James J Chou

List of Publications by Year
in descending order

124	10,424	38742 50	32842 100
papers	citations	h-index	g-index

131	131	131	10396
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Structure of the Streptococcus pyogenes NAD ⁺ Glycohydrolase Translocation Domain and Its Essential Role in Toxin Binding to Oropharyngeal Keratinocytes. Journal of Bacteriology, 2022, 204, JB0036621.	2.2	4
2	Pharmacokinetics of Roxadustat: A Population Analysis of 2855 Dialysis- and Non-Dialysis-Dependent Patients with Chronic Kidney Disease. Clinical Pharmacokinetics, 2021, 60, 759-773.	3.5	8
3	Inhibitor Development against p7 Channel in Hepatitis C Virus. Molecules, 2021, 26, 1350.	3.8	5
4	NMR Model of the Entire Membrane-Interacting Region of the HIV-1 Fusion Protein and Its Perturbation of Membrane Morphology. Journal of the American Chemical Society, 2021, 143, 6609-6615.	13.7	8
5	An amphipathic Bax core dimer forms part of the apoptotic pore wall in the mitochondrialâ£membrane. EMBO Journal, 2021, 40, e106438.	7.8	23
6	A Trimeric Hydrophobic Zipper Mediates the Intramembrane Assembly of SARS-CoV-2 Spike. Journal of the American Chemical Society, 2021, 143, 8543-8546.	13.7	24
7	DNAâ€Mediated Assembly of Multispecific Antibodies for T Cell Engaging and Tumor Killing. Advanced Science, 2020, 7, 1900973.	11.2	14
8	The Diversity and Similarity of Transmembrane Trimerization of TNF Receptors. Frontiers in Cell and Developmental Biology, 2020, 8, 569684.	3.7	19
9	Structural basis of transmembrane coupling of the HIV-1 envelope glycoprotein. Nature Communications, 2020, 11, 2317.	12.8	49
10	HIV-1 fusion inhibitors targeting the membrane-proximal external region of Env spikes. Nature Chemical Biology, 2020, 16, 529-537.	8.0	28
11	Oral Hypoxiaâ€Inducible Factor Prolyl Hydroxylase Inhibitor Roxadustat (FGâ€4592) for Treatment of Anemia in Chronic Kidney Disease: A Placeboâ€Controlled Study of Pharmacokinetic and Pharmacodynamic Profiles in Hemodialysis Patients. Journal of Clinical Pharmacology, 2020, 60, 1432-1440.	2.0	18
12	Higher-order Clustering of the Transmembrane Anchor of DR5 Drives Signaling. Biophysical Journal, 2020, 118, 354a.	0.5	0
13	Multispecific Antibodies: DNAâ€Mediated Assembly of Multispecific Antibodies for T Cell Engaging and Tumor Killing (Adv. Sci. 2/2020). Advanced Science, 2020, 7, 2070010.	11.2	0
14	Structural Characterization of the N-Terminal Domain of the Dictyostelium discoideum Mitochondrial Calcium Uniporter. ACS Omega, 2020, 5, 6452-6460.	3.5	6
15	Structure determination protocol for transmembrane domain oligomers. Nature Protocols, 2019, 14, 2483-2520.	12.0	35
16	Critical Effect of the Detergent:Protein Ratio on the Formation of the Hepatitis C Virus p7 Channel. Biochemistry, 2019, 58, 3834-3837.	2.5	8
17	Unidirectional Presentation of Membrane Proteins in Nanoparticleâ€Supported Liposomes. Angewandte Chemie, 2019, 131, 9971-9975.	2.0	0
18	Unidirectional Presentation of Membrane Proteins in Nanoparticleâ€Supported Liposomes. Angewandte Chemie - International Edition, 2019, 58, 9866-9870.	13.8	9

