

Florentino Fdez-Riverola

List of Publications by Citations

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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	ALTER: program-oriented conversion of DNA and protein alignments. <i>Nucleic Acids Research</i> , 2010 , 38, W14-8	20.1	265
209	Applying lazy learning algorithms to tackle concept drift in spam filtering. <i>Expert Systems With Applications</i> , 2007 , 33, 36-48	7.8	85
208	Selected Extended Papers of the 12th International Conference on Practical Applications of Computational Biology and Bioinformatics (PACBB). <i>Journal of Integrative Bioinformatics</i> , 2019 , 16,	3.8	78
207	Selected Extended Papers of the 11th International Conference on Practical Applications of Computational Biology and Bioinformatics (PACBB). <i>Journal of Integrative Bioinformatics</i> , 2017 , 14,	3.8	78
206	Mass-Up: an all-in-one open software application for MALDI-TOF mass spectrometry knowledge discovery. <i>BMC Bioinformatics</i> , 2015 , 16, 318	3.6	68
205	gene-CBR: A CASE-BASED REASONING TOOL FOR CANCER DIAGNOSIS USING MICROARRAY DATA SETS. <i>Computational Intelligence</i> , 2006 , 22, 254-268	2.5	66
204	SpamHunting: An instance-based reasoning system for spam labelling and filtering. <i>Decision Support Systems</i> , 2007 , 43, 722-736	5.6	65
203	FSFRT: Forecasting System for Red Tides. <i>Applied Intelligence</i> , 2004 , 21, 251-264	4.9	60
202	A Comparative Performance Study of Feature Selection Methods for the Anti-spam Filtering Domain. <i>Lecture Notes in Computer Science</i> , 2006 , 106-120	0.9	50
201	Wireless Body Area Networks for Healthcare Applications: Protocol Stack Review. <i>International Journal of Distributed Sensor Networks</i> , 2015 , 2015, 1-23	1.7	47
200	CBR based system for forecasting red tides. <i>Knowledge-Based Systems</i> , 2003 , 16, 321-328	7.3	44
199	A hybrid artificial intelligence model for river flow forecasting. <i>Applied Soft Computing Journal</i> , 2013 , 13, 3449-3458	7.5	43
198	Reducing the Memory Size of a Fuzzy Case-Based Reasoning System Applying Rough Set Techniques. <i>IEEE Transactions on Systems, Man and Cybernetics, Part C: Applications and Reviews</i> , 2007 , 37, 138-146		43
197	From amino acid sequence to bioactivity: The biomedical potential of antitumor peptides. <i>Protein Science</i> , 2016 , 25, 1084-95	6.3	42
196	Web scraping technologies in an API world. <i>Briefings in Bioinformatics</i> , 2014 , 15, 788-97	13.4	41
195	Assuring the authenticity of northwest Spain white wine varieties using machine learning techniques. <i>Food Research International</i> , 2014 , 60, 230-240	7	37
194	AlBench: a rapid application development framework for translational research in biomedicine. <i>Computer Methods and Programs in Biomedicine</i> , 2010 , 98, 191-203	6.9	37

