupled with Machine Learning. *Journal of Natural Products*, **2016**, 79, 13-23	4.9	22
116	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
115	Automated Network Resilience Optimization Using Computational Intelligence Methods. *Studies in Computational Intelligence*, **2016**, 485-495	0.8	
114	Reconstruction of the Regulatory Network for Bacillus subtilis and Reconciliation with Gene Expression Data. *Frontiers in Microbiology*, **2016**, 7, 275	5.7	7
113	Computing and Applying Atomic Regulons to Understand Gene Expression and Regulation. *Frontiers in Microbiology*, **2016**, 7, 1819	5.7	7
112	Reconstruction of Metabolic Models for Liver Cancer Cells. *Advances in Intelligent Systems and Computing*, **2016**, 213-221	0.4	1
111	In vitro exposure of Ulva lactuca Linnaeus (Chlorophyta) to gasoline - Biochemical and morphological alterations. *Chemosphere*, **2016**, 156, 428-437	8.4	14
110	Toward better understanding of postharvest deterioration: biochemical changes in stored cassava (Manihot esculenta Crantz) roots. *Food Science and Nutrition*, **2016**, 4, 409-22	3.2	9
109	A Text Mining Approach for the Extraction of Kinetic Information from Literature. *Advances in Intelligent Systems and Computing*, **2015**, 89-98	0.4	
108	Carotenoid Analysis of Cassava Genotypes Roots (Manihot Esculenta Crantz) Cultivated in Southern Brazil Using Chemometric Tools. *Advances in Intelligent Systems and Computing*, **2015**, 11-18	0.4	1
107	A Critical Evaluation of Methods for the Reconstruction of Tissue-Specific Models. *Lecture Notes in Computer Science*, **2015**, 340-352	0.9	5

106	Transcript-based reannotation for microarray probesets **2015**,		2
105	Reconstructing genome-scale metabolic models with merlin. *Nucleic Acids Research*, **2015**, 43, 3899-910	20.1	82
104	Reverse engineering of logic-based differential equation models using a mixed-integer dynamic optimization approach. *Bioinformatics*, **2015**, 31, 2999-3007	7.2	16
103	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
102	Integrating data from heterogeneous DNA microarray platforms. *Journal of Integrative Bioinformatics*, **2015**, 12, 39-55	3.8	
101	UV-visible scanning spectrophotometry and chemometric analysis as tools for carotenoids analysis in cassava genotypes (Manihot esculenta Crantz). *Journal of Integrative Bioinformatics*, **2015**, 12, 27-38	3.8	1
100	Discrimination of Brazilian propolis according to the seasoning using chemometrics and machine learning based on UV-Vis scanning data. *Journal of Integrative Bioinformatics*, **2015**, 12, 15-26	3.8	9
99	An Integrated Computational Platform for Metabolomics Data Analysis. *Advances in Intelligent Systems and Computing*, **2015**, 37-47	0.4	1
98	Microarray Gene Expression Data Integration: An Application to Brain Tumor Grade Determination. *Advances in Intelligent Systems and Computing*, **2015**, 127-135	0.4	1
97	UV-Visible Spectrophotometry-Based Metabolomic Analysis of Cedrela Fissilis Velozzo (Meliaceae) Calluses - A Screening Tool for Culture Medium Composition and Cell Metabolic Profiles. *Advances in Intelligent Systems and Computing*, **2015**, 29-36	0.4	0
96	UV-Visible Scanning Spectrophotometry and Chemometric Analysis as Tools to Build Descriptive and Classification Models for Propolis from Southern Brazil. *Advances in Intelligent Systems and Computing*, **2015**, 19-27	0.4	
95	Comparison of Single and Multi-objective Evolutionary Algorithms for Robust Link-State Routing. *Lecture Notes in Computer Science*, **2015**, 573-587	0.9	3
94	Transcriptional profiling of HOXA9-regulated genes in human glioblastoma cell models. *Genomics Data*, **2015**, 5, 54-8		8
93	A transcriptomic signature mediated by HOXA9 promotes human glioblastoma initiation, aggressiveness and resistance to temozolomide. *Oncotarget*, **2015**, 6, 7657-74	3.3	34
92	Discrimination of Brazilian propolis according to the seasoning using chemometrics and machine learning based on UV-Vis scanning data. *Journal of Integrative Bioinformatics*, **2015**, 12, 279	3.8	6
91	Metabolomics combined with chemometric tools (PCA, HCA, PLS-DA and SVM) for screening cassava (Manihot esculenta Crantz) roots during postharvest physiological deterioration. *Food Chemistry*, **2014**, 161, 67-78	8.5	77
90	Optimization of fed-batch fermentation processes with bio-inspired algorithms. *Expert Systems With Applications*, **2014**, 41, 2186-2195	7.8	39
89	Genome-scale bacterial transcriptional regulatory networks: reconstruction and integrated analysis with metabolic models. *Briefings in Bioinformatics*, **2014**, 15, 592-611	13.4	26