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19	Higher-Order Clustering of the Transmembrane Anchor of DR5 Drives Signaling. Cell, 2019, 176, 1477-1489.e14.	28.9	104
20	RÃ¼cktitelbild: Unidirectional Presentation of Membrane Proteins in Nanoparticleâ€Supported Liposomes (Angew. Chem. 29/2019). Angewandte Chemie, 2019, 131, 10114-10114.	2.0	0
21	2590. Streptolysin O Enhances Binding of the Group A Streptococcal NAD+-Glycohydrolase Toxin to Oropharyngeal Keratinocytes. Open Forum Infectious Diseases, 2019, 6, S900-S900.	0.9	0
22	Higherâ€Order Clustering of the Transmembrane Anchor of DR5 Drives Signaling. FASEB Journal, 2019, 33, 792.3.	0.5	0
23	Identification of substrates of the small RNA methyltransferase Hen1 in mouse spermatogonial stem cells and analysis of its methyl-transfer domain. Journal of Biological Chemistry, 2018, 293, 9981-9994.	3.4	13
24	The Unusual Transmembrane Partition of the Hexameric Channel of the Hepatitis C Virus. Structure, 2018, 26, 627-634.e4.	3.3	17
25	Structure of the membrane proximal external region of HIV-1 envelope glycoprotein. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8892-E8899.	7.1	72
26	Reply to â€˜Concerns with yeast mitochondrial ADP/ATP carrierâ€™s integrity in DPCâ€™ and â€˜Dynamics and interactions of AAC3 in DPC are not functionally relevantâ€™. Nature Structural and Molecular Biology, 2018, 25, 749-750.	8.2	6
27	Structural and Functional Properties of Viral Membrane Proteins. , 2018, , 147-181.		5
28	Chen et al. reply. Nature, 2018, 562, E19-E20.	27.8	5
29	Implementation of the prolyl hydroxylase inhibitor Roxadustat (FGâ€4592) and its main metabolites into routine doping controls. Drug Testing and Analysis, 2017, 9, 1768-1778.	2.6	25
30	Pore Architecture and Ion Selectivity Filter of the Mitochondrial Calcium Uniporter. Biophysical Journal, 2017, 112, 3a-4a.	0.5	0
31	Ion and inhibitor binding of the double-ring ion selectivity filter of the mitochondrial calcium uniporter. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2846-E2851.	7.1	54
32	Specific Interaction of the Human Mitochondrial Uncoupling Protein 1 with Free Long-Chain Fatty Acid. Structure, 2017, 25, 1371-1379.e3.	3.3	29
33	Stability and Water Accessibility of the Trimeric Membrane Anchors of the HIV-1 Envelope Spikes. Journal of the American Chemical Society, 2017, 139, 18432-18435.	13.7	25
34	Evaluation of the Carcinogenic Potential of Roxadustat (FG-4592), a Small Molecule Inhibitor of Hypoxia-Inducible Factor Prolyl Hydroxylase in CD-1 Mice and Sprague Dawley Rats. International Journal of Toxicology, 2017, 36, 427-439.	1.2	35
35	Optimal Bicelle Size q for Solution NMR Studies of the Protein Transmembrane Partition. Chemistry - A European Journal, 2017, 23, 1361-1367.	3.3	44
36	Sortase Aâ€Generated Highly Potent Antiâ€CD20â€MMAE Conjugates for Efficient Elimination of Bâ€Lineage Lymphomas. Small, 2017, 13, 1602267.	10.0	45

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37	Structure of the transmembrane domain of <scp>HIV</scp>â€1 envelope glycoprotein. FEBS Journal, 2017, 284, 1171-1177.	4.7	18
38	An Exhaustive Search Algorithm to Aid NMR-Based Structure Determination of Rotationally Symmetric Transmembrane Oligomers. Scientific Reports, 2017, 7, 17373.	3.3	9
39	Architecture of the mitochondrial calcium uniporter. Nature, 2016, 533, 269-273.	27.8	256
40	Specific Lipid Binding of Membrane Proteins in Detergent Micelles Characterized by NMR and Molecular Dynamics. Biochemistry, 2016, 55, 5317-5320.	2.5	7
41	A functional NMR for membrane proteins: dynamics, ligand binding, and allosteric modulation. Protein Science, 2016, 25, 959-973.	7.6	14
42	Structural basis of interaction between the hepatitis C virus p7 channel and its blocker hexamethylene amiloride. Protein and Cell, 2016, 7, 300-304.	11.0	9
43	Structural basis for membrane anchoring of HIV-1 envelope spike. Science, 2016, 353, 172-175.	12.6	169
44	Structural Basis and Functional Role of Intramembrane Trimerization of the Fas/CD95 Death Receptor. Molecular Cell, 2016, 61, 602-613.	9.7	135
45	Developmental Compound E61 Overcomes Proteasome Inhibitor Resistance in Multiple Myeloma Cells By Targeting the Cellular Protein Folding Machinery. Blood, 2016, 128, 1139-1139.	1.4	6
46	Mapping Conformational Heterogeneity of Mitochondrial Nucleotide Transporter in Uninhibited States. Angewandte Chemie, 2015, 127, 2466-2471.	2.0	2
47	Mapping Conformational Heterogeneity of Mitochondrial Nucleotide Transporter in Uninhibited States. Angewandte Chemie - International Edition, 2015, 54, 2436-2441.	13.8	15
48	Structure and Mechanism of the Influenza A M2_{18â€“60} Dimer of Dimers. Journal of the American Chemical Society, 2015, 137, 14877-14886.	13.7	103
49	Molecular Basis of MgATP Selectivity of the Mitochondrial SCaMC Carrier. Structure, 2015, 23, 1394-1403.	3.3	19
50	Transmembrane signaling: A multiplex problem with converging solutions. Progress in Biophysics and Molecular Biology, 2015, 118, 87-88.	2.9	0
51	Substrate-modulated ADP/ATP-transporter dynamics revealed by NMR relaxation dispersion. Nature Structural and Molecular Biology, 2015, 22, 636-641.	8.2	51
52	Transverse relaxation dispersion of the p7 membrane channel from hepatitis C virus reveals conformational breathing. Journal of Biomolecular NMR, 2015, 61, 369-378.	2.8	19
53	Genotype-specific differences in structural features of hepatitis C virus (HCV) p7 membrane protein. Biochimica Et Biophysica Acta - Biomembranes, 2015, 1848, 1383-1392.	2.6	23
54	Structure and multistate function of the transmembrane electron transporter CcdA. Nature Structural and Molecular Biology, 2015, 22, 809-814.	8.2	27

