Minkyung Baek

List of Publications by Year
in descending order

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Version: 2024-02-01

29 papers	4,329 citations	567281 15 h-index	526287 27 g-index
38 all docs	38 docs citations	38 times ranked	3561 citing authors

#	Article	IF	Citations
1	Deep learning and protein structure modeling. Nature Methods, 2022, 19, 13-14.	19.0	75
2	Improved protein structure refinement guided by deep learning based accuracy estimation. Nature Communications, 2021, 12, 1340.	12.8	160
3	Force Field Optimization Guided by Small Molecule Crystal Lattice Data Enables Consistent Sub-Angstrom Proteinâ€“Ligand Docking. Journal of Chemical Theory and Computation, 2021, 17, 2000-2010.	5.3	52
4	GalaxyHeteromer: protein heterodimer structure prediction by template-based and ab initio docking. Nucleic Acids Research, 2021, 49, W237-W241.	14.5	11
5	Accurate prediction of protein structures and interactions using a three-track neural network. Science, 2021, 373, 871-876.	12.6	2,843
6	Structure of the phosphoinositide 3-kinase (PI3K) p110Î³-p101 complex reveals molecular mechanism of GPCR activation. Science Advances, 2021, 7, .	10.3	25
7	Protein tertiary structure prediction and refinement using deep learning and Rosetta in <scp>CASP14</scp>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1722-1733.	2.6	40
8	Protein oligomer modeling guided by predicted interchain contacts in <scp>CASP14</scp>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1824-1833.	2.6	16
9	Accurate protein structure prediction: what comes next?. Biodesign, 2021, 9, 47-50.	0.4	25
10	Computed structures of core eukaryotic protein complexes. Science, 2021, 374, eabm4805.	12.6	316
11	Structure prediction of biological assemblies using GALAXY in CAPRI rounds 38â€45. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1009-1017.	2.6	5
12	Modeling Protein Homo-Oligomer Structures with GalaxyHomomer Web Server. Methods in Molecular Biology, 2020, 2165, 127-137.	0.9	2
13	GalaxyDock3: Proteinâ€“ligand docking that considers the full ligand conformational flexibility. Journal of Computational Chemistry, 2019, 40, 2739-2748.	3.3	15
14	Assessment of protein model structure accuracy estimation in CASP13: Challenges in the era of deep learning. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1351-1360.	2.6	54
15	Prediction of protein oligomer structures using GALAXY in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1233-1240.	2.6	6
16	Blind prediction of homoâ€•and heteroâ€protein complexes: The CASP13â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	2.6	99
17	GalaxyTongDock: Symmetric and asymmetric ab initio proteinâ€“protein docking web server with improved energy parameters. Journal of Computational Chemistry, 2019, 40, 2413-2417.	3.3	41
18	Structural Basis for the Enantioselectivity of Esterase Est-Y29 toward (S)-Ketoprofen. ACS Catalysis, 2019, 9, 755-767.	11.2	14

#	Article	IF	Citations
19	Novel Compound Heterozygote Mutation in IL10RA in a Patient With Very Early-Onset Inflammatory Bowel Disease. Inflammatory Bowel Diseases, 2019, 25, 498-509.	1.9	6
20	The challenge of modeling protein assemblies: the CASP12â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2018, 86, 257-273.	2.6	85
21	Improving Docking Performance of Large Flexible Ligands using Hot Spot Information Predicted by Fragment Docking. Biophysical Journal, 2018, 114, 55a.	0.5	0
22	Cover Image, Volume 85, Issue 3. Proteins: Structure, Function and Bioinformatics, 2017, 85, C4.	2.6	0
23	Absolute binding free energies for octa-acids and guests in SAMPL5. Journal of Computer-Aided Molecular Design, 2017, 31, 107-118.	2.9	16
24	GalaxyDock BP2 score: a hybrid scoring function for accurate proteinâ€“ligand docking. Journal of Computer-Aided Molecular Design, 2017, 31, 653-666.	2.9	44
25	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.	2.6	10
26	Absolute binding free energy calculations of CBClip hostâ€“guest systems in the SAMPL5 blind challenge. Journal of Computer-Aided Molecular Design, 2017, 31, 71-85.	2.9	13
27	GalaxyHomomer: a web server for protein homo-oligomer structure prediction from a monomer sequence or structure. Nucleic Acids Research, 2017, 45, W320-W324.	14.5	102
28	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
29	Binding Site Prediction of Proteins with Organic Compounds or Peptides Using GALAXY Web Servers. Methods in Molecular Biology, 2016, 1414, 33-45.	0.9	4