88	CBFA: phenotype prediction integrating metabolic models with constraints derived from experimental data. *BMC Systems Biology*, **2014**, 8, 123	3.5	6
87	An integrated network visualization framework towards metabolic engineering applications. *BMC Bioinformatics*, **2014**, 15, 420	3.6	6
86	Transcript level and sequence determinants of protein abundance and noise in Escherichia coli. *Nucleic Acids Research*, **2014**, 42, 4791-9	20.1	57
85	D-Tailor: automated analysis and design of DNA sequences. *Bioinformatics*, **2014**, 30, 1087-1094	7.2	23
84	Evaluating Pathway Enumeration Algorithms in Metabolic Engineering Case Studies. *Advances in Intelligent Systems and Computing*, **2014**, 215-223	0.4	
83	Metagenomic Analysis of the Saliva Microbiome with Merlin. *Advances in Intelligent Systems and Computing*, **2014**, 191-199	0.4	1
82	Discrimination of Brazilian Cassava Genotypes (Manihot esculenta Crantz) According to Their Physicochemical Traits and Functional Properties through Bioinformatics Tools. *Advances in Intelligent Systems and Computing*, **2014**, 57-63	0.4	
81	TNA4OptFlux--a software tool for the analysis of strain optimization strategies. *BMC Research Notes*, **2013**, 6, 175	2.3	1
80	Parallel evolutionary computation in bioinformatics applications. *Computer Methods and Programs in Biomedicine*, **2013**, 110, 183-91	6.9	6
79	Evolutionary computation for predicting optimal reaction knockouts and enzyme modulation strategies **2013**,		1
78	Bridging the layers: towards integration of signal transduction, regulation and metabolism into mathematical models. *Molecular BioSystems*, **2013**, 9, 1576-83		65
77	An integrated framework for strain optimization **2013**,		3
76	EMAIL SPAM DETECTION: A SYMBIOTIC FEATURE SELECTION APPROACH FOSTERED BY EVOLUTIONARY COMPUTATION. *International Journal of Information Technology and Decision Making*, **2013**, 12, 863-884	2.8	6
75	Re-annotation of the genome sequence of Helicobacter pylori 26695. *Journal of Integrative Bioinformatics*, **2013**, 10, 66-78	3.8	11
74	Re-annotation of the genome sequence of Helicobacter pylori 26695. *Journal of Integrative Bioinformatics*, **2013**, 10, 233	3.8	10
73	A Framework for Robust Traffic Engineering Using Evolutionary Computation. *Lecture Notes in Computer Science*, **2013**, 1-12	0.9	2
72	Large Scale Metabolic Characterization Using Flux Balance Analysis and Data Mining. *Lecture Notes in Computer Science*, **2013**, 336-345	0.9	
71	Robust Optimization of Intradomain Routing Using Evolutionary Algorithms. *Advances in Intelligent Systems and Computing*, **2013**, 201-208	0.4	