193	A case-based reasoning system for aiding detection and classification of nosocomial infections. <i>Decision Support Systems</i> , 2016 , 84, 104-116	5.6	34
192	Rough sets for spam filtering: Selecting appropriate decision rules for boundary e-mail classification. <i>Applied Soft Computing Journal</i> , 2012 , 12, 3671-3682	7.5	34
191	A ubiquitous and low-cost solution for movement monitoring and accident detection based on sensor fusion. <i>Sensors</i> , 2014 , 14, 8961-83	3.8	30
190	Nextpresso: Next Generation Sequencing Expression Analysis Pipeline. <i>Current Bioinformatics</i> , 2018 , 13, 583-591	4.7	30
189	LA-iMageS: a software for elemental distribution bioimaging using LA-ICP-MS data. <i>Journal of Cheminformatics</i> , 2016 , 8, 65	8.6	29
188	@Note: a workbench for biomedical text mining. <i>Journal of Biomedical Informatics</i> , 2009 , 42, 710-20	10.2	28
187	Fast human serum profiling through chemical depletion coupled to gold-nanoparticle-assisted protein separation. <i>Talanta</i> , 2012 , 100, 239-45	6.2	27
186	geneCBR: a translational tool for multiple-microarray analysis and integrative information retrieval for aiding diagnosis in cancer research. <i>BMC Bioinformatics</i> , 2009 , 10, 187	3.6	27
185	WhichGenes: a web-based tool for gathering, building, storing and exporting gene sets with application in gene set enrichment analysis. <i>Nucleic Acids Research</i> , 2009 , 37, W329-34	20.1	25
184	Deep Neural Networks approaches for detecting and classifying colorectal polyps. <i>Neurocomputing</i> , 2021 , 423, 721-734	5.4	25
183	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> , 2017 , 2017,	5	24
182	Unobstructive Body Area Networks (BAN) for efficient movement monitoring. <i>Sensors</i> , 2012 , 12, 12473-88	3.8	24
181	BioAnnote: a software platform for annotating biomedical documents with application in medical learning environments. <i>Computer Methods and Programs in Biomedicine</i> , 2013 , 111, 139-47	6.9	23
180	Keystrokes and Clicks: Measuring Stress on E-learning Students. <i>Advances in Intelligent Systems and Computing</i> , 2013 , 119-126	0.4	22
179	SDAI: An integral evaluation methodology for content-based spam filtering models. <i>Expert Systems With Applications</i> , 2012 , 39, 12487-12500	7.8	22
178	Using evolutionary computation for discovering spam patterns from e-mail samples. <i>Information Processing and Management</i> , 2018 , 54, 303-317	6.3	21
177	Using Twitter to Understand the Human Bowel Disease Community: Exploratory Analysis of Key Topics. <i>Journal of Medical Internet Research</i> , 2019 , 21, e12610	7.6	21
176	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> , 2016 , 31, 832-840	3.7	20

175	A distributed multiagent system architecture for body area networks applied to healthcare monitoring. <i>BioMed Research International</i> , 2015 , 2015, 192454	3	20
174	Direct matrix assisted laser desorption ionization mass spectrometry-based analysis of wine as a powerful tool for classification purposes. <i>Talanta</i> , 2012 , 91, 72-6	6.2	19
173	Evaluating the effect of unbalanced data in biomedical document classification. <i>Journal of Integrative Bioinformatics</i> , 2011 , 8, 105-117	3.8	19
172	Tracking Concept Drift at Feature Selection Stage in SpamHunting: An Anti-spam Instance-Based Reasoning System. <i>Lecture Notes in Computer Science</i> , 2006 , 504-518	0.9	19
171	A novel ensemble of classifiers that use biological relevant gene sets for microarray classification. <i>Applied Soft Computing Journal</i> , 2014 , 17, 117-126	7.5	18
170	The <i>Drosophila melanogaster</i> methuselah gene: a novel gene with ancient functions. <i>PLoS ONE</i> , 2013 , 8, e63747	3.7	18
169	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> , 2018 , 112, 21-33	5.3	17
168	Marky: a tool supporting annotation consistency in multi-user and iterative document annotation projects. <i>Computer Methods and Programs in Biomedicine</i> , 2015 , 118, 242-51	6.9	16
167	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> , 2013 , 64, 2423-34	7	16
166	Van Hemmen-Kondo model for disordered strongly correlated electron systems. <i>Physical Review B</i> , 2010 , 81,	3.3	16
165	ADOPS--Automatic Detection Of Positively Selected Sites. <i>Journal of Integrative Bioinformatics</i> , 2012 , 9, 200	3.8	16
164	A spam filtering multi-objective optimization study covering parsimony maximization and three-way classification. <i>Applied Soft Computing Journal</i> , 2016 , 48, 111-123	7.5	16
163	A mobile Virtual Butler to bridge the gap between users and ambient assisted living: a Smart Home case study. <i>Sensors</i> , 2014 , 14, 14302-29	3.8	15
162	Screening of the Human Gut Metaproteome Identifies Th17-Promoting Peptides Encrypted in Proteins of Commensal Bacteria. <i>Frontiers in Microbiology</i> , 2017 , 8, 1726	5.7	14
161	ADOPS - Automatic Detection Of Positively Selected Sites. <i>Journal of Integrative Bioinformatics</i> , 2012 , 9, 18-32	3.8	14
160	A dynamic model for integrating simple web spam classification techniques. <i>Expert Systems With Applications</i> , 2015 , 42, 7969-7978	7.8	13
159	Bicycle: a bioinformatics pipeline to analyze bisulfite sequencing data. <i>Bioinformatics</i> , 2018 , 34, 1414-1415	15.2	13
158	Effective scheduling strategies for boosting performance on rule-based spam filtering frameworks. <i>Journal of Systems and Software</i> , 2013 , 86, 3151-3161	3.3	13

