## Hamed Khakzad

List of Publications by Year in descending order

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HAMED KHAKZAD

#	Article	IF	CITATIONS
1	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	19.0	513
2	Rapid determination of quaternary protein structures in complex biological samples. Nature Communications, 2019, 10, 192.	12.8	47
3	A quantitative Streptococcus pyogenes–human protein–protein interaction map reveals localization of opsonizing antibodies. Nature Communications, 2019, 10, 2727.	12.8	36
4	Spike-Dependent Opsonization Indicates Both Dose-Dependent Inhibition of Phagocytosis and That Non-Neutralizing Antibodies Can Confer Protection to SARS-CoV-2. Frontiers in Immunology, 2021, 12, 808932.	4.8	34
5	Structural proteomics, electron cryo-microscopy and structural modeling approaches in bacteria–human protein interactions. Medical Microbiology and Immunology, 2020, 209, 265-275.	4.8	13
6	Streptococcus pyogenes Forms Serotype- and Local Environment-Dependent Interspecies Protein Complexes. MSystems, 2021, 6, e0027121.	3.8	13
7	Structural determination of Streptococcus pyogenes M1 protein interactions with human immunoglobulin G using integrative structural biology. PLoS Computational Biology, 2021, 17, e1008169.	3.2	12
8	In vivo Cross-Linking MS of the Complement System MAC Assembled on Live Gram-Positive Bacteria. Frontiers in Genetics, 2020, 11, 612475.	2.3	7
9	Protein structure prediction using bio-inspired algorithm: A review. , 2012, , .		5
10	PDB2Graph: A toolbox for identifying critical amino acids map in proteins based on graph theory. Computers in Biology and Medicine, 2016, 72, 151-159.	7.0	5
11	Greedy de novo motif discovery to construct motif repositories for bacterial proteomes. BMC Bioinformatics, 2019, 20, 141.	2.6	4
12	The structure of human dermatan sulfate epimerase 1 emphasizes the importance of C5-epimerization of glucuronic acid in higher organisms. Chemical Science, 2021, 12, 1869-1885.	7.4	3
13	Cheetah-MS: a web server to model protein complexes using tandem cross-linking mass spectrometry data. Bioinformatics, 2021, 37, 4871-4872.	4.1	0