Zibo Chen

List of Publications by Year in descending order

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840119 1058022 1,680 16 11 14 h-index citations g-index papers 23 23 23 2546 all docs docs citations times ranked citing authors

#	Article	IF	Citations
1	A cargo-sorting DNA robot. Science, 2017, 357, .	6.0	426
2	De novo design of protein homo-oligomers with modular hydrogen-bond network–mediated specificity. Science, 2016, 352, 680-687.	6.0	262
3	De novo design of bioactive protein switches. Nature, 2019, 572, 205-210.	13.7	190
4	De novo design of protein logic gates. Science, 2020, 368, 78-84.	6.0	151
5	Accurate computational design of multipass transmembrane proteins. Science, 2018, 359, 1042-1046.	6.0	149
6	Programmable design of orthogonal protein heterodimers. Nature, 2019, 565, 106-111.	13.7	139
7	De novo design of tunable, pH-driven conformational changes. Science, 2019, 364, 658-664.	6.0	109
8	Rapid online buffer exchange for screening of proteins, protein complexes and cell lysates by native mass spectrometry. Nature Protocols, 2020, 15, 1132-1157.	5 . 5	88
9	Programmable protein circuit design. Cell, 2021, 184, 2284-2301.	13.5	50
10	Self-Assembling 2D Arrays with <i>de Novo</i> Protein Building Blocks. Journal of the American Chemical Society, 2019, 141, 8891-8895.	6.6	37
11	Functional expression and characterization of the envelope glycoprotein E1E2 heterodimer of hepatitis C virus. PLoS Pathogens, 2019, 15, e1007759.	2.1	28
12	Interpreting neural networks for biological sequences by learning stochastic masks. Nature Machine Intelligence, 2022, 4, 41-54.	8.3	14
13	Modulating mechanical stability of heterodimerization between engineered orthogonal helical domains. Nature Communications, 2020, 11, 4476.	5. 8	13
14	A Game-Theoretic Model of Interactions between Hibiscus Latent Singapore Virus and Tobacco Mosaic Virus. PLoS ONE, 2012, 7, e37007.	1.1	8
15	Competitive Displacement of <i>De Novo</i> Designed HeteroDimers Can Reversibly Control Protein–Protein Interactions and Implement Feedback in Synthetic Circuits. , 2022, 1, 91-100.		4
16	Creating the protein version of DNA base pairing. Science, 2019, 366, 965-965.	6.0	0