

Robin Pearce

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

1,282
citations

567281

15
h-index

839539

18
g-index

21
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docs citations

21
times ranked

1259
citing authors

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