

# Ruben Armananzas Arnedillo

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9119799/publications.pdf>

Version: 2024-02-01

29  
papers

1,878  
citations

471509

17  
h-index

454955

30  
g-index

32  
all docs

32  
docs citations

32  
times ranked

3202  
citing authors

#	ARTICLE	IF	CITATIONS
1	Machine learning in bioinformatics. Briefings in Bioinformatics, 2006, 7, 86-112.	6.5	674
2	Differential Micro RNA Expression in PBMC from Multiple Sclerosis Patients. PLoS ONE, 2009, 4, e6309.	2.5	222
3	A community-based transcriptomics classification and nomenclature of neocortical cell types. Nature Neuroscience, 2020, 23, 1456-1468.	14.8	183
4	Towards the automatic classification of neurons. Trends in Neurosciences, 2015, 38, 307-318.	8.6	90
5	Win-win data sharing in neuroscience. Nature Methods, 2017, 14, 112-116.	19.0	75
6	An open repository for single-cell reconstructions of the brain forest. Scientific Data, 2018, 5, 180006.	5.3	71
7	A review of estimation of distribution algorithms in bioinformatics. BioData Mining, 2008, 1, 6.	4.0	61
8	Machine Learning: An Indispensable Tool in Bioinformatics. Methods in Molecular Biology, 2010, 593, 25-48.	0.9	61
9	Unveiling relevant non-motor Parkinson's disease severity symptoms using a machine learning approach. Artificial Intelligence in Medicine, 2013, 58, 195-202.	6.5	50
10	Machine Learning Approach for the Outcome Prediction of Temporal Lobe Epilepsy Surgery. PLoS ONE, 2013, 8, e62819.	2.5	45
11	Gene Expression Profiling in Limb-Girdle Muscular Dystrophy 2A. PLoS ONE, 2008, 3, e3750.	2.5	41
12	Identification of a biomarker panel for colorectal cancer diagnosis. BMC Cancer, 2012, 12, 43.	2.6	40
13	Voxel-Based Diagnosis of Alzheimer's Disease Using Classifier Ensembles. IEEE Journal of Biomedical and Health Informatics, 2017, 21, 778-784.	6.3	40
14	<b>Mateda-2.0</b> : A MATLAB Package for the Implementation and Analysis of Estimation of Distribution Algorithms. Journal of Statistical Software, 2010, 35, .	3.7	37
15	The importance of metadata to assess information content in digital reconstructions of neuronal morphology. Cell and Tissue Research, 2015, 360, 121-127.	2.9	30
16	Peakbin Selection in Mass Spectrometry Data Using a Consensus Approach with Estimation of Distribution Algorithms. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 760-774.	3.0	26
17	Detecting reliable gene interactions by a hierarchy of Bayesian network classifiers. Computer Methods and Programs in Biomedicine, 2008, 91, 110-121.	4.7	23
18	Doubling up on the Fly: NeuroMorpho.Org Meets Big Data. Neuroinformatics, 2015, 13, 127-129.	2.8	20

#	ARTICLE	IF	CITATIONS
19	Microarray Analysis of Autoimmune Diseases by Machine Learning Procedures. IEEE Transactions on Information Technology in Biomedicine, 2009, 13, 341-350.	3.2	15
20	Comparison of metaheuristic strategies for peakbin selection in proteomic mass spectrometry data. Information Sciences, 2013, 222, 229-246.	6.9	14
21	PaperBot: open-source web-based search and metadata organization of scientific literature. BMC Bioinformatics, 2019, 20, 50.	2.6	14
22	Network measures for information extraction in evolutionary algorithms. International Journal of Computational Intelligence Systems, 2013, 6, 1163-1188.	2.7	13
23	Ensemble transcript interaction networks: A case study on Alzheimer's disease. Computer Methods and Programs in Biomedicine, 2012, 108, 442-450.	4.7	9
24	Genetic algorithms and Gaussian Bayesian networks to uncover the predictive core set of bibliometric indices. Journal of the Association for Information Science and Technology, 2016, 67, 1703-1721.	2.9	8
25	What is behind a summary-evaluation decision?. Behavior Research Methods, 2008, 40, 597-612.	4.0	4
26	Revealing post-transcriptional microRNA-mRNA regulations in Alzheimer's disease through ensemble graphs. BMC Genomics, 2018, 19, 668.	2.8	2
27	Bayesian Classifiers with Consensus Gene Selection: A Case Study in the Systemic Lupus Erythematosus. Mathematics in Industry, 2008, , 560-565.	0.3	2
28	Discretization of Expression Quantitative Trait Loci in Association Analysis Between Genotypes and Expression Data. Current Bioinformatics, 2015, 10, 144-164.	1.5	1
29	Ensemble graphs to reveal post-transcriptional regulatory networks in Alzheimer's disease. , 2017, , .		0