

Wing-Yiu Choy

List of Publications by Year in descending order

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67
papers

4,099
citations

186265
28
h-index

118850
62
g-index

69
all docs

69
docs citations

69
times ranked

4467
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamic equilibrium engagement of a polyvalent ligand with a single-site receptor. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17772-17777.	7.1	304
2	Solution structure and dynamics of the outer membrane enzyme PagP by NMR. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13560-13565.	7.1	302
3	The Hsp70/Hsp90 Chaperone Machinery in Neurodegenerative Diseases. Frontiers in Neuroscience, 2017, 11, 254.	2.8	277
4	CFTR regulatory region interacts with NBD1 predominantly via multiple transient helices. Nature Structural and Molecular Biology, 2007, 14, 738-745.	8.2	267
5	Calculation of ensembles of structures representing the unfolded state of an SH3 domain. Journal of Molecular Biology, 2001, 308, 1011-1032.	4.2	209
6	Solution NMR-derived global fold of a monomeric 82-kDa enzyme. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 622-627.	7.1	203
7	Orienting domains in proteins using dipolar couplings measured by liquid-state NMR: differences in solution and crystal forms of maltodextrin binding protein loaded with β^2 -cyclodextrin. Journal of Molecular Biology, 2000, 295, 1265-1273.	4.2	197
8	Distribution of molecular size within an unfolded state ensemble using small-angle X-ray scattering and pulse field gradient NMR techniques. Journal of Molecular Biology, 2002, 316, 101-112.	4.2	181
9	Comparison of Secondary Structure Formation Using 10 Different Force Fields in Microsecond Molecular Dynamics Simulations. Journal of Chemical Theory and Computation, 2012, 8, 2725-2740.	5.3	171
10	Global folds of proteins with low densities of NOEs using residual dipolar couplings: application to the 370-residue maltodextrin-binding protein. Journal of Molecular Biology, 2000, 300, 197-212.	4.2	165
11	Structural Characterization of Proteins with an Attached ATCUN Motif by Paramagnetic Relaxation Enhancement NMR Spectroscopy. Journal of the American Chemical Society, 2001, 123, 9843-9847.	13.7	162
12	Characterization of disordered proteins with ENSEMBLE. Bioinformatics, 2013, 29, 398-399.	4.1	141
13	Title is missing!. Journal of Biomolecular NMR, 1999, 14, 333-343.	2.8	122
14	Improved Structural Characterizations of the drkN SH3 Domain Unfolded State Suggest a Compact Ensemble with Native-like and Non-native Structure. Journal of Molecular Biology, 2007, 367, 1494-1510.	4.2	109
15	Effects of Molecular Crowding on the Dynamics of Intrinsically Disordered Proteins. PLoS ONE, 2012, 7, e49876.	2.5	85
16	^{15}N NMR Spin Relaxation Dispersion Study of the Molecular Crowding Effects on Protein Folding under Native Conditions. Journal of the American Chemical Society, 2006, 128, 3916-3917.	13.7	83
17	Identification of a Collapsed Intermediate with Non-native Long-range Interactions on the Folding Pathway of a Pair of Fyn SH3 Domain Mutants by NMR Relaxation Dispersion Spectroscopy. Journal of Molecular Biology, 2006, 363, 958-976.	4.2	77
18	AlphaFold2: A Role for Disordered Protein/Region Prediction?. International Journal of Molecular Sciences, 2022, 23, 4591.	4.1	72