70	Network Visualization Tools to Enhance Metabolic Engineering Platforms. *Advances in Intelligent Systems and Computing*, **2013**, 137-144	0.4	1
69	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
68	A Machine Learning and Chemometrics Assisted Interpretation of Spectroscopic Data A NMR-Based Metabolomics Platform for the Assessment of Brazilian Propolis. *Lecture Notes in Computer Science*, **2012**, 129-140	0.9	1
67	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
66	In silico strain optimization by adding reactions to metabolic models. *Journal of Integrative Bioinformatics*, **2012**, 9, 44-56	3.8	
65	An Algorithm to Assemble Gene-Protein-Reaction Associations for Genome-Scale Metabolic Model Reconstruction. *Lecture Notes in Computer Science*, **2012**, 118-128	0.9	1
64	Computational Tools for Strain Optimization by Tuning the Optimal Level of Gene Expression. *Advances in Intelligent and Soft Computing*, **2012**, 251-258		1
63	Computational Tools for Strain Optimization by Adding Reactions. *Advances in Intelligent and Soft Computing*, **2012**, 241-250		
62	In silico strain optimization by adding reactions to metabolic models. *Journal of Integrative Bioinformatics*, **2012**, 9, 202	3.8	
61	Modeling formalisms in Systems Biology. *AMB Express*, **2011**, 1, 45	4.1	107
60	Semantic annotation of biological concepts interplaying microbial cellular responses. *BMC Bioinformatics*, **2011**, 12, 460	3.6	5
59	A computational tool for the simulation and optimization of microbial strains accounting integrated metabolic/regulatory information. *BioSystems*, **2011**, 103, 435-41	1.9	15
58	Symbiotic filtering for spam email detection. *Expert Systems With Applications*, **2011**, 38, 9365-9372	7.8	17
57	Quality of Service constrained routing optimization using Evolutionary Computation. *Applied Soft Computing Journal*, **2011**, 11, 356-364	7.5	19
56	Challenges in integrating Escherichia coli molecular biology data. *Briefings in Bioinformatics*, **2011**, 12, 91-103	13.4	4
55	Traffic Engineering Approaches Using Multicriteria Optimization Techniques. *Lecture Notes in Computer Science*, **2011**, 104-115	0.9	2
54	Highlighting Metabolic Strategies Using Network Analysis over Strain Optimization Results. *Lecture Notes in Computer Science*, **2011**, 109-120	0.9	
53	A Software Platform for Evolutionary Computation with Pluggable Parallelism and Quality Assurance. *International Federation for Information Processing*, **2011**, 45-50		

52	A Study on the Robustness of Strain Optimization Algorithms. *Advances in Intelligent and Soft Computing*, **2011**, 329-336		
51	Interpreting the Regulatory Interplay in E. coli Metabolic Pathways. *Advances in Intelligent and Soft Computing*, **2011**, 303-312		
50	A study of the short and long-term regulation of E. coli metabolic pathways. *Journal of Integrative Bioinformatics*, **2011**, 8, 183	3.8	1
49	A Collaborative Approach for Spam Detection **2010**,		4
48	Merlin: Metabolic Models Reconstruction using Genome-Scale Information*. *IFAC Postprint Volumes IPPV / International Federation of Automatic Control*, **2010**, 43, 120-125		3
47	OptFlux: an open-source software platform for in silico metabolic engineering. *BMC Systems Biology*, **2010**, 4, 45	3.5	258
46	AIBench: a rapid application development framework for translational research in biomedicine. *Computer Methods and Programs in Biomedicine*, **2010**, 98, 191-203	6.9	37
45	BioDR: Semantic indexing networks for biomedical document retrieval. *Expert Systems With Applications*, **2010**, 37, 3444-3453	7.8	9
44	Multi-scale Internet traffic forecasting using neural networks and time series methods. *Expert Systems*, **2010**, 29, no-no	2.1	11
43	Metaheuristics for Strain Optimization Using Transcriptional Information Enriched Metabolic Models. *Lecture Notes in Computer Science*, **2010**, 205-216	0.9	6
42	Analysis of the Effect of Reversibility Constraints on the Predictions of Genome-Scale Metabolic Models. *Advances in Intelligent and Soft Computing*, **2010**, 209-215		1
41	Spam Email Filtering Using Network-Level Properties. *Lecture Notes in Computer Science*, **2010**, 476-489	0.9	5
40	Enhancing Elementary Flux Modes Analysis Using Filtering Techniques in an Integrated Environment. *Advances in Intelligent and Soft Computing*, **2010**, 217-224		
39	A Critical Review on Modelling Formalisms and Simulation Tools in Computational Biosystems. *Lecture Notes in Computer Science*, **2009**, 1063-1070	0.9	1
38	@Note: a workbench for biomedical text mining. *Journal of Biomedical Informatics*, **2009**, 42, 710-20	10.2	28
37	Implementing Metaheuristic Optimization Algorithms with JECoLi **2009**,		6
36	Symbiotic Data Mining for Personalized Spam Filtering **2009**,		5
35	Data Integration Issues in the Reconstruction of the Genome-Scale Metabolic Model of Zymomonas Mobillis. *Advances in Soft Computing*, **2009**, 92-101		1

(2007-2009)

