Juan Esquivel-Rodriguez

List of Publications by Year
in descending order

20 papers	897 citations	623734 14 h-index	839539 18 g-index
21 all docs	21 docs citations	21 times ranked	1058 citing authors

#	Article	IF	Citations
1	Prediction of homoprotein and heteroprotein complexes by protein docking and templateâ€based modeling: A CASPâ€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2016, 84, 323-348.	2.6	148
2	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	4.2	131
3	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1980-1987.	2.6	87
4	Molecular Surface Representation Using 3D Zernike Descriptors for Protein Shape Comparison and Docking. Current Protein and Peptide Science, 2011, 12, 520-530.	1.4	82
5	3D-SURFER: software for high-throughput protein surface comparison and analysis. Bioinformatics, 2009, 25, 2843-2844.	4.1	77
6	Multiâ€LZerD: Multiple protein docking for asymmetric complexes. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1818-1833.	2.6	71
7	Tuning of Pectin Methylesterification. Journal of Biological Chemistry, 2015, 290, 23320-23335.	3.4	52
8	Fitting Multimeric Protein Complexes into Electron Microscopy Maps Using 3D Zernike Descriptors. Journal of Physical Chemistry B, 2012, 116, 6854-6861.	2.6	39
9	Computational methods for constructing protein structure models from 3D electron microscopy maps. Journal of Structural Biology, 2013, 184, 93-102.	2.8	38
10	Pairwise and Multimeric Proteinâ€“Protein Docking Using the LZerD Program Suite. Methods in Molecular Biology, 2014, 1137, 209-234.	0.9	36
11	Ranking proteinâ€“protein docking results using steered molecular dynamics and potential of mean force calculations. Journal of Computational Chemistry, 2016, 37, 1861-1865.	3.3	35
12	Modeling the assembly order of multimeric heteroprotein complexes. PLoS Computational Biology, 2018, 14, e1005937.	3.2	30
13	Navigating 3D electron microscopy maps with EM-SURFER. BMC Bioinformatics, 2015, 16, 181.	2.6	22
14	Human and server docking prediction for CAPRI round 30â€35 using LZerD with combined scoring functions. Proteins: Structure, Function and Bioinformatics, 2017, 85, 513-527.	2.6	18
15	3D-SURFER 2.0: Web Platform for Real-Time Search and Characterization of Protein Surfaces. Methods in Molecular Biology, 2014, 1137, 105-117.	0.9	10
16	Evaluation of multiple protein docking structures using correctly predicted pairwise subunits. BMC Bioinformatics, 2012, 13, S6.	2.6	9
17	Effect of conformation sampling strategies in genetic algorithm for multiple protein docking. BMC Proceedings, 2012, 6, S4.	1.6	5
18	EvoSeg: Automated Electron Microscopy Segmentation through Random Forests and Evolutionary Optimization. Biomimetics, 2021, 6, 37.	3.3	4

#	Article	IF	Citations
19	Matching of EM Map Segments to Structurally-Relevant Bio-molecular Regions. Communications in Computer and Information Science, 2020, , 464-478.	0.5	0
20	Experiment-driven improvements in Human-in-the-loop Machine Learning Annotation via significance-based A/B testing. , 2021, , .		0