Yang Shen

List of Publications by Year
in descending order

54	6,761	236925 25	168389 53
papers	citations	h-index	g-index

58	58	58	8036
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Advances in NMR Spectroscopy of Weakly Aligned Biomolecular Systems. Chemical Reviews, 2022, 122, 9307-9330.	47.7	27
2	De novo design and directed folding of disulfide-bridged peptide heterodimers. Nature Communications, 2022, 13, 1539.	12.8	9
3	Two-Stage Syntheses of Clionastatins A and B. Journal of the American Chemical Society, 2022, 144, 8938-8944.	13.7	7
4	Hybrid measurement of respiratory aerosol reveals a dominant coarse fraction resulting from speech that remains airborne for minutes. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	17
5	Site-Specific Photochemical Desaturation Enables Divergent Syntheses of Illicium Sesquiterpenes. Journal of the American Chemical Society, 2021, 143, 3256-3263.	13.7	26
6	Hydrophobic Gate of Mechanosensitive Channel of Large Conductance in Lipid Bilayers Revealed by Solid-State NMR Spectroscopy. Journal of Physical Chemistry B, 2021, 125, 2477-2490.	2.6	9
7	Structure of membrane diacylglycerol kinase in lipid bilayers. Communications Biology, 2021, 4, 282.	4.4	7
8	A lowly populated, transient Î²-sheet structure in monomeric AÎ²1-42 identified by multinuclear NMR of chemical denaturation. Biophysical Chemistry, 2021, 270, 106531.	2.8	21
9	Concordance of X-ray and AlphaFold2 Models of SARS-CoV-2 Main Protease with Residual Dipolar Couplings Measured in Solution. Journal of the American Chemical Society, 2021, 143, 19306-19310.	13.7	40
10	Merging Câ€“H Vinylation with Switchable 6Ï€-Electrocyclizations for Divergent Heterocycle Synthesis. Journal of the American Chemical Society, 2020, 142, 15585-15594.	13.7	21
11	Modulating the Stiffness of the Myosin VI Single Î±-Helical Domain. Biophysical Journal, 2020, 118, 1119-1128.	0.5	2
12	Conformational Design Principles in Total Synthesis. Angewandte Chemie, 2020, 132, 14302-14314.	2.0	2
13	Conformational Design Principles in Total Synthesis. Angewandte Chemie - International Edition, 2020, 59, 14198-14210.	13.8	30
14	Remarkable Rigidity of the Single Î±-Helical Domain of Myosin-VI As Revealed by NMR Spectroscopy. Journal of the American Chemical Society, 2019, 141, 9004-9017.	13.7	42
15	Stabilizing pâ€Dithiobenzyl Urethane Linkers without Rateâ€Limiting Selfâ€Immolation for Traceless Drug Release. ChemMedChem, 2019, 14, 1196-1203.	3.2	9
16	Probing transient excited states of the bacterial cell division regulator MinE by relaxation dispersion NMR spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25446-25455.	7.1	16
17	Residual Dipolar Couplings for Resolving Cysteine Bridges in Disulfide-Rich Peptides. Frontiers in Chemistry, 2019, 7, 889.	3.6	9
18	Prediction of nearest neighbor effects on backbone torsion angles and NMR scalar coupling constants in disordered proteins. Protein Science, 2018, 27, 146-158.	7.6	24