34	Modelling Fed-Batch Fermentation Processes: An Approach Based on Artificial Neural Networks. *Advances in Soft Computing*, **2009**, 30-39		3
33	Evolutionary Approaches for Strain Optimization Using Dynamic Models under a Metabolic Engineering Perspective. *Lecture Notes in Computer Science*, **2009**, 140-151	0.9	2
32	A Software Tool for the Simulation and Optimization of Dynamic Metabolic Models. *Lecture Notes in Computer Science*, **2009**, 1071-1078	0.9	
31	Modelling of Biotechnological Processes An Approach Based on Artificial Neural Networks. *Studies in Computational Intelligence*, **2009**, 311-332	0.8	
30	Biomedical Text Mining Applied to Document Retrieval and Semantic Indexing. *Lecture Notes in Computer Science*, **2009**, 954-963	0.9	
29	Natural computation meta-heuristics for the in silico optimization of microbial strains. *BMC Bioinformatics*, **2008**, 9, 499	3.6	75
28	Evaluating evolutionary multiobjective algorithms for the in silico optimization of mutant strains **2008**,		8
27	getALife - An Artificial Life Environment for the Evaluation of Agent-Based Systems and Evolutionary Algorithms for Reinforcement Learning. *Studies in Computational Intelligence*, **2008**, 35-44	0.8	1
26	Differential Evolution for the Offline and Online Optimization of Fed-Batch Fermentation Processes. *Studies in Computational Intelligence*, **2008**, 299-317	0.8	5
25	Multiconstrained Optimization of Networks with Multicast and Unicast Traffic. *Lecture Notes in Computer Science*, **2008**, 139-150	0.9	1
24	Evolution of neural networks for classification and regression. *Neurocomputing*, **2007**, 70, 2809-2816	5.4	66
23	Optimization of Bacterial Strains with Variable-Sized Evolutionary Algorithms **2007**,		1
22	A platform for the selection of genes in DNA microarraydata using evolutionary algorithms **2007**,		3
21	Evolutionary Computation for Quality of Service Internet Routing Optimization **2007**, 71-80		1
20	Evaluating Simulated Annealing Algorithms in the Optimization of Bacterial Strains **2007**, 473-484		1
19	Topology Aware Internet Traffic Forecasting Using Neural Networks. *Lecture Notes in Computer Science*, **2007**, 445-454	0.9	4
18	Evaluating Evolutionary Algorithms and Differential Evolution for the Online Optimization of Fermentation Processes **2007**, 236-246		4
17	Class-Based OSPF Traffic Engineering Inspired on Evolutionary Computation **2007**, 141-152		2

16	Time Series Forecasting by Evolutionary Neural Networks **2006**, 47-70		12
15	Efficient OSPF Weight Allocation for Intra-domain QoS Optimization. *Lecture Notes in Computer Science*, **2006**, 37-48	0.9	7
14	Simultaneous Evolution of Neural Network Topologies and Weights for Classification and Regression. *Lecture Notes in Computer Science*, **2005**, 59-66	0.9	9
13	Evolutionary Design of Neural Networks for Classification and Regression **2005**, 304-307		6
12	Evolutionary Algorithms for Static and Dynamic Optimization of Fed-batch Fermentation Processes **2005**, 288-291		6
11	Evolving Time Series Forecasting ARMA Models. *Journal of Heuristics*, **2004**, 10, 415-429	1.9	55
10	Evolutionary Algorithms for Optimal Control in Fed-Batch Fermentation Processes. *Lecture Notes in Computer Science*, **2004**, 84-93	0.9	10
9	Evolutionary Neural Network Learning. *Lecture Notes in Computer Science*, **2003**, 24-28	0.9	15
8	A Lamarckian Approach for Neural Network Training. *Neural Processing Letters*, **2002**, 15, 105-116	2.4	13
7	A Genetic and Evolutionary Programming Environment with Spatially Structured Populations and Built-In Parallelism. *Lecture Notes in Computer Science*, **2001**, 383-392	0.9	
6	A Study of Order Based Genetic and Evolutionary Algorithms in Combinatorial Optimization Problems. *Lecture Notes in Computer Science*, **2000**, 601-611	0.9	3
5	Viewing Scheduling Problems through Genetic and Evolutionary Algorithms. *Lecture Notes in Computer Science*, **2000**, 612-619	0.9	1
4	Preventing Premature Convergence to Local Optima in Genetic Algorithms via Random Offspring Generation. *Lecture Notes in Computer Science*, **1999**, 127-136	0.9	36
3	Reconstruction of consensus tissue-specific metabolic models		1
2	iEC7871 Quercus suber model: the first multi-tissue diel cycle genome-scale metabolic model of a woody tree		2
1	merlinv4.0: an updated platform for the reconstruction of high-quality genome-scale metabolic models		3