

James J Chou

List of Publications by Year in descending order

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124
papers

10,424
citations

38742

50
h-index

32842

100
g-index

131
all docs

131
docs citations

131
times ranked

10396
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Structure and mechanism of the M2 proton channel of influenza A virus. <i>Nature</i> , 2008, 451, 591-595. | 27.8 | 951 |
| 2 | Solution Structure of BID, an Intracellular Amplifier of Apoptotic Signaling. <i>Cell</i> , 1999, 96, 615-624. | 28.9 | 461 |
| 3 | DNA-nanotube-induced alignment of membrane proteins for NMR structure determination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 6644-6648. | 7.1 | 447 |
| 4 | Regulation of T Cell Receptor Activation by Dynamic Membrane Binding of the CD3 ζ Cytoplasmic Tyrosine-Based Motif. <i>Cell</i> , 2008, 135, 702-713. | 28.9 | 391 |
| 5 | Mitochondrial uncoupling protein 2 structure determined by NMR molecular fragment searching. <i>Nature</i> , 2011, 476, 109-113. | 27.8 | 350 |
| 6 | Molecular Basis for Interaction of let-7 MicroRNAs with Lin28. <i>Cell</i> , 2011, 147, 1080-1091. | 28.9 | 335 |
| 7 | The structure of phospholamban pentamer reveals a channel-like architecture in membranes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10870-10875. | 7.1 | 309 |
| 8 | Solution structure of Ca(2+)-calmodulin reveals flexible hand-like properties of its domains. <i>Nature Structural Biology</i> , 2001, 8, 990-997. | 9.7 | 305 |
| 9 | Inhibition of Prolyl Hydroxylases Increases Erythropoietin Production in ESRD. <i>Journal of the American Society of Nephrology: JASN</i> , 2010, 21, 2151-2156. | 6.1 | 304 |
| 10 | Solution Structure of the RAIDD CARD and Model for CARD/CARD Interaction in Caspase-2 and Caspase-9 Recruitment. <i>Cell</i> , 1998, 94, 171-180. | 28.9 | 301 |
| 11 | Mechanism of drug inhibition and drug resistance of influenza A M2 channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 7379-7384. | 7.1 | 281 |
| 12 | Architecture of the mitochondrial calcium uniporter. <i>Nature</i> , 2016, 533, 269-273. | 27.8 | 256 |
| 13 | Rapid Proton-Detected NMR Assignment for Proteins with Fast Magic Angle Spinning. <i>Journal of the American Chemical Society</i> , 2014, 136, 12489-12497. | 13.7 | 254 |
| 14 | Unusual architecture of the p7 channel from hepatitis C virus. <i>Nature</i> , 2013, 498, 521-525. | 27.8 | 236 |
| 15 | A simple apparatus for generating stretched polyacrylamide gels, yielding uniform alignment of proteins and detergent micelles. <i>Journal of Biomolecular NMR</i> , 2001, 21, 377-382. | 2.8 | 223 |
| 16 | The Structure of the β 2-Adrenergic Transmembrane Dimer Reveals Features Essential for Its Assembly with the T Cell Receptor. <i>Cell</i> , 2006, 127, 355-368. | 28.9 | 221 |
| 17 | Micelle-Induced Curvature in a Water-Insoluble HIV-1 Env Peptide Revealed by NMR Dipolar Coupling Measurement in Stretched Polyacrylamide Gel. <i>Journal of the American Chemical Society</i> , 2002, 124, 2450-2451. | 13.7 | 202 |
| 18 | Kinetic studies with the non-nucleoside HIV-1 reverse transcriptase inhibitor U-88204E. <i>Biochemistry</i> , 1993, 32, 6548-6554. | 2.5 | 178 |