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55	Capsid Protein VP4 of Human Rhinovirus Induces Membrane Permeability by the Formation of a Size-Selective Multimeric Pore. PLoS Pathogens, 2014, 10, e1004294.	4.7	88
56	The minimalist architectures of viroporins and their therapeutic implications. Biochimica Et Biophysica Acta - Biomembranes, 2014, 1838, 1058-1067.	2.6	39
57	In Silico Assessment of Bundle Architectures of HCV P7 Protein. Biophysical Journal, 2014, 106, 54a.	0.5	0
58	Fatty Acid Flippase Activity of UCP2 Is Essential for Its Proton Transport in Mitochondria. Cell Metabolism, 2014, 20, 541-552.	16.2	67
59	Proton Association Constants of His 37 in the Influenza-A M2_{18â€“60} Dimer-of-Dimers. Biochemistry, 2014, 53, 5987-5994.	2.5	48
60	Rapid Proton-Detected NMR Assignment for Proteins with Fast Magic Angle Spinning. Journal of the American Chemical Society, 2014, 136, 12489-12497.	13.7	254
61	A Self-Sequestered Calmodulin-like Ca2+ Sensor of Mitochondrial SCaMC Carrier and Its Implication to Ca2+-Dependent ATP-Mg/Pi Transport. Structure, 2014, 22, 209-217.	3.3	28
62	Purification, crystallization and preliminary X-ray diffraction of the N-terminal calmodulin-like domain of the human mitochondrial ATP-Mg/Picarrier SCaMC1. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 68-71.	0.8	3
63	Coordinating the impact of structural genomics on the human Î±-helical transmembrane proteome. Nature Structural and Molecular Biology, 2013, 20, 135-138.	8.2	64
64	Solution Nuclear Magnetic Resonance Spectroscopy. Methods in Molecular Biology, 2013, 955, 495-517.	0.9	2
65	Dynamic Nuclear Polarization Study of Inhibitor Binding to the M2_{18â€“60} Proton Transporter from Influenza A. Biochemistry, 2013, 52, 2774-2782.	2.5	66
66	DNA nanotubes for NMR structure determination of membrane proteins. Nature Protocols, 2013, 8, 755-770.	12.0	58
67	The present and future of solution NMR in investigating the structure and dynamics of channels and transporters. Current Opinion in Structural Biology, 2013, 23, 547-554.	5.7	20
68	Unusual architecture of the p7 channel from hepatitis C virus. Nature, 2013, 498, 521-525.	27.8	236
69	Magic-Angle-Spinning NMR of the Drug Resistant S31N M2 Proton Transporter from Influenza A. Journal of the American Chemical Society, 2012, 134, 7215-7218.	13.7	55
70	Mitochondrial uncoupling protein 2 structure determined by NMR molecular fragment searching. Nature, 2011, 476, 109-113.	27.8	350
71	Molecular Basis for Interaction of let-7 MicroRNAs with Lin28. Cell, 2011, 147, 1080-1091.	28.9	335
72	Influenza M2 proton channels. Biochimica Et Biophysica Acta - Biomembranes, 2011, 1808, 522-529.	2.6	150

