Robin Pearce

List of Publications by Year
in descending order

18	1,282	567281 15	839539 18
papers	citations	h-index	g-index

21	21	21	1259
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Folding non-homologous proteins by coupling deep-learning contact maps with I-TASSER assembly simulations. Cell Reports Methods, 2021, 1, 100014.	2.9	272
2	Deepâ€learning contactâ€map guided protein structure prediction in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1149-1164.	2.6	180
3	LOMETS2: improved meta-threading server for fold-recognition and structure-based function annotation for distant-homology proteins. Nucleic Acids Research, 2019, 47, W429-W436.	14.5	118
4	De novo design of protein peptides to block association of the SARS-CoV-2 spike protein with human ACE2. Aging, 2020, 12, 11263-11276.	3.1	89
5	Deep learning techniques have significantly impacted protein structure prediction and protein design. Current Opinion in Structural Biology, 2021, 68, 194-207.	5.7	77
6	EvoEF2: accurate and fast energy function for computational protein design. Bioinformatics, 2020, 36, 1135-1142.	4.1	73
7	Toward the solution of the protein structure prediction problem. Journal of Biological Chemistry, 2021, 297, 100870.	3.4	73
8	EvoDesign: Designing Proteinâ€“Protein Binding Interactions Using Evolutionary Interface Profiles in Conjunction with an Optimized Physical Energy Function. Journal of Molecular Biology, 2019, 431, 2467-2476.	4.2	60
9	FASPR: an open-source tool for fast and accurate protein side-chain packing. Bioinformatics, 2020, 36, 3758-3765.	4.1	54
10	Protein structure prediction using deep learning distance and hydrogenâ€bonding restraints in <scp>CASP14</scp>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1734-1751.	2.6	53
11	Detecting distant-homology protein structures by aligning deep neural-network based contact maps. PLoS Computational Biology, 2019, 15, e1007411.	3.2	45
12	FUpred: detecting protein domains through deep-learning-based contact map prediction. Bioinformatics, 2020, 36, 3749-3757.	4.1	44
13	Improving fragment-based ab initio protein structure assembly using low-accuracy contact-map predictions. Nature Communications, 2021, 12, 5011.	12.8	44
14	A New Protocol for Atomic-Level Protein Structure Modeling and Refinement Using Low-to-Medium Resolution Cryo-EM Density Maps. Journal of Molecular Biology, 2020, 432, 5365-5377.	4.2	26
15	Computational design of SARS-CoV-2 spike glycoproteins to increase immunogenicity by T cell epitope engineering. Computational and Structural Biotechnology Journal, 2021, 19, 518-529.	4.1	19
16	Identification of 13 Guanidinobenzoyl- or Aminidinobenzoyl-Containing Drugs to Potentially Inhibit TMPRSS2 for COVID-19 Treatment. International Journal of Molecular Sciences, 2021, 22, 7060.	4.1	10
17	Comparative Secretomics Analysis Reveals the Major Components of Penicillium oxalicum 16 and Trichoderma reesei RUT-C30. Microorganisms, 2021, 9, 2042.	3.6	8
18	Fitting Low-Resolution Protein Structures into Cryo-EM Density Maps by Multiobjective Optimization of Global and Local Correlations. Journal of Physical Chemistry B, 2021, 125, 528-538.	2.6	4