

# Vanessa Aguiar-Pulido

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10527392/publications.pdf>

Version: 2024-02-01

16  
papers

258  
citations

1040056

9  
h-index

1058476

14  
g-index

17  
all docs

17  
docs citations

17  
times ranked

452  
citing authors

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