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19	The Prion Protein Ligand, Stress-Inducible Phosphoprotein 1, Regulates Amyloid- β^2 Oligomer Toxicity. <i>Journal of Neuroscience</i> , 2013, 33, 16552-16564.	3.6	70
20	Effects of Zinc Binding on the Structure and Dynamics of the Intrinsically Disordered Protein Prothymosin β : Evidence for Metalation as an Entropic Switch. <i>Biochemistry</i> , 2007, 46, 13120-13130.	2.5	54
21	Solution-Phase Chelators for Suppressing Nonspecific Protein-Metal Interactions in Electrospray Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 5008-5015.	6.5	52
22	Direct structure refinement of high molecular weight proteins against residual dipolar couplings and carbonyl chemical shift changes upon alignment: an application to maltose binding protein. <i>Journal of Biomolecular NMR</i> , 2001, 21, 31-40.	2.8	50
23	Side Chain Dynamics in Unfolded Protein States: An NMR Based ^2H Spin Relaxation Study of ^{13}C . <i>Journal of the American Chemical Society</i> , 2003, 125, 1748-1758.	13.7	44
24	Microsecond Molecular Dynamics Simulations of Intrinsically Disordered Proteins Involved in the Oxidative Stress Response. <i>PLoS ONE</i> , 2011, 6, e27371.	2.5	40
25	Structural Comparison of the Unstable drkN SH3 Domain and a Stable Mutant. <i>Biochemistry</i> , 2005, 44, 15550-15560.	2.5	39
26	Folding or holding? Hsp70 and Hsp90 chaperoning of misfolded proteins in neurodegenerative disease. <i>Journal of Biological Chemistry</i> , 2022, 298, 101905.	3.4	39
27	Fuzzy Complex Formation between the Intrinsically Disordered Prothymosin β and the Kelch Domain of Keap1 Involved in the Oxidative Stress Response. <i>Journal of Molecular Biology</i> , 2013, 425, 1011-1027.	4.2	38
28	Accelerating the Conformational Sampling of Intrinsically Disordered Proteins. <i>Journal of Chemical Theory and Computation</i> , 2014, 10, 5081-5094.	5.3	38
29	An ^{15}N NMR Spin Relaxation Dispersion Study of the Folding of a Pair of Engineered Mutants of Apocytochrome b562. <i>Journal of the American Chemical Society</i> , 2005, 127, 5066-5072.	13.7	30
30	Binding of disordered proteins to a protein hub. <i>Scientific Reports</i> , 2013, 3, 2305.	3.3	28
31	The intrinsically disordered TC1 interacts with Chibby via regions with high helical propensity. <i>Protein Science</i> , 2007, 16, 2510-2518.	7.6	25
32	Domains of STIP1 responsible for regulating PrPC-dependent amyloid- β^2 oligomer toxicity. <i>Biochemical Journal</i> , 2016, 473, 2119-2130.	3.7	23
33	Binding of Disordered Peptides to Kelch: Insights from Enhanced Sampling Simulations. <i>Journal of Chemical Theory and Computation</i> , 2016, 12, 395-404.	5.3	23
34	Structural Analysis of the 14-3-3 η /Chibby Interaction Involved in Wnt/ β^2 -Catenin Signaling. <i>PLoS ONE</i> , 2015, 10, e0123934.	2.5	23
35	Using Neural Network Predicted Secondary Structure Information in Automatic Protein NMR Assignment. <i>Journal of Chemical Information and Computer Sciences</i> , 1997, 37, 1086-1094.	2.8	21
36	Structural Characterization of Partially Disordered Human Chibby: Insights into Its Function in the Wnt-Signaling Pathway. <i>Biochemistry</i> , 2011, 50, 715-726.	2.5	21

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37	Probing Residual Interactions in Unfolded Protein States Using NMR Spin Relaxation Techniques: An Application to ^{131}I . <i>Journal of the American Chemical Society</i> , 2003, 125, 11988-11992.	13.7	19
38	Nrf2, the Major Regulator of the Cellular Oxidative Stress Response, is Partially Disordered. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7434.	4.1	19
39	Conformational Biases of Linear Motifs. <i>Journal of Physical Chemistry B</i> , 2013, 117, 15943-15957.	2.6	18
40	Solution Structure and Dynamics of Human Hemoglobin in the Carbonmonoxy Form. <i>Biochemistry</i> , 2013, 52, 5809-5820.	2.5	17
41	Prediction of Binding Energy of Keap1 Interaction Motifs in the Nrf2 Antioxidant Pathway and Design of Potential High-Affinity Peptides. <i>Journal of Physical Chemistry B</i> , 2018, 122, 5851-5859.	2.6	17
42	Corrigendum to the Paper by Mok et al. (1999) NOE Data Demonstrating a Compact Unfolded State for an SH3 Domain under Non-denaturing Conditions. <i>Journal of Molecular Biology</i> , 2003, 329, 185-187.	4.2	16
43	Modulation of hippocampal neuronal resilience during aging by the Hsp70/Hsp90 co-chaperone ST11. <i>Journal of Neurochemistry</i> , 2020, 153, 727-758.	3.9	16
44	Using Genetic Algorithms with a Priori Knowledge for Quantitative NMR Signal Analysis. <i>Journal of Chemical Information and Computer Sciences</i> , 1998, 38, 685-690.	2.8	15
45	A method for incorporating dipolar couplings into structure calculations in cases of (near) axial symmetry of alignment. <i>Journal of Biomolecular NMR</i> , 2000, 18, 183-188.	2.8	15
46	A new protocol for high-yield purification of recombinant human prothymosin β expressed in <i>Escherichia coli</i> for NMR studies. <i>Protein Expression and Purification</i> , 2008, 57, 1-8.	1.3	15
47	Model selection for the interpretation of protein side chain methyl dynamics. <i>Journal of Biomolecular NMR</i> , 2003, 25, 325-333.	2.8	14
48	Addressing the overlap problem in the quantitative analysis of two dimensional NMR spectra: Application to ^{15}N relaxation measurements. <i>Journal of Biomolecular NMR</i> , 2004, 30, 347-352.	2.8	14
49	Increased levels of Stress-inducible phosphoprotein-1 accelerates amyloid- β^2 deposition in a mouse model of Alzheimer's disease. <i>Acta Neuropathologica Communications</i> , 2020, 8, 143.	5.2	13
50	Characterization of the Free State Ensemble of the CoRNR Box Motif by Molecular Dynamics Simulations. <i>Journal of Physical Chemistry B</i> , 2016, 120, 1060-1068.	2.6	12
51	Exploring the Conformational Landscape of the Neh4 and Neh5 Domains of Nrf2 Using Two Different Force Fields and Circular Dichroism. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 3145-3156.	5.3	11
52	Matrin3: Disorder and ALS Pathogenesis. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 794646.	3.5	10
53	Quantitative determination of glucose in blood plasma and in fruit juices by combined WATR-CPMG ^1H NMR spectroscopy. <i>Analytical Chemistry</i> , 1992, 64, 2570-2574.	6.5	8
54	Solvent-Dependent ^{59}Co NMR-Study of $[\text{Co}(\text{en})_3]\text{Cl}_3$ and cis,trans- $[\text{Co}(\text{en})_2(\text{N}_3)_2]\text{NO}_3$. <i>Journal of Magnetic Resonance Series A</i> , 1994, 108, 196-200.	1.6	8

