# Juan Esquivel-Rodriguez

List of Publications by Year
in descending order



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|---|---|---|---|
| 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 | EvoSeg: Automated Electron Microscopy Segmentation through Random Forests and Evolutionary Optimization. Biomimetics, 2021, 6, 37. | 3.3 | 4 |
| 2 | Experiment-driven improvements in Human-in-the-loop Machine Learning Annotation via significance-based A/B testing. , 2021, , . | | 0 |
| 3 | Matching of EM Map Segments to Structurally-Relevant Bio-molecular Regions. Communications in Computer and Information Science, 2020, , 464-478. | 0.5 | 0 |
| 4 | Modeling the assembly order of multimeric heteroprotein complexes. PLoS Computational Biology, 2018, 14, e1005937. | 3.2 | 30 |
| 5 | 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 |
| 6 | 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 |
| 7 | 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 |
| 8 | Tuning of Pectin Methylesterification. Journal of Biological Chemistry, 2015, 290, 23320-23335. | 3.4 | 52 |
| 9 | Navigating 3D electron microscopy maps with EM-SURFER. BMC Bioinformatics, 2015, 16, 181. | 2.6 | 22 |
| 10 | Pairwise and Multimeric Proteinâ€“Protein Docking Using the LZerD Program Suite. Methods in Molecular Biology, 2014, 1137, 209-234. | 0.9 | 36 |
| 11 | 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 |
| 12 | Computational methods for constructing protein structure models from 3D electron microscopy maps. Journal of Structural Biology, 2013, 184, 93-102. | 2.8 | 38 |
| 13 | 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 |
| 14 | Fitting Multimeric Protein Complexes into Electron Microscopy Maps Using 3D Zernike Descriptors. Journal of Physical Chemistry B, 2012, 116, 6854-6861. | 2.6 | 39 |
| 15 | Evaluation of multiple protein docking structures using correctly predicted pairwise subunits. BMC Bioinformatics, 2012, 13, S6. | 2.6 | 9 |
| 16 | Effect of conformation sampling strategies in genetic algorithm for multiple protein docking. BMC Proceedings, 2012, 6, S4. | 1.6 | 5 |
| 17 | Multiâ€LZerD: Multiple protein docking for asymmetric complexes. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1818-1833. | 2.6 | 71 |
| 18 | Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302. | 4.2 | 131 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | 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 |
| 20 | 3D-SURFER: software for high-throughput protein surface comparison and analysis. Bioinformatics, 2009, 25, 2843-2844. | 4.1 | 77 |