

# Florentino Fdez-Riverola

## List of Publications by Year in Descending Order

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**Version:** 2024-04-27

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

210  
papers

2,462  
citations

25  
h-index

41  
g-index

226  
ext. papers

2,975  
ext. citations

4  
avg, IF

5.4  
L-index

#	Paper	IF	Citations
210	A deep learning relation extraction approach to support a biomedical semi-automatic curation task: The case of the gluten bibliome. <i>Expert Systems With Applications</i> , <b>2022</b> , 195, 116616	7.8	1
209	Hospitality and Hospital Management. <i>Lecture Notes in Networks and Systems</i> , <b>2022</b> , 297-306	0.5	
208	An Entropic Approach to Burnout in the Management of a Kitchen Staff Team. <i>Smart Innovation, Systems and Technologies</i> , <b>2022</b> , 397-409	0.5	
207	Computational Approach to the Systematic Prediction of Glycolytic Abilities: Looking Into Human Microbiota. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2021</b> , 18, 2302-2313	3	1
206	A Health-Related Study from Food Online Reviews. The Case of Gluten-Free Foods. <i>Advances in Intelligent Systems and Computing</i> , <b>2021</b> , 12-22	0.4	
205	The Activity of Bioinformatics Developers and Users in Stack Overflow. <i>Advances in Intelligent Systems and Computing</i> , <b>2021</b> , 23-31	0.4	1
204	On-Device Object Detection for More Efficient and Privacy-Compliant Visual Perception in Context-Aware Systems. <i>Applied Sciences (Switzerland)</i> , <b>2021</b> , 11, 9173	2.6	1
203	Inferences on Mycobacterium Leprae Host Immune Response Escape and Antibiotic Resistance Using Genomic Data and GenomeFastScreen. <i>Advances in Intelligent Systems and Computing</i> , <b>2021</b> , 42-50 <sup>0.4</sup>	0.4	3
202	On the Identification of Clinically Relevant Bacterial Amino Acid Changes at the Whole Genome Level Using Auto-PSS-Genome. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , <b>2021</b> , 13, 334-343	3.5	0
201	Are There Benefits from Thermal Bacteria for Health? The Hydrogenome Role. <i>Water (Switzerland)</i> , <b>2021</b> , 13, 1439	3	1
200	Deep Neural Networks approaches for detecting and classifying colorectal polyps. <i>Neurocomputing</i> , <b>2021</b> , 423, 721-734	5.4	25
199	HaemoKBS: A knowledge-based system for real-time, continuous categorisation of adverse reactions in blood recipients. <i>Neurocomputing</i> , <b>2021</b> , 423, 756-767	5.4	
198	A Multi-valued Logic Assessment of Organizational Performance via Workforce Social Networking. <i>Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering</i> , <b>2021</b> , 63-77	0.2	3
197	A framework to extract biomedical knowledge from gluten-related tweets: The case of dietary concerns in digital era. <i>Artificial Intelligence in Medicine</i> , <b>2021</b> , 118, 102131	7.4	1
196	Real-time polyp detection model using convolutional neural networks. <i>Neural Computing and Applications</i> , <b>2021</b> , 1	4.8	8
195	Revisiting the Metabolic Capabilities of susbp. and subsp. from a Glycoside Hydrolase Perspective. <i>Microorganisms</i> , <b>2020</b> , 8,	4.9	3
194	Metatax: Metataxonomics with a Compi-Based Pipeline for Precision Medicine. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , <b>2020</b> , 12, 252-257	3.5	2