157	Grindstone4Spam: An optimization toolkit for boosting e-mail classification. <i>Journal of Systems and Software</i> , 2012 , 85, 2909-2920	3.3	13
156	Concept drift in e-mail datasets: An empirical study with practical implications. <i>Information Sciences</i> , 2018 , 428, 120-135	7.7	12
155	Wirebrush4SPAM: a novel framework for improving efficiency on spam filtering services. <i>Software - Practice and Experience</i> , 2013 , 43, 1299-1318	2.5	12
154	Active and Assisted Living Ecosystem for the Elderly. <i>Sensors</i> , 2018 , 18,	3.8	11
153	An RNA-seq Based Machine Learning Approach Identifies Latent Tuberculosis Patients With an Active Tuberculosis Profile. <i>Frontiers in Immunology</i> , 2020 , 11, 1470	8.4	11
152	Classifying patients in peritoneal dialysis by mass spectrometry-based profiling. <i>Talanta</i> , 2016 , 152, 364-370	7.0	11
151	Decision peptide-driven: a free software tool for accurate protein quantification using gel electrophoresis and matrix assisted laser desorption ionization time of flight mass spectrometry. <i>Talanta</i> , 2010 , 82, 1412-20	6.2	10
150	Tokenising, Stemming and Stopword Removal on Anti-spam Filtering Domain. <i>Lecture Notes in Computer Science</i> , 2006 , 449-458	0.9	10
149	A JAVA application framework for scientific software development. <i>Software - Practice and Experience</i> , 2012 , 42, 1015-1036	2.5	9
148	DFP: a Bioconductor package for fuzzy profile identification and gene reduction of microarray data. <i>BMC Bioinformatics</i> , 2009 , 10, 37	3.6	9
147	Managing irrelevant knowledge in CBR models for unsolicited e-mail classification. <i>Expert Systems With Applications</i> , 2009 , 36, 1601-1614	7.8	9
146	Elder Care Fall Detection System. <i>Advances in Intelligent and Soft Computing</i> , 2011 , 85-92		9
145	A novel (18)O inverse labeling-based workflow for accurate bottom-up mass spectrometry quantification of proteins separated by gel electrophoresis. <i>Electrophoresis</i> , 2010 , 31, 3407-19	3.6	9
144	BioDR: Semantic indexing networks for biomedical document retrieval. <i>Expert Systems With Applications</i> , 2010 , 37, 3444-3453	7.8	9
143	Bioinformatics Protocols for Quickly Obtaining Large-Scale Data Sets for Phylogenetic Inferences. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019 , 11, 1-9	3.5	9
142	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> , 2016 , 150, 638-45	6.2	8
141	Multiple independent L-gulonolactone oxidase (GULO) gene losses and vitamin C synthesis reacquisition events in non-Deuterostomian animal species. <i>BMC Evolutionary Biology</i> , 2019 , 19, 126	3	8
140	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> , 2015 , 20, 685-693 ¹	3.1	8

139	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> , 2018 , 34, 335-345	3.3	8
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> , 2016 , 2016,	5	8
137	Speeding up the screening of steroids in urine: development of a user-friendly library. <i>Steroids</i> , 2013 , 78, 1226-32	2.8	8
136	Resources and tools for the high-throughput, multi-omic study of intestinal microbiota. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1032-1056	13.4	8
135	BlasterJS: A novel interactive JavaScript visualisation component for BLAST alignment results. <i>PLoS ONE</i> , 2018 , 13, e0205286	3.7	8
134	Real-time polyp detection model using convolutional neural networks. <i>Neural Computing and Applications</i> , 2021 , 1	4.8	8
133	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> , 2019 , 11, 45-56	3.5	7
132	Large Scale Analyses and Visualization of Adaptive Amino Acid Changes Projects. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2018 , 10, 24-32	3.5	7
131	Sequential depletion coupled to C18 sequential extraction as a rapid tool for human serum multiple profiling. <i>Talanta</i> , 2014 , 125, 189-95	6.2	7
130	RUBioSeq+: A multiplatform application that executes parallelized pipelines to analyse next-generation sequencing data. <i>Computer Methods and Programs in Biomedicine</i> , 2017 , 138, 73-81	6.9	7
129	PileLine: a toolbox to handle genome position information in next-generation sequencing studies. <i>BMC Bioinformatics</i> , 2011 , 12, 31	3.6	7
128	Boosting Learning: Non-intrusive Monitoring of Student Efficiency. <i>Advances in Intelligent Systems and Computing</i> , 2015 , 73-80	0.4	7
127	In silico prediction reveals the existence of potential bioactive neuropeptides produced by the human gut microbiota. <i>Food Research International</i> , 2019 , 119, 221-226	7	6
126	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> , 2019 , 11, 57-67	3.5	6
125	DEWE: A novel tool for executing differential expression RNA-Seq workflows in biomedical research. <i>Computers in Biology and Medicine</i> , 2019 , 107, 197-205	7	6
124	Enabling systematic, harmonised and large-scale biofilms data computation: the Biofilms Experiment Workbench. <i>Computer Methods and Programs in Biomedicine</i> , 2015 , 118, 309-21	6.9	6
123	genEnsemble: A new model for the combination of classifiers and integration of biological knowledge applied to genomic data. <i>Expert Systems With Applications</i> , 2013 , 40, 52-63	7.8	6
122	PileLineGUI: a desktop environment for handling genome position files in next-generation sequencing studies. <i>Nucleic Acids Research</i> , 2011 , 39, W562-6	20.1	6

