

Binchen Mao

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3886498/publications.pdf>

Version: 2024-02-01

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	De novo design of a fluorescence-activating β -barrel. <i>Nature</i> , 2018, 561, 485-491.	27.8	269
2	Assessment of template-based protein structure predictions in CASP10. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 43-56.	2.6	93
3	CASD-NMR: critical assessment of automated structure determination by NMR. <i>Nature Methods</i> , 2009, 6, 625-626.	19.0	80
4	Blind Testing of Routine, Fully Automated Determination of Protein Structures from NMR Data. <i>Structure</i> , 2012, 20, 227-236.	3.3	75
5	Protein NMR Structures Refined with Rosetta Have Higher Accuracy Relative to Corresponding X-ray Crystal Structures. <i>Journal of the American Chemical Society</i> , 2014, 136, 1893-1906.	13.7	65
6	PDBStat: a universal restraint converter and restraint analysis software package for protein NMR. <i>Journal of Biomolecular NMR</i> , 2013, 56, 337-351.	2.8	59
7	Accurate Automated Protein NMR Structure Determination Using Unassigned NOESY Data. <i>Journal of the American Chemical Society</i> , 2010, 132, 202-207.	13.7	47
8	Improved Technologies Now Routinely Provide Protein NMR Structures Useful for Molecular Replacement. <i>Structure</i> , 2011, 19, 757-766.	3.3	34
9	A community resource of experimental data for ^{15}N / ^{13}C X-ray crystal structure pairs. <i>Protein Science</i> , 2016, 25, 30-45.	7.6	24
10	Segmental isotope labeling of proteins for NMR structural study using a protein S tag for higher expression and solubility. <i>Journal of Biomolecular NMR</i> , 2012, 52, 303-313.	2.8	16
11	Guiding automated NMR structure determination using a global optimization metric, the NMR DP score. <i>Journal of Biomolecular NMR</i> , 2015, 62, 439-451.	2.8	16
12	A web server for transcription factor binding site prediction. <i>Bioinformatics</i> , 2006, 1, 156-157.	0.5	6
13	MACO: a gapped-alignment scoring tool for comparing transcription factor binding sites. <i>In Silico Biology</i> , 2006, 6, 307-10.	0.9	5
14	Diastolic dysfunction and impaired cardiac output reserve in dysmetabolic nonhuman primate with proteinuria. <i>Journal of Diabetes and Its Complications</i> , 2021, 35, 107881.	2.3	4