Jooyoung Lee

List of Publications by Year in descending order

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30 papers	2,559 citations	331670 21 h-index	477307 29 g-index
30 all docs	30 docs citations	30 times ranked	3737 citing authors

#	Article	IF	Citations
1	Improving physical realism, stereochemistry, and sideâ€chain accuracy in homology modeling: Four approaches that performed well in CASP8. Proteins: Structure, Function and Bioinformatics, 2009, 77, 114-122.	2.6	1,105
2	New optimization method for conformational energy calculations on polypeptides: Conformational space annealing. Journal of Computational Chemistry, 1997, 18, 1222-1232.	3.3	291
3	SVMQA: supportâ€“vector-machine-based protein single-model quality assessment. Bioinformatics, 2017, 33, 2496-2503.	4.1	145
4	Unbiased Global Optimization of Lennard-Jones Clusters forNâ‰201Using the Conformational Space Annealing Method. Physical Review Letters, 2003, 91, 080201.	7.8	115
5	Random Forest-Based Protein Model Quality Assessment (RFMQA) Using Structural Features and Potential Energy Terms. PLoS ONE, 2014, 9, e106542.	2.5	77
6	Conformational analysis of the 20-residue membrane-bound portion of melittin by conformational space annealing. , 1998, 46, 103-115.		73
7	High accuracy template based modeling by global optimization. Proteins: Structure, Function and Bioinformatics, 2007, 69, 83-89.	2.6	70
8	Computational search for direct band gap silicon crystals. Physical Review B, 2014, 90, .	3.2	63
9	Structure optimization by conformational space annealing in an off-lattice protein model. Physical Review E, 2005, 72, 011916.	2.1	57
10	Ab initio materials design using conformational space annealing and its application to searching for direct band gap silicon crystals. Computer Physics Communications, 2016, 203, 110-121.	7.5	55
11	De novo protein structure prediction by dynamic fragment assembly and conformational space annealing. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2403-2417.	2.6	54
12	Modularity optimization by conformational space annealing. Physical Review E, 2012, 85, 056702.	2.1	43
13	Allâ€atom chainâ€building by optimizing MODELLER energy function using conformational space annealing. Proteins: Structure, Function and Bioinformatics, 2009, 75, 1010-1023.	2.6	42
14	Efficient parallel algorithms in global optimization of potential energy functions for peptides, proteins, and crystals. Computer Physics Communications, 2000, 128, 399-411.	7.5	38
15	Dipole-allowed direct band gap silicon superlattices. Scientific Reports, 2015, 5, 18086.	3.3	37
16	Protein structure modeling for CASP10 by multiple layers of global optimization. Proteins: Structure, Function and Bioinformatics, 2014, 82, 188-195.	2.6	36
17	Multiple Sequence Alignment by Conformational Space Annealing. Biophysical Journal, 2008, 95, 4813-4819.	0.5	35
18	Conformational space annealing and an off-lattice frustrated model protein. Journal of Chemical Physics, 2003, 119, 10274-10279.	3.0	33

#	Article	IF	Citations
19	Finding multiple reaction pathways via global optimization of action. Nature Communications, 2017, 8, 15443.	12.8	29
20	An efficient molecular docking using conformational space annealing. Journal of Computational Chemistry, 2005, 26, 78-87.	3.3	28
21	Template based protein structure modeling by global optimization in <scp>CASP</scp>11. Proteins: Structure, Function and Bioinformatics, 2016, 84, 221-232.	2.6	28
22	Methods for estimation of model accuracy in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 361-373.	2.6	27
23	Protein structure determination by conformational space annealing using <scp>NMR</scp> geometric restraints. Proteins: Structure, Function and Bioinformatics, 2015, 83, 2251-2262.	2.6	16
24	Conformational Space Annealing explained: A general optimization algorithm, with diverse applications. Computer Physics Communications, 2018, 223, 28-33.	7.5	16
25	Ground-state energy and energy landscape of the Sherrington-Kirkpatrick spin glass. Physical Review B, 2007, 76, .	3.2	12
26	Contactâ€assisted protein structure modeling by global optimization in CASP11. Proteins: Structure, Function and Bioinformatics, 2016, 84, 189-199.	2.6	11
27	Supramolecular tholos-like architecture constituted by archaeal proteins without functional annotation. Scientific Reports, 2020, 10, 1540.	3.3	8
28	Templateâ€free modeling by <scp>LEE</scp> and <scp>LEER</scp> in <scp>CASP</scp>11. Proteins: Structure, Function and Bioinformatics, 2016, 84, 118-130.	2.6	7
29	Dataâ€assisted protein structure modeling by global optimization in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 240-246.	2.6	6
30	Non-sequential protein structure alignment by conformational space annealing and local refinement. PLoS ONE, 2019, 14, e0210177.	2.5	2