121	A novel ensemble approach for multiclass classification of DNA microarray data using biological relevant gene sets. <i>International Journal of Data Mining and Bioinformatics</i> , 2012 , 6, 602-16	0.5	6
120	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> , 2016 , 2016,	5	6
119	Boosting Accuracy of Classical Machine Learning Antispam Classifiers in Real Scenarios by Applying Rough Set Theory. <i>Scientific Programming</i> , 2016 , 2016, 1-10	1.4	6
118	Using new scheduling heuristics based on resource consumption information for increasing throughput on rule-based spam filtering systems. <i>Software - Practice and Experience</i> , 2016 , 46, 1035-1051	1.5	6
117	Online visibility of software-related web sites: The case of biomedical text mining tools. <i>Information Processing and Management</i> , 2019 , 56, 565-583	6.3	6
116	geneCommittee: a web-based tool for extensively testing the discriminatory power of biologically relevant gene sets in microarray data classification. <i>BMC Bioinformatics</i> , 2014 , 15, 31	3.6	5
115	Agent-based spatiotemporal simulation of biomolecular systems within the open source MASON framework. <i>BioMed Research International</i> , 2015 , 2015, 769471	3	5
114	Rapid development of proteomic applications with the AIBench framework. <i>Journal of Integrative Bioinformatics</i> , 2011 , 8, 16-30	3.8	5
113	Indirect ultrasonication for protein quantification and peptide mass mapping through mass spectrometry-based techniques. <i>Talanta</i> , 2010 , 82, 587-93	6.2	5
112	FSFRT: FORECASTING SYSTEM FOR RED TIDES. A HYBRID AUTONOMOUS AI MODEL. <i>Applied Artificial Intelligence</i> , 2003 , 17, 955-982	2.3	5
111	Reconstruction of the Network of Experimentally Validated AMP-Drug Combinations Against <i>Pseudomonas aeruginosa</i> Infections. <i>Current Bioinformatics</i> , 2016 , 11, 523-530	4.7	5
110	Determining the Influence of Class Imbalance for the Triage of Biomedical Documents. <i>Current Bioinformatics</i> , 2018 , 13, 592-605	4.7	5
109	Inferring Positive Selection in Large Viral Datasets. <i>Advances in Intelligent Systems and Computing</i> , 2020 , 61-69	0.4	5
108	WSF2: A Novel Framework for Filtering Web Spam. <i>Scientific Programming</i> , 2016 , 2016, 1-18	1.4	5
107	GC4S: A bioinformatics-oriented Java software library of reusable graphical user interface components. <i>PLoS ONE</i> , 2018 , 13, e0204474	3.7	5
106	Improving Gene Selection in Microarray Data Analysis Using Fuzzy Patterns Inside a CBR System. <i>Lecture Notes in Computer Science</i> , 2005 , 191-205	0.9	5
105	WARCProcessor: An Integrative Tool for Building and Management of Web Spam Corpora. <i>Sensors</i> , 2017 , 18,	3.8	4
104	Next generation community assessment of biomedical entity recognition web servers: metrics, performance, interoperability aspects of BeCalm. <i>Journal of Cheminformatics</i> , 2019 , 11, 42	8.6	4