193	In silico and functional analyses of immunomodulatory peptides encrypted in the human gut metaproteome. <i>Journal of Functional Foods</i> , <b>2020</b> , 70, 103969	5.1	2
192	Mining the sociome for Health Informatics: Analysis of therapeutic lifestyle adherence of diabetic patients in Twitter. <i>Future Generation Computer Systems</i> , <b>2020</b> , 110, 214-232	7.5	3
191	Inferring Positive Selection in Large Viral Datasets. <i>Advances in Intelligent Systems and Computing</i> , <b>2020</b> , 61-69	0.4	5
190	Enhancing sepsis management through machine learning techniques: A review. <i>Medicina Intensiva</i> , <b>2020</b> , 46, 140-140	1.2	2
189	The extracellular proteins of <i>Lactobacillus acidophilus</i> DSM 20079T display anti-inflammatory effect in both in piglets, healthy human donors and Crohn's Disease patients. <i>Journal of Functional Foods</i> , <b>2020</b> , 64, 103660	5.1	2
188	Understanding the social evolution of the Java community in Stack Overflow: A 10-year study of developer interactions. <i>Future Generation Computer Systems</i> , <b>2020</b> , 105, 446-454	7.5	3
187	An RNA-seq Based Machine Learning Approach Identifies Latent Tuberculosis Patients With an Active Tuberculosis Profile. <i>Frontiers in Immunology</i> , <b>2020</b> , 11, 1470	8.4	11
186	SEDA: a Desktop Tool Suite for FASTA Files Processing. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2020</b> , PP,	3	4
185	Proposal of a New Bioinformatics Pipeline for Metataxonomics in Precision Medicine. <i>Advances in Intelligent Systems and Computing</i> , <b>2020</b> , 8-15	0.4	3
184	Gold Standard Evaluation of an Automatic HAIs Surveillance System. <i>BioMed Research International</i> , <b>2019</b> , 2019, 1049575	3	2
183	EvoPPI 1.0: a Web Platform for Within- and Between-Species Multiple Interactome Comparisons and Application to Nine PolyQ Proteins Determining Neurodegenerative Diseases. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , <b>2019</b> , 11, 45-56	3.5	7
182	In silico prediction reveals the existence of potential bioactive neuropeptides produced by the human gut microbiota. <i>Food Research International</i> , <b>2019</b> , 119, 221-226	7	6
181	BDBM 1.0: A Desktop Application for Efficient Retrieval and Processing of High-Quality Sequence Data and Application to the Identification of the Putative Coffea S-Locus. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , <b>2019</b> , 11, 57-67	3.5	6
180	Multiple independent L-gulonolactone oxidase (GULO) gene losses and vitamin C synthesis reacquisition events in non-Deuterostomian animal species. <i>BMC Evolutionary Biology</i> , <b>2019</b> , 19, 126	3	8
179	DEWE: A novel tool for executing differential expression RNA-Seq workflows in biomedical research. <i>Computers in Biology and Medicine</i> , <b>2019</b> , 107, 197-205	7	6
178	Application of agent-based modelling to assess single-molecule transport across the cell envelope of <i>E. coli</i> . <i>Computers in Biology and Medicine</i> , <b>2019</b> , 107, 218-226	7	2
177	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
176	Computational prediction of the bioactivity potential of proteomes based on expert knowledge. <i>Journal of Biomedical Informatics</i> , <b>2019</b> , 91, 103121	10.2	1

