

Quan Chen

List of Publications by Year in descending order

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15
papers

522
citations

1040056

9
h-index

996975

15
g-index

16
all docs

16
docs citations

16
times ranked

492
citing authors

#	ARTICLE	IF	CITATIONS
1	Computational Redesign of a PETase for Plastic Biodegradation under Ambient Condition by the GRAPE Strategy. <i>ACS Catalysis</i> , 2021, 11, 1340-1350.	11.2	263
2	Protein design with a comprehensive statistical energy function and boosted by experimental selection for foldability. <i>Nature Communications</i> , 2014, 5, 5330.	12.8	74
3	A backbone-centred energy function of neural networks for protein design. <i>Nature</i> , 2022, 602, 523-528.	27.8	48
4	Increasing the efficiency and accuracy of the ABACUS protein sequence design method. <i>Bioinformatics</i> , 2020, 36, 136-144.	4.1	25
5	Solution structure and backbone dynamics of the AF-6 PDZ domain/Bcr peptide complex. <i>Protein Science</i> , 2007, 16, 1053-1062.	7.6	20
6	Computational protein design for given backbone: recent progresses in general method-related aspects. <i>Current Opinion in Structural Biology</i> , 2016, 39, 89-95.	5.7	20
7	Proteins of well-defined structures can be designed without backbone readjustment by a statistical model. <i>Journal of Structural Biology</i> , 2016, 196, 350-357.	2.8	12
8	Computational Protein Design Under a Given Backbone Structure with the ABACUS Statistical Energy Function. <i>Methods in Molecular Biology</i> , 2017, 1529, 217-226.	0.9	11
9	De novo sequence redesign of a functional Ras-binding domain globally inverted the surface charge distribution and led to extreme thermostability. <i>Biotechnology and Bioengineering</i> , 2021, 118, 2031-2042.	3.3	11
10	Integrating genome sequence and structural data for statistical learning to predict transcription factor binding sites. <i>Nucleic Acids Research</i> , 2020, 48, 12604-12617.	14.5	11
11	Selection and analyses of variants of a designed protein suggest importance of hydrophobicity of partially buried sidechains for protein stability at high temperatures. <i>Protein Science</i> , 2019, 28, 1437-1447.	7.6	6
12	Crystal structure and activation mechanism of DR3 death domain. <i>FEBS Journal</i> , 2019, 286, 2593-2610.	4.7	6
13	Biochemical characterization of G64W mutant of acidic beta-crystallin 4. <i>Experimental Eye Research</i> , 2019, 186, 107712.	2.6	5
14	Recurring sequence-structure motifs in (β ₂) ₈ -barrel proteins and experimental optimization of a chimeric protein designed based on such motifs. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 165-175.	2.3	4
15	DEPACT and PACMatch: A Workflow of Designing <i>De Novo</i> Protein Pockets to Bind Small Molecules. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 971-985.	5.4	4