103	The Artificial Intelligence Workbench: a retrospective review. <i>Advances in Distributed Computing and Artificial Intelligence Journal</i> , 2016 , 5, 73-85	0.4	4
102	SEDA: a Desktop Tool Suite for FASTA Files Processing. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , PP,	3	4
101	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> , 2018 , 155, 1-9	6.9	4
100	Applying GCS Networks to Fuzzy Discretized Microarray Data for Tumour Diagnosis. <i>Lecture Notes in Computer Science</i> , 2006 , 1095-1102	0.9	4
99	PathJam: a new service for integrating biological pathway information. <i>Journal of Integrative Bioinformatics</i> , 2010 , 7,	3.8	4
98	Revisiting the Metabolic Capabilities of susbp. and subsp. from a Glycoside Hydrolase Perspective. <i>Microorganisms</i> , 2020 , 8,	4.9	3
97	Mining the sociome for Health Informatics: Analysis of therapeutic lifestyle adherence of diabetic patients in Twitter. <i>Future Generation Computer Systems</i> , 2020 , 110, 214-232	7.5	3
96	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> , 2016 , 60, 137-41	6	3
95	Approach for Unveiling the Glycoside Hydrolase Activities in Through a Systematic and Integrative Large-Scale Analysis. <i>Frontiers in Microbiology</i> , 2019 , 10, 517	5.7	3
94	Predicting Specificities Under the Non-self Gametophytic Self-Incompatibility Recognition Model. <i>Frontiers in Plant Science</i> , 2019 , 10, 879	6.2	3
93	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> , 2014 , 139, 992-5	5	3
92	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> , 2014 , 10, 455-73	0.5	3
91	A new approach to bacterial colony morphotyping by matrix-assisted laser desorption ionization time of flight-based mass spectrometry. <i>Talanta</i> , 2013 , 116, 100-7	6.2	3
90	Removing Barriers to Promote Social Computing among Senior Population. <i>International Journal of Distributed Sensor Networks</i> , 2015 , 2015, 1-13	1.7	3
89	Improving Phylogeny Reconstruction at the Strain Level Using Peptidome Datasets. <i>PLoS Computational Biology</i> , 2016 , 12, e1005271	5	3
88	Inferences on Mycobacterium Leprae Host Immune Response Escape and Antibiotic Resistance Using Genomic Data and GenomeFastScreen. <i>Advances in Intelligent Systems and Computing</i> , 2021 , 42-50 ^{0.4}		3
87	Fuzzy Patterns and GCS Networks to Clustering Gene Expression Data. <i>Studies in Fuzziness and Soft Computing</i> , 2009 , 103-125	0.7	3
86	Understanding the social evolution of the Java community in Stack Overflow: A 10-year study of developer interactions. <i>Future Generation Computer Systems</i> , 2020 , 105, 446-454	7.5	3

85	RuleSIM: a toolkit for simulating the operation and improving throughput of rule-based spam filters. <i>Software - Practice and Experience</i> , 2016 , 46, 1091-1108	2.5	3
84	ATXN1 N-terminal region explains the binding differences of wild-type and expanded forms. <i>BMC Medical Genomics</i> , 2019 , 12, 145	3.7	3
83	Proposal of a New Bioinformatics Pipeline for Metataxonomics in Precision Medicine. <i>Advances in Intelligent Systems and Computing</i> , 2020 , 8-15	0.4	3
82	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> , 2021 , 63-77	0.2	3
81	Using Fuzzy Patterns for Gene Selection and Data Reduction on Microarray Data. <i>Lecture Notes in Computer Science</i> , 2006 , 1087-1094	0.9	3
80	An Automated Hybrid CBR System for Forecasting. <i>Lecture Notes in Computer Science</i> , 2002 , 519-533	0.9	3
79	Evaluating the effect of unbalanced data in biomedical document classification. <i>Journal of Integrative Bioinformatics</i> , 2011 , 8, 177	3.8	3
78	Gold Standard Evaluation of an Automatic HAIs Surveillance System. <i>BioMed Research International</i> , 2019 , 2019, 1049575	3	2
77	Application of agent-based modelling to assess single-molecule transport across the cell envelope of E. coli. <i>Computers in Biology and Medicine</i> , 2019 , 107, 218-226	7	2
76	Metatax: Metataxonomics with a Compi-Based Pipeline for Precision Medicine. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2020 , 12, 252-257	3.5	2
75	In silico and functional analyses of immunomodulatory peptides encrypted in the human gut metaproteome. <i>Journal of Functional Foods</i> , 2020 , 70, 103969	5.1	2
74	High performance computing for three-dimensional agent-based molecular models. <i>Journal of Molecular Graphics and Modelling</i> , 2016 , 68, 68-77	2.8	2
73	A Workflow for the Application of Biclustering to Mass Spectrometry Data. <i>Advances in Intelligent Systems and Computing</i> , 2013 , 145-153	0.4	2
72	Analysis of student's context in e-Learning 2014 ,		2
71	Using CBR as Design Methodology for Developing Adaptable Decision Support Systems 2011 ,		2
70	On the Development of a Pipeline for the Automatic Detection of Positively Selected Sites. <i>Advances in Intelligent and Soft Computing</i> , 2012 , 225-229		2
69	Sistemas híbridos neuro-simbólicos: Una revisión.. <i>Inteligencia Artificial</i> , 2000 , 4,	1.5	2
68	Applying Rough Sets Reduction Techniques to the Construction of a Fuzzy Rule Base for Case Based Reasoning. <i>Lecture Notes in Computer Science</i> , 2004 , 83-92	0.9	2

