Joe G Greener

List of Publications by Year
in descending order

13	1,384	933264	1125617
papers	citations	10 h-index	13 g-index

17	17	17	1234
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A guide to machine learning for biologists. Nature Reviews Molecular Cell Biology, 2022, 23, 40-55.	16.1	626
2	Ultrafast end-to-end protein structure prediction enables high-throughput exploration of uncharacterized proteins. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	26
3	Differentiable molecular simulation can learn all the parameters in a coarse-grained force field for proteins. PLoS ONE, 2021, 16, e0256990.	1.1	13
4	BioStructures.jl: read, write and manipulate macromolecular structures in Julia. Bioinformatics, 2020, 36, 4206-4207.	1.8	11
5	Prediction of interresidue contacts with DeepMetaPSICOV in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1092-1099.	1.5	102
6	Recent developments in deep learning applied to protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1179-1189.	1.5	56
7	Deep learning extends de novo protein modelling coverage of genomes using iteratively predicted structural constraints. Nature Communications, 2019, 10, 3977.	5.8	144
8	Highâ€Throughput Kinetic Analysis for Targetâ€Directed Covalent Ligand Discovery. Angewandte Chemie - International Edition, 2018, 57, 5257-5261.	7.2	59
9	Highâ€Throughput Kinetic Analysis for Targetâ€Directed Covalent Ligand Discovery. Angewandte Chemie, 2018, 130, 5355-5359.	1.6	5
10	Structure-based prediction of protein allostery. Current Opinion in Structural Biology, 2018, 50, 1-8.	2.6	90
11	Design of metalloproteins and novel protein folds using variational autoencoders. Scientific Reports, 2018, 8, 16189.	1.6	82
12	Predicting Protein Dynamics and Allostery Using Multi-Protein Atomic Distance Constraints. Structure, 2017, 25, 546-558.	1.6	45
13	AlloPred: prediction of allosteric pockets on proteins using normal mode perturbation analysis. BMC Bioinformatics, 2015, 16, 335.	1.2	88