175	A Bioinformatics Protocol for Quickly Creating Large-Scale Phylogenetic Trees. <i>Advances in Intelligent Systems and Computing</i> , <b>2019</b> , 88-96	0.4	1
174	EvoPPI: A Web Application to Compare Protein-Protein Interactions (PPIs) from Different Databases and Species. <i>Advances in Intelligent Systems and Computing</i> , <b>2019</b> , 149-156	0.4	1
173	Approach for Unveiling the Glycoside Hydrolase Activities in Through a Systematic and Integrative Large-Scale Analysis. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 517	5.7	3
172	Predicting Specificities Under the Non-self Gametophytic Self-Incompatibility Recognition Model. <i>Frontiers in Plant Science</i> , <b>2019</b> , 10, 879	6.2	3
171	Next generation community assessment of biomedical entity recognition web servers: metrics, performance, interoperability aspects of BeCalm. <i>Journal of Cheminformatics</i> , <b>2019</b> , 11, 42	8.6	4
170	Using Twitter to Understand the Human Bowel Disease Community: Exploratory Analysis of Key Topics. <i>Journal of Medical Internet Research</i> , <b>2019</b> , 21, e12610	7.6	21
169	ATXN1 N-terminal region explains the binding differences of wild-type and expanded forms. <i>BMC Medical Genomics</i> , <b>2019</b> , 12, 145	3.7	3
168	Online visibility of software-related web sites: The case of biomedical text mining tools. <i>Information Processing and Management</i> , <b>2019</b> , 56, 565-583	6.3	6
167	Bioinformatics Protocols for Quickly Obtaining Large-Scale Data Sets for Phylogenetic Inferences. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , <b>2019</b> , 11, 1-9	3.5	9
166	Resources and tools for the high-throughput, multi-omic study of intestinal microbiota. <i>Briefings in Bioinformatics</i> , <b>2019</b> , 20, 1032-1056	13.4	8
165	Agent-based model of diffusion of N-acyl homoserine lactones in a multicellular environment of <i>Pseudomonas aeruginosa</i> and <i>Candida albicans</i> . <i>Biofouling</i> , <b>2018</b> , 34, 335-345	3.3	8
164	Large Scale Analyses and Visualization of Adaptive Amino Acid Changes Projects. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , <b>2018</b> , 10, 24-32	3.5	7
163	Perceptions of the use of intelligent information access systems in university level active learning activities among teachers of biomedical subjects. <i>International Journal of Medical Informatics</i> , <b>2018</b> , 112, 21-33	5.3	17
162	Using evolutionary computation for discovering spam patterns from e-mail samples. <i>Information Processing and Management</i> , <b>2018</b> , 54, 303-317	6.3	21
161	Bicycle: a bioinformatics pipeline to analyze bisulfite sequencing data. <i>Bioinformatics</i> , <b>2018</b> , 34, 1414-1415	11.5	13
160	Concept drift in e-mail datasets: An empirical study with practical implications. <i>Information Sciences</i> , <b>2018</b> , 428, 120-135	7.7	12
159	Active and Assisted Living Ecosystem for the Elderly. <i>Sensors</i> , <b>2018</b> , 18,	3.8	11
158	Determining the Influence of Class Imbalance for the Triage of Biomedical Documents. <i>Current Bioinformatics</i> , <b>2018</b> , 13, 592-605	4.7	5