67	Employing TSK Fuzzy Models to Automate the Revision Stage of a CBR System. <i>Lecture Notes in Computer Science</i> , 2004 , 302-311	0.9	2
66	Marky: A Lightweight Web Tracking Tool for Document Annotation. <i>Advances in Intelligent Systems and Computing</i> , 2014 , 269-276	0.4	2
65	Analyzing the Performance of Spam Filtering Methods When Dimensionality of Input Vector Changes. <i>Lecture Notes in Computer Science</i> , 2007 , 364-378	0.9	2
64	Assessing Classification Accuracy in the Revision Stage of a CBR Spam Filtering System. <i>Lecture Notes in Computer Science</i> , 2007 , 374-388	0.9	2
63	Building Proteomics Applications with the AIBench Application Framework. <i>Advances in Intelligent and Soft Computing</i> , 2011 , 99-107		2
62	Assessing the Suitability of MeSH Ontology for Classifying Medline Documents. <i>Advances in Intelligent and Soft Computing</i> , 2011 , 337-344		2
61	Assessing the Impact of Class-Imbalanced Data for Classifying Relevant/Irrelevant Medline Documents. <i>Advances in Intelligent and Soft Computing</i> , 2011 , 345-353		2
60	Enhancing sepsis management through machine learning techniques: A review. <i>Medicina Intensiva</i> , 2020 , 46, 140-140	1.2	2
59	Intelligent Tutoring. <i>Advances in Linguistics and Communication Studies</i> , 2016 , 205-224	0.3	2
58	Elder Care Alert Management - Decision Support by a Logistic Regression Model. <i>Advances in Intelligent and Soft Computing</i> , 2011 , 9-16		2
57	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> , 2020 , 64, 103660	5.1	2
56	BIOMedical Search Engine Framework: Lightweight and customized implementation of domain-specific biomedical search engines. <i>Computer Methods and Programs in Biomedicine</i> , 2016 , 131, 63-77	6.9	2
55	The Evolving Role of Information Technology in Haemovigilance Systems. <i>Journal of Healthcare Engineering</i> , 2018 , 2018, 6183468	3.7	2
54	Autonomous Internal Control System for Small to Medium Firms. <i>Lecture Notes in Computer Science</i> , 2005 , 106-121	0.9	2
53	Optimized convolutional neural network architectures for efficient on-device vision-based object detection. <i>Neural Computing and Applications</i> , 1	4.8	2
52	Computational prediction of the bioactivity potential of proteomes based on expert knowledge. <i>Journal of Biomedical Informatics</i> , 2019 , 91, 103121	10.2	1
51	Computational Approach to the Systematic Prediction of Glycolytic Abilities: Looking Into Human Microbiota. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 2302-2313	3	1
50	Collaborative relation annotation and quality analysis in Markyt environment. <i>Database: the Journal of Biological Databases and Curation</i> , 2017 , 2017,	5	1

49	A Bioinformatics Protocol for Quickly Creating Large-Scale Phylogenetic Trees. <i>Advances in Intelligent Systems and Computing</i> , 2019 , 88-96	0.4	1
48	EvoPPI: A Web Application to Compare Protein-Protein Interactions (PPIs) from Different Databases and Species. <i>Advances in Intelligent Systems and Computing</i> , 2019 , 149-156	0.4	1
47	Incorporating biological knowledge to microarray data classification through genomic data fusion 2010 ,		1
46	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> , 2022 , 195, 116616	7.8	1
45	The Activity of Bioinformatics Developers and Users in Stack Overflow. <i>Advances in Intelligent Systems and Computing</i> , 2021 , 23-31	0.4	1
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