Vanessa Aguiar-Pulido

List of Publications by Year
in descending order

16	258	1040056	1058476
papers	citations	9	14
		h-index	g-index

17	17	17	452
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genome-wide investigation identifies a rare copy-number variant burden associated with human spina bifida. Genetics in Medicine, 2021, 23, 1211-1218.	2.4	10
2	Systems biology analysis of human genomes points to key pathways conferring spina bifida risk. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	11
3	Loss of *RAD9B* impairs early neural development and contributes to the risk for human spina bifida. Human Mutation, 2020, 41, 786-799.	2.5	14
4	Threshold for neural tube defect risk by accumulated singleton loss-of-function variants. Cell Research, 2018, 28, 1039-1041.	12.0	48
5	Computational Methods in Epigenetics. , 2015, , 153-180.		0
6	Unbiased high-throughput characterization of mussel transcriptomic responses to sublethal concentrations of the biotoxin okadaic acid. PeerJ, 2015, 3, e1429.	2.0	15
7	Random Forest classification based on star graph topological indices for antioxidant proteins. Journal of Theoretical Biology, 2013, 317, 331-337.	1.7	45
8	Exploring Patterns of Epigenetic Information with Data Mining Techniques. Current Pharmaceutical Design, 2013, 19, 779-789.	1.9	15
9	The CHROMEVALOA Database: A Resource for the Evaluation of Okadaic Acid Contamination in the Marine Environment Based on the Chromatin-Associated Transcriptome of the Mussel Mytilus galloprovincialis. Marine Drugs, 2013, 11, 830-841.	4.6	22
10	Applied Computational Techniques on Schizophrenia Using Genetic Mutations. Current Topics in Medicinal Chemistry, 2013, 13, 675-684.	2.1	3
11	Evolutionary Computation and QSAR Research. Current Computer-Aided Drug Design, 2013, 9, 206-225.	1.2	28
12	Exploring patterns of epigenetic information with data mining techniques. Current Pharmaceutical Design, 2013, 19, 779-89.	1.9	3
13	Naïve Bayes QSDR classification based on spiral-graph Shannon entropies for protein biomarkers in human colon cancer. Molecular BioSystems, 2012, 8, 1716.	2.9	26
14	Exploring Patterns of Epigenetic Information with Data Mining Techniques. Current Pharmaceutical Design, 2012, 19, 779-789.	1.9	0
15	SNP-Schizo: A Web Tool for Schizophrenia SNP Sequence Classification. Lecture Notes in Computer Science, 2011, , 252-259.	1.3	1
16	Machine Learning Techniques for Single Nucleotide Polymorphism—Disease Classification Models in Schizophrenia. Molecules, 2010, 15, 4875-4889.	3.8	17