

Gaohua Liu

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	REDCRAFT: A computational platform using residual dipolar coupling NMR data for determining structures of perdeuterated proteins in solution. <i>PLoS Computational Biology</i> , 2021, 17, e1008060.	3.2	8
2	A common binding motif in the ET domain of BRD3 forms polymorphic structural interfaces with host and viral proteins. <i>Structure</i> , 2021, 29, 886-898.e6.	3.3	16
3	Assessment of prediction methods for protein structures determined by <i>NMR</i> in <i>CASP14</i> : Impact of <i>AlphaFold2</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1959-1976.	2.6	30
4	Protein structure prediction assisted with sparse NMR data in <i>CASP13</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1315-1332.	2.6	21
5	De novo protein design by citizen scientists. <i>Nature</i> , 2019, 570, 390-394.	27.8	105
6	Backbone and Ile- β 1, Leu, Val methyl 1H, 15N, and 13C, chemical shift assignments for <i>Rhizopus chinensis</i> lipase. <i>Biomolecular NMR Assignments</i> , 2018, 12, 63-68.	0.8	3
7	Principles for designing proteins with cavities formed by curved β^2 sheets. <i>Science</i> , 2017, 355, 201-206.	12.6	117
8	Aromatic claw: A new fold with high aromatic content that evades structural prediction. <i>Protein Science</i> , 2017, 26, 208-217.	7.6	0
9	Introduction of a polar core into the de novo designed protein <i>Top7</i> . <i>Protein Science</i> , 2016, 25, 1299-1307.	7.6	7
10	A community resource of experimental data for <i>NMR</i> / <i>X-ray</i> crystal structure pairs. <i>Protein Science</i> , 2016, 25, 30-45.	7.6	24
11	Structural/Functional Properties of Human NFU1, an Intermediate [4Fe-4S] Carrier in Human Mitochondrial Iron-Sulfur Cluster Biogenesis. <i>Structure</i> , 2016, 24, 2080-2091.	3.3	45
12	The second round of Critical Assessment of Automated Structure Determination of Proteins by NMR: <i>CASP-NMR-2013</i> . <i>Journal of Biomolecular NMR</i> , 2015, 62, 413-424.	2.8	27
13	Control over overall shape and size in de novo designed proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5478-85.	7.1	113
14	NMR structure of <i>Actin</i> binding domain of <i>Arg/Abl2</i> from <i>Homo sapiens</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1326-1330.	2.6	7
15	Solution NMR structure of the ARID domain of human AT-rich interactive domain-containing protein 3A: A human cancer protein interaction network target. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2170-2175.	2.6	16