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55	Molecular effects of cancer-associated somatic mutations on the structural and target recognition properties of Keap1. <i>Biochemical Journal</i> , 2015, 467, 141-151.	3.7	7
56	KEAP1 Cancer Mutants: A Large-Scale Molecular Dynamics Study of Protein Stability. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5408.	4.1	7
57	Conformational characterization of the intrinsically disordered protein Chibby: Interplay between structural elements in target recognition. <i>Protein Science</i> , 2016, 25, 1420-1429.	7.6	6
58	Molecular basis for the interaction between stress-inducible phosphoprotein 1 (STIP1) and S100A1. <i>Biochemical Journal</i> , 2017, 474, 1853-1866.	3.7	6
59	¹ H, ¹⁵ N and ¹³ C backbone resonance assignments of the TPR1 and TPR2A domains of mouse STI1. <i>Biomolecular NMR Assignments</i> , 2013, 7, 305-310.	0.8	5
60	A novel yeast model detects Nrf2 and Keap1 interactions with Hsp90. <i>DMM Disease Models and Mechanisms</i> , 2022, 15, .	2.4	5
61	Expression of a recombinant Phoneytria toxin active in calcium channels. <i>Toxicon</i> , 2012, 60, 907-918.	1.6	3
62	Hypothetical protein AF2241 from <i>Archaeoglobus fulgidus</i> adopts a cyclophilin-like fold. <i>Journal of Biomolecular NMR</i> , 2007, 38, 353-358.	2.8	2
63	¹ H, ¹⁵ N and ¹³ C backbone resonance assignments of the Kelch domain of mouse Keap1. <i>Biomolecular NMR Assignments</i> , 2013, 7, 149-153.	0.8	2
64	Oxidative Stress-Induced Misfolding and Inclusion Formation of Nrf2 and Keap1. <i>Antioxidants</i> , 2022, 11, 243.	5.1	2
65	The hypothetical protein Atu4866 from <i>Agrobacterium tumefaciens</i> adopts a streptavidin-like fold. <i>Protein Science</i> , 2007, 17, 154-158.	7.6	1
66	Backbone and side chain ¹ H, ¹³ C, and ¹⁵ N resonance assignments of AF2241 from <i>Archaeoglobus fulgidus</i> . <i>Journal of Biomolecular NMR</i> , 2007, 38, 183-183.	2.8	1
67	Quantitative determination of glucose in blood plasma by homonuclear proton decoupled water attenuation transverse relaxation Carr-Purcell-Meiboom-Gill (WATR-HDCPMG) NMR spectroscopy. <i>Fresenius' Journal of Analytical Chemistry</i> , 1998, 361, 500-503.	1.5	0