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|----|---|------|-----------|
| 19 | The structural basis for intramembrane assembly of an activating immunoreceptor complex. <i>Nature Immunology</i> , 2010, 11, 1023-1029. | 14.5 | 176 |
| 20 | Structural basis for membrane anchoring of HIV-1 envelope spike. <i>Science</i> , 2016, 353, 172-175. | 12.6 | 169 |
| 21 | Solution structure and functional analysis of the influenza B proton channel. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 1267-1271. | 8.2 | 156 |
| 22 | Influenza M2 proton channels. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011, 1808, 522-529. | 2.6 | 150 |
| 23 | Solution structure of Apaf-1 CARD and its interaction with caspase-9 CARD: A structural basis for specific adaptor/caspase interaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 11265-11270. | 7.1 | 139 |
| 24 | Structural Basis and Functional Role of Intramembrane Trimerization of the Fas/CD95 Death Receptor. <i>Molecular Cell</i> , 2016, 61, 602-613. | 9.7 | 135 |
| 25 | Insights into the Mobility of Methyl-Bearing Side Chains in Proteins from ³ JCC and ³ JNC Couplings. <i>Journal of the American Chemical Society</i> , 2003, 125, 8959-8966. | 13.7 | 131 |
| 26 | Characterization of Phospholipid Mixed Micelles by Translational Diffusion. <i>Journal of Biomolecular NMR</i> , 2004, 29, 299-308. | 2.8 | 127 |
| 27 | MemBrain: Improving the Accuracy of Predicting Transmembrane Helices. <i>PLoS ONE</i> , 2008, 3, e2399. | 2.5 | 105 |
| 28 | Higher-Order Clustering of the Transmembrane Anchor of DR5 Drives Signaling. <i>Cell</i> , 2019, 176, 1477-1489.e14. | 28.9 | 104 |
| 29 | Structure and Mechanism of the Influenza A M2 ₁₈₀ Dimer of Dimers. <i>Journal of the American Chemical Society</i> , 2015, 137, 14877-14886. | 13.7 | 103 |
| 30 | Solution NMR structure of the V27A drug resistant mutant of influenza A M2 channel. <i>Biochemical and Biophysical Research Communications</i> , 2010, 401, 58-63. | 2.1 | 97 |
| 31 | 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. <i>Cell</i> , 1999, 99, 747-755. | 28.9 | 94 |
| 32 | Study of conformational rearrangement and refinement of structural homology models by the use of heteronuclear dipolar couplings. <i>Journal of Biomolecular NMR</i> , 2000, 18, 217-227. | 2.8 | 92 |
| 33 | Capsid Protein VP4 of Human Rhinovirus Induces Membrane Permeability by the Formation of a Size-Selective Multimeric Pore. <i>PLoS Pathogens</i> , 2014, 10, e1004294. | 4.7 | 88 |
| 34 | Structure of a Central Component of the Yeast Kinetochores: The Spc24p/Spc25p Globular Domain. <i>Structure</i> , 2006, 14, 1003-1009. | 3.3 | 86 |
| 35 | Magic Angle Spinning NMR Investigation of Influenza A M2 ₁₈₀ : Support for an Allosteric Mechanism of Inhibition. <i>Journal of the American Chemical Society</i> , 2010, 132, 10958-10960. | 13.7 | 82 |
| 36 | Flu channel drug resistance: a tale of two sites. <i>Protein and Cell</i> , 2010, 1, 246-258. | 11.0 | 80 |

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|----|---|------|-----------|
| 37 | Kinetic studies with the non-nucleoside human immunodeficiency virus type-1 reverse transcriptase inhibitor U-90152E. <i>Biochemical Pharmacology</i> , 1994, 47, 2017-2028. | 4.4 | 75 |
| 38 | Structural Investigation of Rimantadine Inhibition of the AM2-BM2 Chimera Channel of Influenza Viruses. <i>Structure</i> , 2011, 19, 1655-1663. | 3.3 | 74 |
| 39 | A Joint Prediction of the Folding Types of 1490 Human Proteins from their Genetic Codons. <i>Journal of Theoretical Biology</i> , 1993, 161, 251-262. | 1.7 | 72 |
| 40 | Structure of the membrane proximal external region of HIV-1 envelope glycoprotein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8892-E8899. | 7.1 | 72 |
| 41 | Amantadine partition and localization in phospholipid membrane: a solution NMR study. <i>Biochemical and Biophysical Research Communications</i> , 2004, 324, 212-217. | 2.1 | 71 |
| 42 | Fatty Acid Flippase Activity of UCP2 Is Essential for Its Proton Transport in Mitochondria. <i>Cell Metabolism</i> , 2014, 20, 541-552. | 16.2 | 67 |
| 43 | Dynamic Nuclear Polarization Study of Inhibitor Binding to the M2 ₆₀ Proton Transporter from Influenza A. <i>Biochemistry</i> , 2013, 52, 2774-2782. | 2.5 | 66 |
| 44 | Solution structure of an informationally complex high-affinity RNA aptamer to GTP. <i>Rna</i> , 2006, 12, 567-579. | 3.5 | 64 |
| 45 | Coordinating the impact of structural genomics on the human α -helical transmembrane proteome. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 135-138. | 8.2 | 64 |
| 46 | Predicting cleavability of peptide sequences by HIV protease via correlation-angle approach. <i>The Protein Journal</i> , 1993, 12, 291-302. | 1.1 | 62 |
| 47 | DNA nanotubes for NMR structure determination of membrane proteins. <i>Nature Protocols</i> , 2013, 8, 755-770. | 12.0 | 58 |
| 48 | Steady-state kinetic studies with the polysulfonate U-9843, an HIV reverse transcriptase inhibitor. <i>Experientia</i> , 1994, 50, 23-28. | 1.2 | 57 |
| 49 | Probing the Interaction between the Coiled Coil Leucine Zipper of cGMP-dependent Protein Kinase α and the C Terminus of the Myosin Binding Subunit of the Myosin Light Chain Phosphatase. <i>Journal of Biological Chemistry</i> , 2008, 283, 32860-32869. | 3.4 | 57 |
| 50 | Measurement of one-bond ¹⁵ N- ¹³ C' dipolar couplings in medium sized proteins. <i>Journal of Biomolecular NMR</i> , 2000, 18, 101-105. | 2.8 | 56 |
| 51 | Magic-Angle-Spinning NMR of the Drug Resistant S31N M2 Proton Transporter from Influenza A. <i>Journal of the American Chemical Society</i> , 2012, 134, 7215-7218. | 13.7 | 55 |
| 52 | Ion and inhibitor binding of the double-ring ion selectivity filter of the mitochondrial calcium uniporter. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E2846-E2851. | 7.1 | 54 |
| 53 | Substrate-modulated ADP/ATP-transporter dynamics revealed by NMR relaxation dispersion. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 636-641. | 8.2 | 51 |
| 54 | Structural basis of transmembrane coupling of the HIV-1 envelope glycoprotein. <i>Nature Communications</i> , 2020, 11, 2317. | 12.8 | 49 |