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19	Conformational Bias by a Removable Silyl Group: Construction of Bicyclo[n.3.1]alkenes by Ring Closing Metathesis. Chemistry - A European Journal, 2018, 24, 2334-2338.	3.3	10
20	Gating Mechanism of Aquaporin Z in Synthetic Bilayers and Native Membranes Revealed by Solid-State NMR Spectroscopy. Journal of the American Chemical Society, 2018, 140, 7885-7895.	13.7	26
21	Total Synthesis of Aplydactone by a Conformationally Controlled Câ^'H Functionalization. Angewandte Chemie, 2017, 129, 8299-8302.	2.0	8
22	Total Synthesis of Aplydactone by a Conformationally Controlled Câ^'H Functionalization. Angewandte Chemie - International Edition, 2017, 56, 8187-8190.	13.8	46
23	Innentitelbild: Total Synthesis of Aplydactone by a Conformationally Controlled Câ^'H Functionalization (Angew. Chem. 28/2017). Angewandte Chemie, 2017, 129, 8130-8130.	2.0	0
24	ARTSY-J: Convenient and precise measurement of 3JHNHÎ± couplings in medium-size proteins from TROSY-HSQC spectra. Journal of Magnetic Resonance, 2016, 268, 73-81.	2.1	8
25	Monomeric AÎ²^{1â€“40} and AÎ²^{1â€“42} Peptides in Solution Adopt Very Similar Ramachandran Map Distributions That Closely Resemble Random Coil. Biochemistry, 2016, 55, 762-775.	2.5	168
26	Homology modeling of larger proteins guided by chemical shifts. Nature Methods, 2015, 12, 747-750.	19.0	51
27	MERA: a webserver for evaluating backbone torsion angle distributions in dynamic and disordered proteins from NMR data. Journal of Biomolecular NMR, 2015, 63, 85-95.	2.8	40
28	Protecting-Group-Free Total Synthesis of (â^')-Jiadifenolide: Development of a [4 + 1] Annulation toward Multisubstituted Tetrahydrofurans. Organic Letters, 2015, 17, 5480-5483.	4.6	44
29	Protein Structural Information Derived from NMR Chemical Shift with the Neural Network Program TALOS-N. Methods in Molecular Biology, 2015, 1260, 17-32.	0.9	196
30	A maximum entropy approach to the study of residueâ€specific backbone angle distributions in Î±â€synuclein, an intrinsically disordered protein. Protein Science, 2014, 23, 1275-1290.	7.6	73
31	Improving 3D structure prediction from chemical shift data. Journal of Biomolecular NMR, 2013, 57, 27-35.	2.8	25
32	Protein backbone and sidechain torsion angles predicted from NMR chemical shifts using artificial neural networks. Journal of Biomolecular NMR, 2013, 56, 227-241.	2.8	939
33	Improved chemical shift based fragment selection for CS-Rosetta using Rosetta3 fragment picker. Journal of Biomolecular NMR, 2013, 57, 117-127.	2.8	38
34	Identification of helix capping and Î²-turn motifs from NMR chemical shifts. Journal of Biomolecular NMR, 2012, 52, 211-232.	2.8	81
35	Prediction of Xaa-Pro peptide bond conformation from sequence and chemical shifts. Journal of Biomolecular NMR, 2010, 46, 199-204.	2.8	124
36	SPARTA+: a modest improvement in empirical NMR chemical shift prediction by means of an artificial neural network. Journal of Biomolecular NMR, 2010, 48, 13-22.	2.8	468

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37	Fully automated high-quality NMR structure determination of small 2H-enriched proteins. Journal of Structural and Functional Genomics, 2010, 11, 223-232.	1.2	12
38	De novo structure generation using chemical shifts for proteins with highâ€sequence identity but different folds. Protein Science, 2010, 19, 349-356.	7.6	59
39	Solution Conformation and Dynamics of the HIV-1 Integrase Core Domain. Journal of Biological Chemistry, 2010, 285, 18072-18084.	3.4	24
40	Simultaneous prediction of protein folding and docking at high resolution. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18978-18983.	7.1	145
41	De novo protein structure generation from incomplete chemical shift assignments. Journal of Biomolecular NMR, 2009, 43, 63-78.	2.8	234
42	TALOS+: a hybrid method for predicting protein backbone torsion angles from NMR chemical shifts. Journal of Biomolecular NMR, 2009, 44, 213-223.	2.8	2,305
43	Structure of the Protein BPTI Derived with NOESY in Supercooled Water: Validation and Refinement of Solution Structures. Angewandte Chemie - International Edition, 2008, 47, 324-326.	13.8	5
44	Consistent blind protein structure generation from NMR chemical shift data. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 4685-4690.	7.1	776
45	J-GFT NMR for Precise Measurement of Mutually Correlated Nuclear Spinâ'Spin Couplings. Journal of the American Chemical Society, 2007, 129, 680-692.	13.7	24
46	Building native protein conformation from NMR backbone chemical shifts using Monte Carlo fragment assembly. Protein Science, 2007, 16, 1515-1521.	7.6	33
47	Protein backbone chemical shifts predicted from searching a database for torsion angle and sequence homology. Journal of Biomolecular NMR, 2007, 38, 289-302.	2.8	287
48	NMR structure of protein PA2021 fromPseudomonas aeruginosa. Proteins: Structure, Function and Bioinformatics, 2006, 65, 767-770.	2.6	1
49	NMR structure of protein yqbG from Bacillus subtilis reveals a novel Î±-helical protein fold. Proteins: Structure, Function and Bioinformatics, 2005, 62, 288-291.	2.6	3
50	NMR data collection and analysis protocol for high-throughput protein structure determination. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10487-10492.	7.1	108
51	G-Matrix Fourier Transform NOESY-Based Protocol for High-Quality Protein Structure Determination. Journal of the American Chemical Society, 2005, 127, 9085-9099.	13.7	54
52	Letter to the Editor: Resonance assignments for the 18ÂkDa protein CC1736 from Caulobacter crescentus. Journal of Biomolecular NMR, 2004, 29, 549-550.	2.8	3
53	NMR structure of the 18 kDa protein CC1736 from Caulobacter crescentus identifies a member of the â€œSTARTâ€•domain superfamily and suggests residues mediating substrate specificity. Proteins: Structure, Function and Bioinformatics, 2004, 58, 747-750.	2.6	18
54	Simultaneous Determination of Vitamin B Complex Using Wavelet Neural Network. Chinese Journal of Chemistry, 2001, 19, 836-841.	4.9	2