Minkyung Baek

List of Publications by Year
in descending order

29 papers	4,329 citations	567281 15 h-index
38 all docs	38 docs citations	38 times ranked

526287 27 g-index
3561 citing authors

#	Article	IF	Citations
1	Accurate prediction of protein structures and interactions using a three-track neural network. Science, 2021, 373, 871-876.	12.6	2,843
2	Computed structures of core eukaryotic protein complexes. Science, 2021, 374, eabm4805.	12.6	316
3	Improved protein structure refinement guided by deep learning based accuracy estimation. Nature Communications, 2021, 12, 1340.	12.8	160
4	Prediction of homoprotein and heteroprotein complexes by protein docking and template‐based modeling: A CASP‐CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2016, 84, 323-348.	2.6	148
5	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
6	Blind prediction of homo‐and hetero‐protein complexes: The CASP13‐CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	2.6	99
7	The challenge of modeling protein assemblies: the CASP12‐CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2018, 86, 257-273.	2.6	85
8	Deep learning and protein structure modeling. Nature Methods, 2022, 19, 13-14.	19.0	75
9	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
10	Force Field Optimization Guided by Small Molecule Crystal Lattice Data Enables Consistent Sub-Angstrom Protein–Ligand Docking. Journal of Chemical Theory and Computation, 2021, 17, 2000-2010.	5.3	52
11	GalaxyDock BP2 score: a hybrid scoring function for accurate protein–ligand docking. Journal of Computer-Aided Molecular Design, 2017, 31, 653-666.	2.9	44
12	GalaxyTongDock: Symmetric and asymmetric *ab initio* protein–protein docking web server with improved energy parameters. Journal of Computational Chemistry, 2019, 40, 2413-2417.	3.3	41
13	Protein tertiary structure prediction and refinement using deep learning and Rosetta in CASP14. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1722-1733.	2.6	40
14	Structure of the phosphoinositide 3-kinase (PI3K) p110γ-p101 complex reveals molecular mechanism of GPCR activation. Science Advances, 2021, 7, .	10.3	25
15	Accurate protein structure prediction: what comes next?. Biodesign, 2021, 9, 47-50.	0.4	25
16	Absolute binding free energies for octa-acids and guests in SAMPL5. Journal of Computer-Aided Molecular Design, 2017, 31, 107-118.	2.9	16
17	Protein oligomer modeling guided by predicted interchain contacts in CASP14. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1824-1833.	2.6	16
18	GalaxyDock3: Protein–ligand docking that considers the full ligand conformational flexibility. Journal of Computational Chemistry, 2019, 40, 2739-2748.	3.3	15

#	Article	IF	Citations
19	Structural Basis for the Enantioselectivity of Esterase Est-Y29 toward (*S*)-Ketoprofen. ACS Catalysis, 2019, 9, 755-767.	11.2	14
20	Absolute binding free energy calculations of CBClip host–guest systems in the SAMPL5 blind challenge. Journal of Computer-Aided Molecular Design, 2017, 31, 71-85.	2.9	13
21	GalaxyHeteromer: protein heterodimer structure prediction by template-based and *ab initio* docking. Nucleic Acids Research, 2021, 49, W237-W241.	14.5	11
22	Template-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
23	Prediction of protein oligomer structures using GALAXY in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1233-1240.	2.6	6
24	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
25	Structure prediction of biological assemblies using GALAXY in CAPRI rounds 38–45. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1009-1017.	2.6	5
26	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
27	Modeling Protein Homo-Oligomer Structures with GalaxyHomomer Web Server. Methods in Molecular Biology, 2020, 2165, 127-137.	0.9	2
28	Cover Image, Volume 85, Issue 3. Proteins: Structure, Function and Bioinformatics, 2017, 85, C4.	2.6	0
29	Improving Docking Performance of Large Flexible Ligands using Hot Spot Information Predicted by Fragment Docking. Biophysical Journal, 2018, 114, 55a.	0.5	0