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	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
2	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
3	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
4	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
5	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
6	De novo protein structure generation from incomplete chemical shift assignments. Journal of Biomolecular NMR, 2009, 43, 63-78.	2.8	234
7	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
8	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
9	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
10	Prediction of Xaa-Pro peptide bond conformation from sequence and chemical shifts. Journal of Biomolecular NMR, 2010, 46, 199-204.	2.8	124
11	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
12	Identification of helix capping and Î²-turn motifs from NMR chemical shifts. Journal of Biomolecular NMR, 2012, 52, 211-232.	2.8	81
13	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
14	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
15	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
16	Homology modeling of larger proteins guided by chemical shifts. Nature Methods, 2015, 12, 747-750.	19.0	51
17	Total Synthesis of Aplydactone by a Conformationally Controlled Câ€“H Functionalization. Angewandte Chemie - International Edition, 2017, 56, 8187-8190.	13.8	46
18	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

#	Article	IF	Citations
19	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
20	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
21	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
22	Improved chemical shift based fragment selection for CS-Rosetta using Rosetta3 fragment picker. Journal of Biomolecular NMR, 2013, 57, 117-127.	2.8	38
23	Building native protein conformation from NMR backbone chemical shifts using Monte Carlo fragment assembly. Protein Science, 2007, 16, 1515-1521.	7.6	33
24	Conformational Design Principles in Total Synthesis. Angewandte Chemie - International Edition, 2020, 59, 14198-14210.	13.8	30
25	Advances in NMR Spectroscopy of Weakly Aligned Biomolecular Systems. Chemical Reviews, 2022, 122, 9307-9330.	47.7	27
26	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
27	Site-Specific Photochemical Desaturation Enables Divergent Syntheses of Illicium Sesquiterpenes. Journal of the American Chemical Society, 2021, 143, 3256-3263.	13.7	26
28	Improving 3D structure prediction from chemical shift data. Journal of Biomolecular NMR, 2013, 57, 27-35.	2.8	25
29	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
30	Solution Conformation and Dynamics of the HIV-1 Integrase Core Domain. Journal of Biological Chemistry, 2010, 285, 18072-18084.	3.4	24
31	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
32	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
33	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
34	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
35	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
36	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

#	Article	IF	Citations
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	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
39	Stabilizing pâ€Dithiobenzyl Urethane Linkers without Rateâ€Limiting Selfâ€Immolation for Traceless Drug Release. ChemMedChem, 2019, 14, 1196-1203.	3.2	9
40	Residual Dipolar Couplings for Resolving Cysteine Bridges in Disulfide-Rich Peptides. Frontiers in Chemistry, 2019, 7, 889.	3.6	9
41	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
42	De novo design and directed folding of disulfide-bridged peptide heterodimers. Nature Communications, 2022, 13, 1539.	12.8	9
43	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
44	Total Synthesis of Aplydactone by a Conformationally Controlled Câ^'H Functionalization. Angewandte Chemie, 2017, 129, 8299-8302.	2.0	8
45	Structure of membrane diacylglycerol kinase in lipid bilayers. Communications Biology, 2021, 4, 282.	4.4	7
46	Two-Stage Syntheses of Clionastatins A and B. Journal of the American Chemical Society, 2022, 144, 8938-8944.	13.7	7
47	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
48	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
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	Simultaneous Determination of Vitamin B Complex Using Wavelet Neural Network. Chinese Journal of Chemistry, 2001, 19, 836-841.	4.9	2
51	Modulating the Stiffness of the Myosin VI Single Î±-Helical Domain. Biophysical Journal, 2020, 118, 1119-1128.	0.5	2
52	Conformational Design Principles in Total Synthesis. Angewandte Chemie, 2020, 132, 14302-14314.	2.0	2
53	NMR structure of protein PA2021 fromPseudomonas aeruginosa. Proteins: Structure, Function and Bioinformatics, 2006, 65, 767-770.	2.6	1
54	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