Xiaoqiang Huang

List of Publications by Year
in descending order

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28	1,085	567281 15	501196 28
papers	citations	h-index	g-index

35	35	35	1416
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Recent Advances in Improving Gene-Editing Specificity through CRISPRâ€“Cas9 Nuclease Engineering. Cells, 2022, 11, 2186.	4.1	25
2	Effects of SARSâ€CoVâ€2 mutations on protein structures and intraviral proteinâ€“protein interactions. Journal of Medical Virology, 2021, 93, 2132-2140.	5.0	85
3	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
4	The Fungal Effector Mlp37347 Alters Plasmodesmata Fluxes and Enhances Susceptibility to Pathogen. Microorganisms, 2021, 9, 1232.	3.6	9
5	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
6	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
7	EvoEF2: accurate and fast energy function for computational protein design. Bioinformatics, 2020, 36, 1135-1142.	4.1	73
8	Toward the Accuracy and Speed of Protein Side-Chain Packing: AÂSystematic Study on Rotamer Libraries. Journal of Chemical Information and Modeling, 2020, 60, 410-420.	5.4	15
9	SSIPe: accurately estimating proteinâ€“protein binding affinity change upon mutations using evolutionary profiles in combination with an optimized physical energy function. Bioinformatics, 2020, 36, 2429-2437.	4.1	42
10	Identifying the Zoonotic Origin of SARS-CoV-2 by Modeling the Binding Affinity between the Spike Receptor-Binding Domain and Host ACE2. Journal of Proteome Research, 2020, 19, 4844-4856.	3.7	27
11	A Poplar Rust Effector Protein Associates with Protein Disulfide Isomerase and Enhances Plant Susceptibility. Biology, 2020, 9, 294.	2.8	8
12	Landscape of variable domain of heavyâ€chainâ€only antibody repertoire from alpaca. Immunology, 2020, 161, 53-65.	4.4	17
13	Protein Structure and Sequence Reanalysis of 2019-nCoV Genome Refutes Snakes as Its Intermediate Host and the Unique Similarity between Its Spike Protein Insertions and HIV-1. Journal of Proteome Research, 2020, 19, 1351-1360.	3.7	242
14	FASPR: an open-source tool for fast and accurate protein side-chain packing. Bioinformatics, 2020, 36, 3758-3765.	4.1	54
15	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
16	Using molecular dynamics simulations to evaluate active designs of cephradine hydrolase by molecular mechanics/Poissonâ€“Boltzmann surface area and molecular mechanics/generalized Born surface area methods. RSC Advances, 2019, 9, 13868-13877.	3.6	19
17	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
18	Changing the Apoptosis Pathway through Evolutionary Protein Design. Journal of Molecular Biology, 2019, 431, 825-841.	4.2	16

#	Article	IF	Citations
19	Computational redesign of penicillin acylase for cephradine synthesis with high kinetic selectivity. Green Chemistry, 2018, 20, 5484-5490.	9.0	30
20	Computational design of cephradine synthase in a new scaffold identified from structural databases. Chemical Communications, 2017, 53, 7604-7607.	4.1	19
21	Computational design to improve catalytic activity of cephalosporin C acylase from Pseudomonas strain N176. RSC Advances, 2017, 7, 30370-30375.	3.6	9
22	Computational design of variants for cephalosporin C acylase from Pseudomonas strain N176 with improved stability and activity. Applied Microbiology and Biotechnology, 2017, 101, 621-632.	3.6	22
23	Use of an Improved Matching Algorithm to Select Scaffolds for Enzyme Design Based on a Complex Active Site Model. PLoS ONE, 2016, 11, e0156559.	2.5	14
24	A fast loop-closure algorithm to accelerate residue matching in computational enzyme design. Journal of Molecular Modeling, 2016, 22, 49.	1.8	7
25	Computational design of enzymeâ€“ligand binding using a combined energy function and deterministic sequence optimization algorithm. Journal of Molecular Modeling, 2015, 21, 191.	1.8	23
26	Evaluation of active designs of cephalosporin C acylase by molecular dynamics simulation and molecular docking. Journal of Molecular Modeling, 2014, 20, 2314.	1.8	11
27	A solvated ligand rotamer approach and its application in computational protein design. Journal of Molecular Modeling, 2013, 19, 1355-1367.	1.8	9
28	Systematic optimization model and algorithm for binding sequence selection in computational enzyme design. Protein Science, 2013, 22, 929-941.	7.6	34