157	Nextpresso: Next Generation Sequencing Expression Analysis Pipeline. <i>Current Bioinformatics</i> , <b>2018</b> , 13, 583-591	4.7	30
156	S2P: A software tool to quickly carry out reproducible biomedical research projects involving 2D-gel and MALDI-TOF MS protein data. <i>Computer Methods and Programs in Biomedicine</i> , <b>2018</b> , 155, 1-9	6.9	4
155	Quadcriteria Optimization of Binary Classifiers: Error Rates, Coverage, and Complexity. <i>Advances in Intelligent Systems and Computing</i> , <b>2018</b> , 37-49	0.4	0
154	Advanced Practical Applications of Computational Biology & Bioinformatics: PACBB15. <i>Current Bioinformatics</i> , <b>2018</b> , 13, 565-565	4.7	
153	BlasterJS: A novel interactive JavaScript visualisation component for BLAST alignment results. <i>PLoS ONE</i> , <b>2018</b> , 13, e0205286	3.7	8
152	GC4S: A bioinformatics-oriented Java software library of reusable graphical user interface components. <i>PLoS ONE</i> , <b>2018</b> , 13, e0204474	3.7	5
151	The Evolving Role of Information Technology in Haemovigilance Systems. <i>Journal of Healthcare Engineering</i> , <b>2018</b> , 2018, 6183468	3.7	2
150	S2P: A Desktop Application for Fast and Easy Processing of 2D-Gel and MALDI-Based Mass Spectrometry Protein Data. <i>Advances in Intelligent Systems and Computing</i> , <b>2017</b> , 1-8	0.4	
149	Collaborative relation annotation and quality analysis in Markyt environment. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2017</b> , 2017,	5	1
148	WARCProcessor: An Integrative Tool for Building and Management of Web Spam Corpora. <i>Sensors</i> , <b>2017</b> , 18,	3.8	4
147	MAHMI database: a comprehensive MetaHit-based resource for the study of the mechanism of action of the human microbiota. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2017</b> , 2017,	5	24
146	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
145	P4P: a peptidome-based strain-level genome comparison web tool. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, W265-W269	6.5	269
144	RUBioSeq+: A multiplatform application that executes parallelized pipelines to analyse next-generation sequencing data. <i>Computer Methods and Programs in Biomedicine</i> , <b>2017</b> , 138, 73-81	6.9	7
143	Screening of the Human Gut Metaproteome Identifies Th17-Promoting Peptides Encrypted in Proteins of Commensal Bacteria. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 1726	5.7	14
142	The Complexity of Promoter Regions Based on a Vector Topological Entropy. <i>Current Bioinformatics</i> , <b>2017</b> , 12,	4.7	1
141	Automated Collection and Sharing of Adaptive Amino Acid Changes Data. <i>Advances in Intelligent Systems and Computing</i> , <b>2017</b> , 18-25	0.4	
140	A methodological approach based on gold-nanoparticles followed by matrix assisted laser desorption ionization time of flight mass spectrometry for the analysis of urine profiling of knee osteoarthritis. <i>Talanta</i> , <b>2016</b> , 150, 638-45	6.2	8

139	A peptidome-based phylogeny pipeline reveals differential peptides at the strain level within <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> . <i>Food Microbiology</i> , <b>2016</b> , 60, 137-41	6	3
138	The Markyt visualisation, prediction and benchmark platform for chemical and gene entity recognition at BioCreative/CHEMDNER challenge. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2016</b> , 2016,	5	8
137	RUBioSeq+: An Application that Executes Parallelized Pipelines to Analyse Next-Generation Sequencing Data. <i>Advances in Intelligent Systems and Computing</i> , <b>2016</b> , 141-149	0.4	
136	High performance computing for three-dimensional agent-based molecular models. <i>Journal of Molecular Graphics and Modelling</i> , <b>2016</b> , 68, 68-77	2.8	2
135	Laser ablation and inductively coupled plasma mass spectrometry focusing on bioimaging from elemental distribution using MatLab software: a practical guide. <i>Journal of Analytical Atomic Spectrometry</i> , <b>2016</b> , 31, 832-840	3.7	20
134	A case-based reasoning system for aiding detection and classification of nosocomial infections. <i>Decision Support Systems</i> , <b>2016</b> , 84, 104-116	5.6	34
133	Improving Phylogeny Reconstruction at the Strain Level Using Peptidome Datasets. <i>PLoS Computational Biology</i> , <b>2016</b> , 12, e1005271	5	3
132	The Artificial Intelligence Workbench: a retrospective review. <i>Advances in Distributed Computing and Artificial Intelligence Journal</i> , <b>2016</b> , 5, 73-85	0.4	4
131	Reconstruction of the Network of Experimentally Validated AMP-Drug Combinations Against <i>Pseudomonas aeruginosa</i> Infections. <i>Current Bioinformatics</i> , <b>2016</b> , 11, 523-530	4.7	5
130	Construction of antimicrobial peptide-drug combination networks from scientific literature based on a semi-automated curation workflow. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2016</b> , 2016,	5	6
129	Intelligent Tutoring. <i>Advances in Linguistics and Communication Studies</i> , <b>2016</b> , 205-224	0.3	2
128	Implementing effective machine learning-based workflows for the analysis of mass spectrometry data. <i>Journal of Integrated OMICS</i> , <b>2016</b> , 6,	0.5	1
127	Boosting Accuracy of Classical Machine Learning Antispam Classifiers in Real Scenarios by Applying Rough Set Theory. <i>Scientific Programming</i> , <b>2016</b> , 2016, 1-10	1.4	6
126	WSF2: A Novel Framework for Filtering Web Spam. <i>Scientific Programming</i> , <b>2016</b> , 2016, 1-18	1.4	5
125	From amino acid sequence to bioactivity: The biomedical potential of antitumor peptides. <i>Protein Science</i> , <b>2016</b> , 25, 1084-95	6.3	42
124	RuleSIM: a toolkit for simulating the operation and improving throughput of rule-based spam filters. <i>Software - Practice and Experience</i> , <b>2016</b> , 46, 1091-1108	2.5	3
123	Using new scheduling heuristics based on resource consumption information for increasing throughput on rule-based spam filtering systems. <i>Software - Practice and Experience</i> , <b>2016</b> , 46, 1035-1051	2.5	6
122	A spam filtering multi-objective optimization study covering parsimony maximization and three-way classification. <i>Applied Soft Computing Journal</i> , <b>2016</b> , 48, 111-123	7.5	16

