Gaohua Liu

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4475199/publications.pdf

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15	540	933447 10	1058476 14
papers	citations	h-index	g-index

17	17	17	983
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Principles for designing proteins with cavities formed by curved Î² sheets. Science, 2017, 355, 201-206.	12.6	117
2	Control over overall shape and size in de novo designed proteins. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5478-85.	7.1	113
3	De novo protein design by citizen scientists. Nature, 2019, 570, 390-394.	27.8	105
4	Structural/Functional Properties of Human NFU1, an Intermediate [4Fe-4S] Carrier in Human Mitochondrial Iron-Sulfur Cluster Biogenesis. Structure, 2016, 24, 2080-2091.	3.3	45
5	Assessment of prediction methods for protein structures determined by <scp>NMR</scp> in <scp>CASP14</scp>: Impact of <scp>AlphaFold2</scp>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1959-1976.	2.6	30
6	The second round of Critical Assessment of Automated Structure Determination of Proteins by NMR: CASD-NMR-2013. Journal of Biomolecular NMR, 2015, 62, 413-424.	2.8	27
7	A community resource of experimental data for <scp>NMR</scp> / <scp>X</scp>â€ray crystal structure pairs. Protein Science, 2016, 25, 30-45.	7.6	24
8	Protein structure prediction assisted with sparse NMR data in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1315-1332.	2.6	21
9	Solution NMR structure of the ARID domain of human AT-rich interactive domain-containing protein 3A: A human cancer protein interaction network target. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2170-2175.	2.6	16
10	A common binding motif in the ET domain of BRD3 forms polymorphic structural interfaces with host and viral proteins. Structure, 2021, 29, 886-898.e6.	3.3	16
11	REDCRAFT: A computational platform using residual dipolar coupling NMR data for determining structures of perdeuterated proteins in solution. PLoS Computational Biology, 2021, 17, e1008060.	3.2	8
12	NMR structure of Fâ€actinâ€binding domain of Arg/Abl2 from Homo sapiens. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1326-1330.	2.6	7
13	Introduction of a polar core into the de novo designed protein <scp>T</scp>op7. Protein Science, 2016, 25, 1299-1307.	7.6	7
14	Backbone and Ile-Î´1, Leu, Val methyl 1H, 15N, and 13C, chemical shift assignments for Rhizopus chinensis lipase. Biomolecular NMR Assignments, 2018, 12, 63-68.	0.8	3
15	Aromatic claw: A new fold with high aromatic content that evades structural prediction. Protein Science, 2017, 26, 208-217.	7.6	0