

# Áscar Álvarez-Machancoses

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3470164/publications.pdf>

Version: 2024-02-01

15  
papers

167  
citations

1307594

7  
h-index

1125743

13  
g-index

15  
all docs

15  
docs citations

15  
times ranked

189  
citing authors

#	ARTICLE	IF	CITATIONS
1	Using artificial intelligence methods to speed up drug discovery. Expert Opinion on Drug Discovery, 2019, 14, 769-777.	5.0	54
2	Modeling the Effect of Polymer Chain Stiffness on the Behavior of Polymer Nanocomposites. Journal of Physical Chemistry B, 2017, 121, 6245-6256.	2.6	25
3	Particle Swarm Optimization and Uncertainty Assessment in Inverse Problems. Entropy, 2018, 20, 96.	2.2	14
4	Sampling Defective Pathways in Phenotype Prediction Problems via the Holdout Sampler. Lecture Notes in Computer Science, 2018, , 24-32.	1.3	11
5	<p></p>On the Role of Artificial Intelligence in Genomics to Enhance Precision Medicine</p>. Pharmacogenomics and Personalized Medicine, 2020, Volume 13, 105-119.	0.7	10
6	Robust Sampling of Defective Pathways in Alzheimer’s Disease. Implications in Drug Repositioning. International Journal of Molecular Sciences, 2020, 21, 3594.	4.1	9
7	Sampling Defective Pathways in Phenotype Prediction Problems via the Fisher’s Ratio Sampler. Lecture Notes in Computer Science, 2018, , 15-23.	1.3	9
8	Robust Prediction of Single and Multiple Point Protein Mutations Stability Changes. Biomolecules, 2020, 10, 67.	4.0	7
9	Predicting protein tertiary structure and its uncertainty analysis via particle swarm sampling. Journal of Molecular Modeling, 2019, 25, 79.	1.8	6
10	Robust pathway sampling in phenotype prediction. Application to triple negative breast cancer. BMC Bioinformatics, 2020, 21, 89.	2.6	6
11	Comparison of Different Sampling Algorithms for Phenotype Prediction. Lecture Notes in Computer Science, 2018, , 33-45.	1.3	6
12	Principal component analysis in protein tertiary structure prediction. Journal of Bioinformatics and Computational Biology, 2018, 16, 1850005.	0.8	4
13	Prediction of Protein Tertiary Structure via Regularized Template Classification Techniques. Molecules, 2020, 25, 2467.	3.8	3
14	Protein Tertiary Structure Prediction via SVD and PSO Sampling. Lecture Notes in Computer Science, 2018, , 211-220.	1.3	2
15	The Utilization of Different Classifiers to Perform Drug Repositioning in Inclusion Body Myositis Supports the Concept of Biological Invariance. Lecture Notes in Computer Science, 2020, , 589-598.	1.3	1