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73	Structural Investigation of Rimantadine Inhibition of the AM2-BM2 Chimera Channel of Influenza Viruses. Structure, 2011, 19, 1655-1663.	3.3	74
74	Flu channel drug resistance: a tale of two sites. Protein and Cell, 2010, 1, 246-258.	11.0	80
75	A View into the Blind Spot: Solution NMR Provides New Insights into Signal Transduction Across the Lipid Bilayer. Structure, 2010, 18, 1559-1569.	3.3	27
76	The structural basis for intramembrane assembly of an activating immunoreceptor complex. Nature Immunology, 2010, 11, 1023-1029.	14.5	176
77	Inhibition of Prolyl Hydroxylases Increases Erythropoietin Production in ESRD. Journal of the American Society of Nephrology: JASN, 2010, 21, 2151-2156.	6.1	304
78	Magic Angle Spinning NMR Investigation of Influenza A M2_{18â˜60}: Support for an Allosteric Mechanism of Inhibition. Journal of the American Chemical Society, 2010, 132, 10958-10960.	13.7	82
79	Kinetic Analysis of the M2 Proton Conduction of the Influenza Virus. Journal of the American Chemical Society, 2010, 132, 17695-17697.	13.7	45
80	Solution NMR structure of the V27A drug resistant mutant of influenza A M2 channel. Biochemical and Biophysical Research Communications, 2010, 401, 58-63.	2.1	97
81	Response Multilayered Control of T Cell Receptor Phosphorylation. Cell, 2010, 142, 669-671.	28.9	32
82	Structure and Mechanism of Influenza Proton Channels. Biophysical Journal, 2010, 98, 198a-199a.	0.5	0
83	Mechanism of drug inhibition and drug resistance of influenza A M2 channel. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 7379-7384.	7.1	281
84	Correction for Pielak et al., Mechanism of drug inhibition and drug resistance of influenza A M2 channel. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11425-11425.	7.1	0
85	Residual structure within the disordered Câ€terminal segment of p21^{Waf1/Cip1/Sdi1} and its implications for molecular recognition. Protein Science, 2009, 18, 337-347.	7.6	34
86	Solution structure and functional analysis of the influenza B proton channel. Nature Structural and Molecular Biology, 2009, 16, 1267-1271.	8.2	156
87	Structure and mechanism of the M2 proton channel of influenza A virus. Nature, 2008, 451, 591-595.	27.8	951
88	Regulation of T Cell Receptor Activation by Dynamic Membrane Binding of the CD3É› Cytoplasmic Tyrosine-Based Motif. Cell, 2008, 135, 702-713.	28.9	391
89	Probing the Interaction between the Coiled Coil Leucine Zipper of cGMP-dependent Protein Kinase Iα and the C Terminus of the Myosin Binding Subunit of the Myosin Light Chain Phosphatase. Journal of Biological Chemistry, 2008, 283, 32860-32869.	3.4	57
90	MemBrain: Improving the Accuracy of Predicting Transmembrane Helices. PLoS ONE, 2008, 3, e2399.	2.5	105

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91	Extended Abstract: Structure Determination of Symmetric Protein Complexes by a Complete Search of Symmetry Configuration Space Using NMR Distance Restraints. Springer Tracts in Advanced Robotics, 2008, , 335-340.	0.4	0
92	DNA-nanotube-induced alignment of membrane proteins for NMR structure determination. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6644-6648.	7.1	447
93	Structure and Evolutionary Analysis of a Non-biological ATP-binding Protein. Journal of Molecular Biology, 2007, 371, 501-513.	4.2	18
94	Nonuniform sampling and maximum entropy reconstruction applied to the accurate measurement of residual dipolar couplings. Journal of Magnetic Resonance, 2007, 186, 201-211.	2.1	19
95	Comparing the structure and dynamics of phospholamban pentamer in its unphosphorylated and pseudoâ€phosphorylated states. Protein Science, 2007, 16, 1977-1983.	7.6	25
96	The Structure of the Î¶Î¶ Transmembrane Dimer Reveals Features Essential for Its Assembly with the T Cell Receptor. Cell, 2006, 127, 355-368.	28.9	221
97	Structure determination of symmetric homo-oligomers by a complete search of symmetry configuration space, using NMR restraints and van der Waals packing. Proteins: Structure, Function and Bioinformatics, 2006, 65, 203-219.	2.6	38
98	Structure of a Central Component of the Yeast Kinetochore: The Spc24p/Spc25p Globular Domain. Structure, 2006, 14, 1003-1009.	3.3	86
99	Protein structure similarity from Principle Component Correlation analysis. BMC Bioinformatics, 2006, 7, 40.	2.6	19
100	Solution structure of an informationally complex high-affinity RNA aptamer to GTP. Rna, 2006, 12, 567-579.	3.5	64
101	Rapid and accurate structure determination of coiled-coil domains using NMR dipolar couplings: Application to cGMP-dependent protein kinase IÎ±. Protein Science, 2005, 14, 2421-2428.	7.6	43
102	The structure of phospholamban pentamer reveals a channel-like architecture in membranes. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10870-10875.	7.1	309
103	Determination of the Packing Mode of the Coiled-Coil Domain of cGMP-Dependent Protein Kinase IÎ± in Solution Using Charge-Predicted Dipolar Couplings. Journal of the American Chemical Society, 2005, 127, 11918-11919.	13.7	9
104	Characterization of Phospholipid Mixed Micelles by Translational Diffusion. Journal of Biomolecular NMR, 2004, 29, 299-308.	2.8	127
105	Amantadine partition and localization in phospholipid membrane: a solution NMR study. Biochemical and Biophysical Research Communications, 2004, 324, 212-217.	2.1	71
106	The Three-Dimensional Structure of the cGMP-Dependent Protein Kinase I - Î± Leucine Zipper Domain and Its Interaction with the Myosin Binding Subunit.. Blood, 2004, 104, 3539-3539.	1.4	14
107	Insights into the Mobility of Methyl-Bearing Side Chains in Proteins from3JCCand3JCNCouplings. Journal of the American Chemical Society, 2003, 125, 8959-8966.	13.7	131
108	Micelle-Induced Curvature in a Water-Insoluble HIV-1 Env Peptide Revealed by NMR Dipolar Coupling Measurement in Stretched Polyacrylamide Gel. Journal of the American Chemical Society, 2002, 124, 2450-2451.	13.7	202

