

Gyu Rie Lee

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6759311/publications.pdf>

Version: 2024-02-01

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. <i>Science</i> , 2021, 373, 871-876.	6.0	2,843
2	Accurate protein structure prediction: what comes next?. <i>BioDesign</i> , 2021, 9, 47-50.	0.2	25
3	De Novo Protein Design Using the Blueprint Builder in Rosetta. <i>Current Protocols in Protein Science</i> , 2020, 102, e116.	2.8	6
4	High-accuracy refinement using Rosetta in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1276-1282.	1.5	41
5	GalaxyRefine2: simultaneous refinement of inaccurate local regions and overall protein structure. <i>Nucleic Acids Research</i> , 2019, 47, W451-W455.	6.5	66
6	Simultaneous refinement of inaccurate local regions and overall structure in the CASP12 protein model refinement experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 168-176.	1.5	14
7	From Single Structures to Ensembles: Application of the Galaxy Program Suite to Ubiquitin, Cyclophilin a and PTP1B. <i>Biophysical Journal</i> , 2018, 114, 575a.	0.2	0
8	GalaxyGPCRloop: Template-Based and <i>Ab Initio</i> Structure Sampling of the Extracellular Loops of G-Protein-Coupled Receptors. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 1234-1243.	2.5	10
9	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. <i>Scientific Reports</i> , 2018, 8, 9939.	1.6	19
10	Biophysical and functional characterization of Norrin signaling through Frizzled4. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 8787-8792.	3.3	30
11	Cover Image, Volume 85, Issue 3. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, C4.	1.5	0
12	Benchmarking predictions of allostery in liver pyruvate kinase in CAGI4. <i>Human Mutation</i> , 2017, 38, 1123-1131.	1.1	17
13	Cover Image, Volume 38, Issue 9. <i>Human Mutation</i> , 2017, 38, i.	1.1	0
14	Template-based modeling and <i>ab initio</i> refinement of protein oligomer structures using GALAXY in CAPRI round 30. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 399-407.	1.5	10
15	Cell-cell adhesion in metazoans relies on evolutionarily conserved features of the β -catenin- β -catenin binding interface. <i>Journal of Biological Chemistry</i> , 2017, 292, 16477-16490.	1.6	9
16	Prediction of homoprotein and heteroprotein complexes by protein docking and template-based modeling: A CASP-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 323-348.	1.5	148
17	Galaxy7TM: flexible GPCR ligand docking by structure refinement. <i>Nucleic Acids Research</i> , 2016, 44, W502-W506.	6.5	33
18	Effective protein model structure refinement by loop modeling and overall relaxation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 293-301.	1.5	79

#	ARTICLE	IF	CITATIONS
19	Evaluation of GalaxyDock Based on the Community Structureâ€™Activity Resource 2013 and 2014 Benchmark Studies. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 988-995.	2.5	9
20	Protein Loop Modeling Using a New Hybrid Energy Function and Its Application to Modeling in Inaccurate Structural Environments. <i>PLoS ONE</i> , 2014, 9, e113811.	1.1	78