

Joe G Greener

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4863167/publications.pdf>

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13
papers

1,384
citations

933264

10
h-index

1125617

13
g-index

17
all docs

17
docs citations

17
times ranked

1234
citing authors

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