Mariana Recamonde-Mendoza

List of Publications by Year
in descending order

40 papers	720 citations	687220
		13 h-index

580701	
25 g-index	

43 all docs	43 docs citations	43 times ranked	1280 citing authors

#	Article	IF	Citations
1	MicroRNA expression profiles and type 1 diabetes mellitus: systematic review and bioinformatic analysis. Endocrine Connections, 2017, 6, 773-790.	0.8	118
2	MicroRNAs and diabetic kidney disease: Systematic review and bioinformatic analysis. Molecular and Cellular Endocrinology, 2018, 477, 90-102.	1.6	83
3	Identifying outbreaks of Porcine Epidemic Diarrhea virus through animal movements and spatial neighborhoods. Scientific Reports, 2019, 9, 457.	1.6	61
4	What variables are important in predicting bovine viral diarrhea virus? A random forest approach. Veterinary Research, 2015, 46, 85.	1.1	54
5	MicroRNA expression profile in plasma from type 1 diabetic patients: Case-control study and bioinformatic analysis. Diabetes Research and Clinical Practice, 2018, 141, 35-46.	1.1	49
6	Circulating miRNAs in diabetic kidney disease: caseâ€"control study and in silico analyses. Acta Diabetologica, 2019, 56, 55-65.	1.2	41
7	RFMirTarget: Predicting Human MicroRNA Target Genes with a Random Forest Classifier. PLoS ONE, 2013, 8, e70153.	1.1	34
8	How to make more from exposure data? An integrated machine learning pipeline to predict pathogen exposure. Journal of Animal Ecology, 2019, 88, 1447-1461.	1.3	33
9	Spectral Alignment of Graphs. IEEE Transactions on Network Science and Engineering, 2020, 7, 1182-1197.	4.1	27
10	Synergistic effects between ADORA2A and DRD2 genes on anxiety disorders in children with ADHD. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2019, 93, 214-220.	2.5	22
11	Detecting Aedes aegypti mosquitoes through audio classification with convolutional neural networks. Computers in Biology and Medicine, 2021, 129, 104152.	3.9	22
12	Circulating microRNAs in obese and lean heart failure patients: A caseâ€"control study with computational target prediction analysis. Gene, 2015, 574, 1-10.	1.0	21
13	Urinary peptidomics and bioinformatics for the detection of diabetic kidney disease. Scientific Reports, 2020, 10, 1242.	1.6	19
14	Calcium Signaling Alterations Caused by Epigenetic Mechanisms in Pancreatic Cancer: From Early Markers to Prognostic Impact. Cancers, 2020, 12, 1735.	1.7	14
15	A comparative evaluation of aggregation methods for machine learning over vertically partitioned data. Expert Systems With Applications, 2020, 152, 113406.	4.4	11
16	Reverse engineering of GRNs. , 2012, , .		10
17	Social choice in distributed classification tasks: Dealing with vertically partitioned data. Information Sciences, 2016, 332, 56-71.	4.0	10
18	TULP3: A potential biomarker in colorectal cancer?. PLoS ONE, 2019, 14, e0210762.	1.1	10

#	Article	IF	Citations
19	The role of protein intrinsic disorder in major psychiatric disorders. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2016, 171, 848-860.	1.1	9
20	Systems biology approach identifies key regulators and the interplay between miRNAs and transcription factors for pathological cardiac hypertrophy. Gene, 2019, 698, 157-169.	1.0	9
21	Meta-analysis of Transcriptomic Data Reveals Pathophysiological Modules Involved with Atrial Fibrillation. Molecular Diagnosis and Therapy, 2020, 24, 737-751.	1.6	9
22	CRL4-Cereblon complex in Thalidomide Embryopathy: a translational investigation. Scientific Reports, 2020, 10, 851.	1.6	8
23	EPGAT: Gene Essentiality Prediction With Graph Attention Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	1.9	8
24	Evolving random boolean networks with genetic algorithms for regulatory networks reconstruction. , 2011, , .		6
25	Identification of Candidate Biomarkers for Transplant Rejection from Transcriptome Data: A Systematic Review. Molecular Diagnosis and Therapy, 2019, 23, 439-458.	1.6	5
26	Decreased expression of the thyroid hormone-inactivating enzyme type 3 deiodinase is associated with lower survival rates in breast cancer. Scientific Reports, 2020, 10, 13914.	1.6	5
27	Roux-en-Y Gastric Bypass Downregulates Angiotensin-Converting Enzyme 2 (ACE2) Gene Expression in Subcutaneous White Adipose Tissue: A Putative Protective Mechanism Against Severe COVID-19. Obesity Surgery, 2021, 31, 2831-2834.	1.1	5
28	Patterns of high-risk drinking among medical students: A web-based survey with machine learning. Computers in Biology and Medicine, 2021, 136, 104747.	3.9	4
29	Transcriptome meta-analysis of valproic acid exposure in human embryonic stem cells. European Neuropsychopharmacology, 2022, 60, 76-88.	0.3	3
30	A comprehensive analysis of core polyadenylation sequences and regulation by microRNAs in a set of cancer predisposition genes. Gene, 2019, 712, 143943.	1.0	2
31	Anticonvulsants and Chromatin-Genes Expression: A Systems Biology Investigation. Frontiers in Neuroscience, 2020, 14, 591196.	1.4	2
32	Comparative Genomics Identifies Putative Interspecies Mechanisms Underlying Crbn-Sall4-Linked Thalidomide Embryopathy. Frontiers in Genetics, 2021, 12, 680217.	1.1	2
33	Social-Training: Ensemble Learning with Voting Aggregation for Semi-supervised Classification Tasks. , 2017, , .		1
34	Adaptive Incremental Gaussian Mixture Network for Non-Stationary Data Stream Classification. , 2018, , .		1
35	Ensemble Feature Selection Compares toÂMeta-analysis for Breast Cancer Biomarker Identification from Microarray Data. Lecture Notes in Computer Science, 2021, , 162-178.	1.0	1
36	Thalidomide embryopathy as a phenocopy: applying protein conservation and gene expression analyses for the understanding of interspecific differences. Reproductive Toxicology, 2019, 88, 35-36.	1.3	0

#	ARTICLE	IF	CITATIONS
37	Abstract 4926: Loss of deiodinase type 3 expression distinguishes patients with poor prognosis in breast cancer. , 2019, , .		0
38	Gene Expression Analysis Platform (GEAP): A highly customizable, fast, versatile and ready-to-use microarray analysis platform. Genetics and Molecular Biology, 2022, 45, e20210077.	0.6	0
39	Identifying posttraumatic stress disorder staging from clinical and sociodemographic features: a proof-of-concept study using a machine learning approach. Psychiatry Research, 2022, 311, 114489.	1.7	0
40	A transcriptome meta-analysis of ethanol embryonic exposure: implications in neurodevelopment and neuroinflammatory genes. Neuroscience Informatics, 2022, , 100094.	2.8	0