Quan Chen

List of Publications by Year
in descending order

15	522	1040056	996975
15 papers	**522** citations	**9** h-index	**15** g-index

16	16	16	492
16 all docs	**16** docs citations	**16** times ranked	**492** citing authors

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