Hahnbeom Park

List of Publications by Citations

48 papers	4,509 citations	27 h-index	62 g-index
62 ext. papers	7,511 ext. citations	8.5 avg, IF	5.92 L-index

#	Paper	IF	Citations
48	Accurate prediction of protein structures and interactions using a three-track neural network. *Science*, **2021**, 373, 871-876	33.3	522
47	Improved protein structure prediction using predicted interresidue orientations. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 1496-1503	11.5	496
46	The Rosetta All-Atom Energy Function for Macromolecular Modeling and Design. *Journal of Chemical Theory and Computation*, **2017**, 13, 3031-3048	6.4	486
45	GalaxyRefine: Protein structure refinement driven by side-chain repacking. *Nucleic Acids Research*, **2013**, 41, W384-8	20.1	403
44	Protein structure determination using metagenome sequence data. *Science*, **2017**, 355, 294-298	33.3	346
43	GalaxyWEB server for protein structure prediction and refinement. *Nucleic Acids Research*, **2012**, 40, W294-7	20.1	335
42	Simultaneous Optimization of Biomolecular Energy Functions on Features from Small Molecules and Macromolecules. *Journal of Chemical Theory and Computation*, **2016**, 12, 6201-6212	6.4	199
41	Large-scale determination of previously unsolved protein structures using evolutionary information. *ELife*, **2015**, 4, e09248	8.9	173
40	Macromolecular modeling and design in Rosetta: recent methods and frameworks. *Nature Methods*, **2020**, 17, 665-680	21.6	165
39	De novo design of a fluorescence-activating β-barrel. *Nature*, **2018**, 561, 485-491	50.4	156
38	Advances in GPCR modeling evaluated by the GPCR Dock 2013 assessment: meeting new challenges. *Structure*, **2014**, 22, 1120-1139	5.2	136
37	Community-wide assessment of protein-interface modeling suggests improvements to design methodology. *Journal of Molecular Biology*, **2011**, 414, 289-302	6.5	114
36	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. *Proteins: Structure, Function and Bioinformatics*, **2013**, 81, 1980-7	4.2	78
35	Protein loop modeling by using fragment assembly and analytical loop closure. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 3428-36	4.2	77
34	The FALC-Loop web server for protein loop modeling. *Nucleic Acids Research*, **2011**, 39, W210-4	20.1	72
33	GalaxyTBM: template-based modeling by building a reliable core and refining unreliable local regions. *BMC Bioinformatics*, **2012**, 13, 198	3.6	64
32	Protein structure prediction using Rosetta in CASP12. *Proteins: Structure, Function and Bioinformatics*, **2018**, 86 Suppl 1, 113-121	4.2	63

31	Protein loop modeling using a new hybrid energy function and its application to modeling in inaccurate structural environments. *PLoS ONE*, **2014**, 9, e113811	3.7	54
30	Improved protein structure refinement guided by deep learning based accuracy estimation. *Nature Communications*, **2021**, 12, 1340	17.4	50
29	Protein homology model refinement by large-scale energy optimization. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 3054-3059	11.5	49
28	Refinement of unreliable local regions in template-based protein models. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 1974-86	4.2	47
27	Blind prediction of interfacial water positions in CAPRI. *Proteins: Structure, Function and Bioinformatics*, **2014**, 82, 620-32	4.2	43
26	Strength of Calpha-H...O=C hydrogen bonds in transmembrane proteins. *Journal of Physical Chemistry B*, **2008**, 112, 1041-8	3.4	35
25	Transmembrane signaling of chemotaxis receptor tar: insights from molecular dynamics simulation studies. *Biophysical Journal*, **2011**, 100, 2955-63	2.9	32
24	High-resolution protein-protein docking by global optimization: recent advances and future challenges. *Current Opinion in Structural Biology*, **2015**, 35, 24-31	8.1	30
23	GalaxyGemini: a web server for protein homo-oligomer structure prediction based on similarity. *Bioinformatics*, **2013**, 29, 1078-80	7.2	30
22	Automatic structure prediction of oligomeric assemblies using Robetta in CASP12. *Proteins: Structure, Function and Bioinformatics*, **2018**, 86 Suppl 1, 283-291	4.2	29
21	High-accuracy refinement using Rosetta in CASP13. *Proteins: Structure, Function and Bioinformatics*, **2019**, 87, 1276-1282	4.2	26
20	Sampling and energy evaluation challenges in ligand binding protein design. *Protein Science*, **2017**, 26, 2426-2437	6.3	23
19	Refinement of protein termini in template-based modeling using conformational space annealing. *Proteins: Structure, Function and Bioinformatics*, **2011**, 79, 2725-34	4.2	19
18	Efficient consideration of coordinated water molecules improves computational protein-protein and protein-ligand docking discrimination. *PLoS Computational Biology*, **2020**, 16, e1008103	5	19
17	CASP11 refinement experiments with ROSETTA. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84 Suppl 1, 314-22	4.2	18
16	Improved protein structure prediction using predicted inter-residue orientations		17
15	The origin of consistent protein structure refinement from structural averaging. *Structure*, **2015**, 23, 1123-8	5.2	14
14	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	6.4	12

13	Prediction of Protein Mutational Free Energy: Benchmark and Sampling Improvements Increase Classification Accuracy. *Frontiers in Bioengineering and Biotechnology*, **2020**, 8, 558247	5.8	11
12	Structure prediction using sparse simulated NOE restraints with Rosetta in CASP11. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84 Suppl 1, 181-8	4.2	11
11	Improved protein structure refinement guided by deep learning based accuracy estimation		10
10	Accurate prediction of protein structures and interactions using a 3-track network		9
9	Protein tertiary structure prediction and refinement using deep learning and Rosetta in CASP14. *Proteins: Structure, Function and Bioinformatics*, **2021**, 89, 1722-1733	4.2	9
8	How does a registry change in dyneins coiled-coil stalk drive binding of dynein to microtubules?. *Biochemistry*, **2011**, 50, 7629-36	3.2	5
7	Conformational Sampling of Flexible Ligand-binding Protein Loops. *Bulletin of the Korean Chemical Society*, **2012**, 33, 770-774	1.2	4
6	Protein oligomer modeling guided by predicted interchain contacts in CASP14. *Proteins: Structure, Function and Bioinformatics*, **2021**, 89, 1824-1833	4.2	4
5	Accurate protein structure prediction: what comes next?. *Biodesign*, **2021**, 9, 47-50	0	4
4	The Rosetta all-atom energy function for macromolecular modeling and design		3
3	Efficient consideration of coordinated water molecules improves computational protein-protein and protein-ligand docking		3
2	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	6.1	3
1	Prediction of protein mutational free energy: benchmark and sampling improvements increase classification accuracy		1