121	LA-iMageS: a software for elemental distribution bioimaging using LA-ICP-MS data. <i>Journal of Cheminformatics</i> , <b>2016</b> , 8, 65	8.6	29
120	Classifying patients in peritoneal dialysis by mass spectrometry-based profiling. <i>Talanta</i> , <b>2016</b> , 152, 364-70	7.0	11
119	BIOMedical Search Engine Framework: Lightweight and customized implementation of domain-specific biomedical search engines. <i>Computer Methods and Programs in Biomedicine</i> , <b>2016</b> , 131, 63-77	6.9	2
118	A dynamic model for integrating simple web spam classification techniques. <i>Expert Systems With Applications</i> , <b>2015</b> , 42, 7969-7978	7.8	13
117	Enabling systematic, harmonised and large-scale biofilms data computation: the Biofilms Experiment Workbench. <i>Computer Methods and Programs in Biomedicine</i> , <b>2015</b> , 118, 309-21	6.9	6
116	Gene knockout identification for metabolite production improvement using a hybrid of genetic ant colony optimization and flux balance analysis. <i>Biotechnology and Bioprocess Engineering</i> , <b>2015</b> , 20, 685-693	6.3	8
115	Marky: a tool supporting annotation consistency in multi-user and iterative document annotation projects. <i>Computer Methods and Programs in Biomedicine</i> , <b>2015</b> , 118, 242-51	6.9	16
114	Mass-Up: an all-in-one open software application for MALDI-TOF mass spectrometry knowledge discovery. <i>BMC Bioinformatics</i> , <b>2015</b> , 16, 318	3.6	68
113	A distributed multiagent system architecture for body area networks applied to healthcare monitoring. <i>BioMed Research International</i> , <b>2015</b> , 2015, 192454	3	20
112	Agent-based spatiotemporal simulation of biomolecular systems within the open source MASON framework. <i>BioMed Research International</i> , <b>2015</b> , 2015, 769471	3	5
111	A New Bioinformatic Pipeline to Address the Most Common Requirements in RNA-seq Data Analysis. <i>Advances in Intelligent Systems and Computing</i> , <b>2015</b> , 117-125	0.4	
110	Wireless Body Area Networks for Healthcare Applications: Protocol Stack Review. <i>International Journal of Distributed Sensor Networks</i> , <b>2015</b> , 2015, 1-23	1.7	47
109	Removing Barriers to Promote Social Computing among Senior Population. <i>International Journal of Distributed Sensor Networks</i> , <b>2015</b> , 2015, 1-13	1.7	3
108	Boosting Learning: Non-intrusive Monitoring of Student Efficiency. <i>Advances in Intelligent Systems and Computing</i> , <b>2015</b> , 73-80	0.4	7
107	A Novel Search Engine Supporting Specific Drug Queries and Literature Management. <i>Advances in Intelligent Systems and Computing</i> , <b>2015</b> , 99-106	0.4	
106	Combining Scheduling Heuristics to Improve e-mail Filtering Throughput. <i>Advances in Intelligent Systems and Computing</i> , <b>2015</b> , 235-242	0.4	1
105	Analyzing the Impact of Unbalanced Data on Web Spam Classification. <i>Advances in Intelligent Systems and Computing</i> , <b>2015</b> , 243-250	0.4	1
104	geneCommittee: a web-based tool for extensively testing the discriminatory power of biologically relevant gene sets in microarray data classification. <i>BMC Bioinformatics</i> , <b>2014</b> , 15, 31	3.6	5

