Gyu Rie Lee

List of Publications by Year
in descending order

20 papers	3,437 citations	758635 12 h-index	887659 17 g-index
20 all docs	20 docs citations	20 times ranked	3144 citing authors

#	Article	IF	Citations
1	Accurate prediction of protein structures and interactions using a three-track neural network. Science, 2021, 373, 871-876.	6.0	2,843
2	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
3	Effective protein model structure refinement by loop modeling and overall relaxation. Proteins: Structure, Function and Bioinformatics, 2016, 84, 293-301.	1.5	79
4	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
5	GalaxyRefine2: simultaneous refinement of inaccurate local regions and overall protein structure. Nucleic Acids Research, 2019, 47, W451-W455.	6.5	66
6	Highâ€accuracy refinement using Rosetta in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1276-1282.	1.5	41
7	Galaxy7TM: flexible GPCRâ€“ligand docking by structure refinement. Nucleic Acids Research, 2016, 44, W502-W506.	6.5	33
8	Biophysical and functional characterization of Norrin signaling through Frizzled4. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 8787-8792.	3.3	30
9	Accurate protein structure prediction: what comes next?. Biodesign, 2021, 9, 47-50.	0.2	25
10	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
11	Benchmarking predictions of allostery in liver pyruvate kinase in CAGI4. Human Mutation, 2017, 38, 1123-1131.	1.1	17
12	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
13	Templateâ€based modeling and ab initio refinement of protein oligomer structures using GALAXY in CAPRI round 30. Proteins: Structure, Function and Bioinformatics, 2017, 85, 399-407.	1.5	10
14	GalaxyGPCRloop: Template-Based and Ab Initio Structure Sampling of the Extracellular Loops of G-Protein-Coupled Receptors. Journal of Chemical Information and Modeling, 2018, 58, 1234-1243.	2.5	10
15	Evaluation of GalaxyDock Based on the Community Structureâ€“Activity Resource 2013 and 2014 Benchmark Studies. Journal of Chemical Information and Modeling, 2016, 56, 988-995.	2.5	9
16	Cellâ€“cell adhesion in metazoans relies on evolutionarily conserved features of the Î±-cateninÂ·Î²-cateninâ€“binding interface. Journal of Biological Chemistry, 2017, 292, 16477-16490.	1.6	9
17	De Novo Protein Design Using the Blueprint Builder in Rosetta. Current Protocols in Protein Science, 2020, 102, e116.	2.8	6
18	Cover Image, Volume 85, Issue 3. Proteins: Structure, Function and Bioinformatics, 2017, 85, C4.	1.5	0

#	Article	IF	Citations
19	Cover Image, Volume 38, Issue 9. Human Mutation, 2017, 38, i.	1.1	0
20	From Single Structures to Ensembles: Application of the Galaxy Program Suite to Ubiquitin, Cyclophilin a and PTP1B. Biophysical Journal, 2018, 114, 575a.	0.2	0