Fa-An Chao

List of Publications by Year
in descending order

15 papers	528 citations	840776 11 h-index	1058476 14 g-index
15 all docs	15 docs citations	15 times ranked	992 citing authors

#	Article	IF	Citations
1	Facilitating spectral analyses, simplification, and new tools through deep neural networks. Magnetic Resonance Letters, 2022, 2, 56-58.	1.3	0
2	Insights into the Cross Talk between Effector and Allosteric Lobes of KRAS from Methyl Conformational Dynamics. Journal of the American Chemical Society, 2022, 144, 4196-4205.	13.7	14
3	Theoretical classification of exchange geometries from the perspective of NMR relaxation dispersion. Journal of Magnetic Resonance, 2021, 328, 107003.	2.1	3
4	Achieving pure spin effects by artifact suppression in methyl adiabatic relaxation experiments. Journal of Biomolecular NMR, 2020, 74, 223-228.	2.8	3
5	Optimization of sortase A ligation for flexible engineering of complex protein systems. Journal of Biological Chemistry, 2020, 295, 2664-2675.	3.4	29
6	Probing the Broad Time Scale and Heterogeneous Conformational Dynamics in the Catalytic Core of the Arf-GAP ASAP1 via Methyl Adiabatic Relaxation Dispersion. Journal of the American Chemical Society, 2019, 141, 11881-11891.	13.7	15
7	Protein dynamics revealed by NMR relaxation methods. Emerging Topics in Life Sciences, 2018, 2, 93-105.	2.6	17
8	Application of geometric approximation to the CPMG experiment: Two- and three-site exchange. Journal of Magnetic Resonance, 2017, 277, 8-14.	2.1	8
9	A dynamic hydrophobic core orchestrates allostery in protein kinases. Science Advances, 2017, 3, e1600663.	10.3	89
10	Geometric Approximation: A New Computational Approach To Characterize Protein Dynamics from NMR Adiabatic Relaxation Dispersion Experiments. Journal of the American Chemical Society, 2016, 138, 7337-7345.	13.7	22
11	FLAMEnGO 2.0: An enhanced fuzzy logic algorithm for structure-based assignment of methyl group resonances. Journal of Magnetic Resonance, 2014, 245, 17-23.	2.1	41
12	Structure and dynamics of a primordial catalytic fold generated by in vitro evolution. Nature Chemical Biology, 2013, 9, 81-83.	8.0	80
13	FLAMEnGO: A fuzzy logic approach for methyl group assignment using NOESY and paramagnetic relaxation enhancement data. Journal of Magnetic Resonance, 2012, 214, 103-110.	2.1	23
14	Heteronuclear Adiabatic Relaxation Dispersion (HARD) for quantitative analysis of conformational dynamics in proteins. Journal of Magnetic Resonance, 2012, 219, 75-82.	2.1	14
15	Multiple Nucleic Acid Binding Sites and Intrinsic Disorder of Severe Acute Respiratory Syndrome Coronavirus Nucleocapsid Protein: Implications for Ribonucleocapsid Protein Packaging. Journal of Virology, 2009, 83, 2255-2264.	3.4	170