Binchen Mao

List of Publications by Year
in descending order

14 papers	793 citations	840776 11 h-index	1058476 14 g-index
14 all docs	14 docs citations	14 times ranked	1335 citing authors

#	Article	IF	Citations
1	Diastolic dysfunction and impaired cardiac output reserve in dysmetabolic nonhuman primate with proteinuria. Journal of Diabetes and Its Complications, 2021, 35, 107881.	2.3	4
2	De novo design of a fluorescence-activating Î²-barrel. Nature, 2018, 561, 485-491.	27.8	269
3	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
4	Guiding automated NMR structure determination using a global optimization metric, the NMR DP score. Journal of Biomolecular NMR, 2015, 62, 439-451.	2.8	16
5	Assessment of templateâ€based protein structure predictions in CASP10. Proteins: Structure, Function and Bioinformatics, 2014, 82, 43-56.	2.6	93
6	Protein NMR Structures Refined with Rosetta Have Higher Accuracy Relative to Corresponding X-ray Crystal Structures. Journal of the American Chemical Society, 2014, 136, 1893-1906.	13.7	65
7	PDBStat: a universal restraint converter and restraint analysis software package for protein NMR. Journal of Biomolecular NMR, 2013, 56, 337-351.	2.8	59
8	Segmental isotope labeling of proteins for NMR structural study using a protein S tag for higher expression and solubility. Journal of Biomolecular NMR, 2012, 52, 303-313.	2.8	16
9	Blind Testing of Routine, Fully Automated Determination of Protein Structures from NMR Data. Structure, 2012, 20, 227-236.	3.3	75
10	Improved Technologies Now Routinely Provide Protein NMR Structures Useful for Molecular Replacement. Structure, 2011, 19, 757-766.	3.3	34
11	Accurate Automated Protein NMR Structure Determination Using Unassigned NOESY Data. Journal of the American Chemical Society, 2010, 132, 202-207.	13.7	47
12	CASD-NMR: critical assessment of automated structure determination by NMR. Nature Methods, 2009, 6, 625-626.	19.0	80
13	A web server for transcription factor binding site prediction. Bioinformation, 2006, 1, 156-157.	0.5	6
14	MACO: a gapped-alignment scoring tool for comparing transcription factor binding sites. In Silico Biology, 2006, 6, 307-10.	0.9	5