103	A novel ensemble of classifiers that use biological relevant gene sets for microarray classification. <i>Applied Soft Computing Journal</i> , <b>2014</b> , 17, 117-126	7.5	18
102	A mesofluidic platform integrating on-chip probe ultrasonication for multiple sample pretreatment involving denaturation, reduction, and digestion in protein identification assays by mass spectrometry. <i>Analyst, The</i> , <b>2014</b> , 139, 992-5	5	3
101	A comprehensive analysis about the influence of low-level preprocessing techniques on mass spectrometry data for sample classification. <i>International Journal of Data Mining and Bioinformatics</i> , <b>2014</b> , 10, 455-73	0.5	3
100	Web scraping technologies in an API world. <i>Briefings in Bioinformatics</i> , <b>2014</b> , 15, 788-97	13.4	41
99	Sequential depletion coupled to C18 sequential extraction as a rapid tool for human serum multiple profiling. <i>Talanta</i> , <b>2014</b> , 125, 189-95	6.2	7
98	Assuring the authenticity of northwest Spain white wine varieties using machine learning techniques. <i>Food Research International</i> , <b>2014</b> , 60, 230-240	7	37
97	A mobile Virtual Butler to bridge the gap between users and ambient assisted living: a Smart Home case study. <i>Sensors</i> , <b>2014</b> , 14, 14302-29	3.8	15
96	A ubiquitous and low-cost solution for movement monitoring and accident detection based on sensor fusion. <i>Sensors</i> , <b>2014</b> , 14, 8961-83	3.8	30
95	Analysis of student's context in e-Learning <b>2014</b> ,		2
94	Marky: A Lightweight Web Tracking Tool for Document Annotation. <i>Advances in Intelligent Systems and Computing</i> , <b>2014</b> , 269-276	0.4	2
93	BEW: Bioinformatics Workbench for Analysis of Biofilms Experimental Data. <i>Advances in Intelligent Systems and Computing</i> , <b>2014</b> , 49-56	0.4	1
92	Wirebrush4SPAM: a novel framework for improving efficiency on spam filtering services. <i>Software - Practice and Experience</i> , <b>2013</b> , 43, 1299-1318	2.5	12
91	A hybrid artificial intelligence model for river flow forecasting. <i>Applied Soft Computing Journal</i> , <b>2013</b> , 13, 3449-3458	7.5	43
90	A Workflow for the Application of Biclustering to Mass Spectrometry Data. <i>Advances in Intelligent Systems and Computing</i> , <b>2013</b> , 145-153	0.4	2
89	Keystrokes and Clicks: Measuring Stress on E-learning Students. <i>Advances in Intelligent Systems and Computing</i> , <b>2013</b> , 119-126	0.4	22
88	Speeding up the screening of steroids in urine: development of a user-friendly library. <i>Steroids</i> , <b>2013</b> , 78, 1226-32	2.8	8
87	Effective scheduling strategies for boosting performance on rule-based spam filtering frameworks. <i>Journal of Systems and Software</i> , <b>2013</b> , 86, 3151-3161	3.3	13
86	A new approach to bacterial colony morphotyping by matrix-assisted laser desorption ionization time of flight-based mass spectrometry. <i>Talanta</i> , <b>2013</b> , 116, 100-7	6.2	3