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109	Protein Side-Chain Rotamers from Dipolar Couplings in a Liquid Crystalline Phase. Journal of the American Chemical Society, 2001, 123, 3844-3845.	13.7	41
110	A simple apparatus for generating stretched polyacrylamide gels, yielding uniform alignment of proteins and detergent micelles. Journal of Biomolecular NMR, 2001, 21, 377-382.	2.8	223
111	Solution structure of Ca(2+)-calmodulin reveals flexible hand-like properties of its domains. Nature Structural Biology, 2001, 8, 990-997.	9.7	305
112	Measurement of one-bond 15N-13C' dipolar couplings in medium sized proteins. Journal of Biomolecular NMR, 2000, 18, 101-105.	2.8	56
113	Study of conformational rearrangement and refinement of structural homology models by the use of heteronuclear dipolar couplings. Journal of Biomolecular NMR, 2000, 18, 217-227.	2.8	92
114	Solution structure of Apaf-1 CARD and its interaction with caspase-9 CARD: A structural basis for specific adaptor/caspase interaction. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 11265-11270.	7.1	139
115	Solution Structure of BID, an Intracellular Amplifier of Apoptotic Signaling. Cell, 1999, 96, 615-624.	28.9	461
116	Solution Structure of the CIDE-N Domain of CIDE-B and a Model for CIDE-N/CIDE-N Interactions in the DNA Fragmentation Pathway of Apoptosis. Cell, 1999, 99, 747-755.	28.9	94
117	A Study on Local-Global Cooperativity in Protein Collapse. Journal of Physical Chemistry B, 1999, 103, 2535-2542.	2.6	10
118	Solution Structure of the RAIDD CARD and Model for CARD/CARD Interaction in Caspase-2 and Caspase-9 Recruitment. Cell, 1998, 94, 171-180.	28.9	301
119	Steady-state kinetic studies with the polysulfonate U-9843, an HIV reverse transcriptase inhibitor. Experientia, 1994, 50, 23-28.	1.2	57
120	Kinetic studies with the non-nucleoside human immunodeficiency virus type-1 reverse transcriptase inhibitor U-90152E. Biochemical Pharmacology, 1994, 47, 2017-2028.	4.4	75
121	A Joint Prediction of the Folding Types of 1490 Human Proteins from their Genetic Codons. Journal of Theoretical Biology, 1993, 161, 251-262.	1.7	72
122	A formulation for correlating properties of peptides and its application to predicting human immunodeficiency virus protease-cleavable sites in proteins. Biopolymers, 1993, 33, 1405-1414.	2.4	40
123	Predicting cleavability of peptide sequences by HIV protease via correlation-angle approach. The Protein Journal, 1993, 12, 291-302.	1.1	62
124	Kinetic studies with the non-nucleoside HIV-1 reverse transcriptase inhibitor U-88204E. Biochemistry, 1993, 32, 6548-6554.	2.5	178