

Francisco M Ortuño

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1160420/publications.pdf>

Version: 2024-02-01

30
papers

448
citations

686830

13
h-index

752256

20
g-index

37
all docs

37
docs citations

37
times ranked

790
citing authors

#	ARTICLE	IF	CITATIONS
1	Uniform genomic data analysis in the NCI Genomic Data Commons. Nature Communications, 2021, 12, 1226.	5.8	61
2	The NCI Genomic Data Commons. Nature Genetics, 2021, 53, 257-262.	9.4	52
3	Optimizing multiple sequence alignments using a genetic algorithm based on three objectives: structural information, non-gaps percentage and totally conserved columns. Bioinformatics, 2013, 29, 2112-2121.	1.8	48
4	Serum Cytokine Profile in Patients With Pancreatic Cancer. Pancreas, 2014, 43, 1042-1049.	0.5	41
5	CSVS, a crowdsourcing database of the Spanish population genetic variability. Nucleic Acids Research, 2021, 49, D1130-D1137.	6.5	34
6	Collaborating to Compete: Blood Profiling Atlas in Cancer (BloodPAC) Consortium. Clinical Pharmacology and Therapeutics, 2017, 101, 589-592.	2.3	32
7	Integrative multi-platform meta-analysis of gene expression profiles in pancreatic ductal adenocarcinoma patients for identifying novel diagnostic biomarkers. PLoS ONE, 2018, 13, e0194844.	1.1	24
8	Multiclass classification for skin cancer profiling based on the integration of heterogeneous gene expression series. PLoS ONE, 2018, 13, e0196836.	1.1	19
9	Prognosis Relevance of Serum Cytokines in Pancreatic Cancer. BioMed Research International, 2015, 2015, 1-12.	0.9	16
10	Towards Improving Skin Cancer Diagnosis by Integrating Microarray and RNA-Seq Datasets. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 2119-2130.	3.9	16
11	KnowSeq R-Bioc package: The automatic smart gene expression tool for retrieving relevant biological knowledge. Computers in Biology and Medicine, 2021, 133, 104387.	3.9	16
12	Identification of gene expression profiling associated with erlotinib-related skin toxicity in pancreatic adenocarcinoma patients. Toxicology and Applied Pharmacology, 2016, 311, 113-116.	1.3	15
13	Using cited references to improve the retrieval of related biomedical documents. BMC Bioinformatics, 2013, 14, 113.	1.2	14
14	Predicting the accuracy of multiple sequence alignment algorithms by using computational intelligent techniques. Nucleic Acids Research, 2013, 41, e26-e26.	6.5	13
15	Comparing different machine learning and mathematical regression models to evaluate multiple sequence alignments. Neurocomputing, 2015, 164, 123-136.	3.5	12
16	Optimization of multiple sequence alignment methodologies using a multiobjective evolutionary algorithm based on NSGA-II. , 2012, , .		9
17	A versatile workflow to integrate RNA-seq genomic and transcriptomic data into mechanistic models of signaling pathways. PLoS Computational Biology, 2021, 17, e1008748.	1.5	6
18	An effective, practical and low computational cost framework for the integration of heterogeneous data to predict functional associations between proteins by means of Artificial Neural Networks. Neurocomputing, 2013, 121, 64-78.	3.5	3

#	ARTICLE	IF	CITATIONS
19	New trends in biomedical engineering and bioinformatics applied to biomedicine - special issue of IWBBIO 2014. BioMedical Engineering OnLine, 2015, 14, 11.	1.3	3
20	Highly accurate whole-genome imputation of SARS-CoV-2 from partial or low-quality sequences. GigaScience, 2021, 10, .	3.3	2
21	Intelligent Systems to Autonomously Classify Several Arrhythmia Using Information from ECG. , 2013, , .		1
22	Advances in bioinformatics and biomedical engineering - special issue of IWBBIO 2013. Theoretical Biology and Medical Modelling, 2014, 11, 11.	2.1	1
23	Emerging Methodologies in Multiple Sequence Alignment Using High Throughput Data. Advances in Intelligent and Soft Computing, 2011, , 183-190.	0.2	1
24	Creation of a Database Including a Set of Biological Features Related to Protein Sequences and Their Corresponding Alignment. , 2014, , .		0
25			