Lim Heo

List of Publications by Year
in descending order

34 papers	6,634 citations	394286 19 h-index	377752 34 g-index
41 all docs	41 docs citations	41 times ranked	5101 citing authors

#	Article	IF	Citations
1	Protein assembly and crowding simulations. Current Opinion in Structural Biology, 2022, 73, 102340.	2.6	18
2	Multiâ€state modeling of Gâ€protein coupled receptors at experimental accuracy. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1873-1885.	1.5	84
3	ColabFold: making protein folding accessible to all. Nature Methods, 2022, 19, 679-682.	9.0	3,242
4	Improved Sampling Strategies for Protein Model Refinement Based on Molecular Dynamics Simulation. Journal of Chemical Theory and Computation, 2021, 17, 1931-1943.	2.3	19
5	GalaxyWater-wKGB: Prediction of Water Positions on Protein Structure Using wKGB Statistical Potential. Journal of Chemical Information and Modeling, 2021, 61, 2283-2293.	2.5	9
6	Physicsâ€based protein structure refinement in the era of artificial intelligence. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1870-1887.	1.5	17
7	Biosynthesis and trafficking of heme o and heme a: new structural insights and their implications for reaction mechanisms and prenylated heme transfer. Critical Reviews in Biochemistry and Molecular Biology, 2021, 56, 1-29.	2.3	5
8	Highâ€accuracy protein structures by combining machineâ€learning with physicsâ€based refinement. Proteins: Structure, Function and Bioinformatics, 2020, 88, 637-642.	1.5	48
9	Modeling Protein Homo-Oligomer Structures with GalaxyHomomer Web Server. Methods in Molecular Biology, 2020, 2165, 127-137.	0.4	2
10	Driven to nearâ€experimental accuracy by refinement via molecular dynamics simulations. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1263-1275.	1.5	40
11	GalaxyRefine2: simultaneous refinement of inaccurate local regions and overall protein structure. Nucleic Acids Research, 2019, 47, W451-W455.	6.5	66
12	Structure refinement of membrane proteins via molecular dynamics simulations. Proteins: Structure, Function and Bioinformatics, 2018, 86, 738-750.	1.5	15
13	PREFMD: a web server for protein structure refinement via molecular dynamics simulations. Bioinformatics, 2018, 34, 1063-1065.	1.8	31
14	What makes it difficult to refine protein models further via molecular dynamics simulations?. Proteins: Structure, Function and Bioinformatics, 2018, 86, 177-188.	1.5	35
15	Simultaneous refinement of inaccurate local regions and overall structure in the CASP12 protein model refinement experiment. Proteins: Structure, Function and Bioinformatics, 2018, 86, 168-176.	1.5	14
16	The challenge of modeling protein assemblies: the CASP12â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2018, 86, 257-273.	1.5	85
17	Experimental accuracy in protein structure refinement via molecular dynamics simulations. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 13276-13281.	3.3	68
18	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. Scientific Reports, 2018, 8, 9939.	1.6	19

#	Article	IF	Citations
19	Protein Structure Refinement via Molecular Dynamics Simulations. Biophysical Journal, 2018, 114, 575a.	0.2	3
20	GalaxyHomomer: a web server for protein homo-oligomer structure prediction from a monomer sequence or structure. Nucleic Acids Research, 2017, 45, W320-W324.	6.5	102
21	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.	1.5	148
22	Binding Site Prediction of Proteins with Organic Compounds or Peptides Using GALAXY Web Servers. Methods in Molecular Biology, 2016, 1414, 33-45.	0.4	4
23	GalaxyRefineComplex: Refinement of protein-protein complex model structures driven by interface repacking. Scientific Reports, 2016, 6, 32153.	1.6	94
24	Effective protein model structure refinement by loop modeling and overall relaxation. Proteins: Structure, Function and Bioinformatics, 2016, 84, 293-301.	1.5	79
25	Factors affecting redox potential and differential sensitivity of <scp>SoxR</scp> to redoxâ€active compounds. Molecular Microbiology, 2015, 97, 808-821.	1.2	18
26	GalaxyPepDock: a proteinâ€“peptide docking tool based on interaction similarity and energy optimization. Nucleic Acids Research, 2015, 43, W431-W435.	6.5	236
27	Structure of vaccinia virus A46, an inhibitor of TLR4 signaling pathway, shows the conformation of VIPER motif. Protein Science, 2014, 23, 906-914.	3.1	13
28	GalaxySite: ligand-binding-site prediction by using molecular docking. Nucleic Acids Research, 2014, 42, W210-W214.	6.5	80
29	Protein Loop Modeling Using a New Hybrid Energy Function and Its Application to Modeling in Inaccurate Structural Environments. PLoS ONE, 2014, 9, e113811.	1.1	78
30	New molecular interaction of IIA^{Ntr} and HPr from Burkholderia pseudomallei identified by Xâ€ray crystallography and docking studies. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1499-1508.	1.5	2
31	Alternative zincâ€binding sites explain the redox sensitivity of zincâ€containing antiâ€sigma factors. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1644-1652.	1.5	6
32	GalaxyRefine: protein structure refinement driven by side-chain repacking. Nucleic Acids Research, 2013, 41, W384-W388.	6.5	735
33	GalaxyWEB server for protein structure prediction and refinement. Nucleic Acids Research, 2012, 40, W294-W297.	6.5	603
34	LigDockCSA: Proteinâ€“ligand docking using conformational space annealing. Journal of Computational Chemistry, 2011, 32, 3226-3232.	1.5	40