85	genEnsemble: A new model for the combination of classifiers and integration of biological knowledge applied to genomic data. <i>Expert Systems With Applications</i> , <b>2013</b> , 40, 52-63	7.8	6
84	BioAnnote: a software platform for annotating biomedical documents with application in medical learning environments. <i>Computer Methods and Programs in Biomedicine</i> , <b>2013</b> , 111, 139-47	6.9	23
83	Patterns of evolution at the gametophytic self-incompatibility <i>Sorbus aucuparia</i> (Pyrinae) S pollen genes support the non-self recognition by multiple factors model. <i>Journal of Experimental Botany</i> , <b>2013</b> , 64, 2423-34	7	16
82	The <i>Drosophila melanogaster</i> methuselah gene: a novel gene with ancient functions. <i>PLoS ONE</i> , <b>2013</b> , 8, e63747	3.7	18
81	Rough sets for spam filtering: Selecting appropriate decision rules for boundary e-mail classification. <i>Applied Soft Computing Journal</i> , <b>2012</b> , 12, 3671-3682	7.5	34
80	Grindstone4Spam: An optimization toolkit for boosting e-mail classification. <i>Journal of Systems and Software</i> , <b>2012</b> , 85, 2909-2920	3.3	13
79	Fast human serum profiling through chemical depletion coupled to gold-nanoparticle-assisted protein separation. <i>Talanta</i> , <b>2012</b> , 100, 239-45	6.2	27
78	Direct matrix assisted laser desorption ionization mass spectrometry-based analysis of wine as a powerful tool for classification purposes. <i>Talanta</i> , <b>2012</b> , 91, 72-6	6.2	19
77	SDAI: An integral evaluation methodology for content-based spam filtering models. <i>Expert Systems With Applications</i> , <b>2012</b> , 39, 12487-12500	7.8	22
76	A JAVA application framework for scientific software development. <i>Software - Practice and Experience</i> , <b>2012</b> , 42, 1015-1036	2.5	9
75	Unobstructive Body Area Networks (BAN) for efficient movement monitoring. <i>Sensors</i> , <b>2012</b> , 12, 12473-88	3.8	24
74	On the Development of a Pipeline for the Automatic Detection of Positively Selected Sites. <i>Advances in Intelligent and Soft Computing</i> , <b>2012</b> , 225-229		2
73	ADOPS - Automatic Detection Of Positively Selected Sites. <i>Journal of Integrative Bioinformatics</i> , <b>2012</b> , 9, 18-32	3.8	14
72	A novel ensemble approach for multiclassification of DNA microarray data using biological relevant gene sets. <i>International Journal of Data Mining and Bioinformatics</i> , <b>2012</b> , 6, 602-16	0.5	6
71	ADOPS--Automatic Detection Of Positively Selected Sites. <i>Journal of Integrative Bioinformatics</i> , <b>2012</b> , 9, 200	3.8	16
70	Developing Anti-spam Filters Using Automatically Generated Rough Sets Rules. <i>Advances in Intelligent Systems and Computing</i> , <b>2012</b> , 325-334	0.4	1
69	Applying AIBench Framework to Develop Rich User Interfaces in NGS Studies. <i>Advances in Intelligent and Soft Computing</i> , <b>2012</b> , 189-196		
68	Biological Knowledge Integration in DNA Microarray Gene Expression Classification Based on Rough Set Theory. <i>Advances in Intelligent and Soft Computing</i> , <b>2012</b> , 53-61		1

67	Using variable precision rough set for selection and classification of biological knowledge integrated in DNA gene expression. <i>Journal of Integrative Bioinformatics</i> , <b>2012</b> , 9, 199	3.8	1
66	Using CBR as Design Methodology for Developing Adaptable Decision Support Systems <b>2011</b> ,		2
65	Rapid development of proteomic applications with the AIBench framework. <i>Journal of Integrative Bioinformatics</i> , <b>2011</b> , 8, 16-30	3.8	5
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