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|----|---|------|-----------|
| 55 | Proton Association Constants of His 37 in the Influenza-A M2 ₁₈ Dimer-of-Dimers. <i>Biochemistry</i> , 2014, 53, 5987-5994. | 2.5 | 48 |
| 56 | Kinetic Analysis of the M2 Proton Conduction of the Influenza Virus. <i>Journal of the American Chemical Society</i> , 2010, 132, 17695-17697. | 13.7 | 45 |
| 57 | Sortase A-Generated Highly Potent Anti-CD20-mMAE Conjugates for Efficient Elimination of B-Lineage Lymphomas. <i>Small</i> , 2017, 13, 1602267. | 10.0 | 45 |
| 58 | Optimal Bicelle Size $\langle i \rangle$ for Solution NMR Studies of the Protein Transmembrane Partition. <i>Chemistry - A European Journal</i> , 2017, 23, 1361-1367. | 3.3 | 44 |
| 59 | Rapid and accurate structure determination of coiled-coil domains using NMR dipolar couplings: Application to cGMP-dependent protein kinase II \pm . <i>Protein Science</i> , 2005, 14, 2421-2428. | 7.6 | 43 |
| 60 | Protein Side-Chain Rotamers from Dipolar Couplings in a Liquid Crystalline Phase. <i>Journal of the American Chemical Society</i> , 2001, 123, 3844-3845. | 13.7 | 41 |
| 61 | A formulation for correlating properties of peptides and its application to predicting human immunodeficiency virus protease-cleavable sites in proteins. <i>Biopolymers</i> , 1993, 33, 1405-1414. | 2.4 | 40 |
| 62 | The minimalist architectures of viroporins and their therapeutic implications. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014, 1838, 1058-1067. | 2.6 | 39 |
| 63 | Structure determination of symmetric homo-oligomers by a complete search of symmetry configuration space, using NMR restraints and van der Waals packing. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 203-219. | 2.6 | 38 |
| 64 | 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. <i>International Journal of Toxicology</i> , 2017, 36, 427-439. | 1.2 | 35 |
| 65 | Structure determination protocol for transmembrane domain oligomers. <i>Nature Protocols</i> , 2019, 14, 2483-2520. | 12.0 | 35 |
| 66 | Residual structure within the disordered C-terminal segment of p21 ^{Waf1/Cip1/Sdi1} and its implications for molecular recognition. <i>Protein Science</i> , 2009, 18, 337-347. | 7.6 | 34 |
| 67 | Response Multilayered Control of T Cell Receptor Phosphorylation. <i>Cell</i> , 2010, 142, 669-671. | 28.9 | 32 |
| 68 | Specific Interaction of the Human Mitochondrial Uncoupling Protein 1 with Free Long-Chain Fatty Acid. <i>Structure</i> , 2017, 25, 1371-1379.e3. | 3.3 | 29 |
| 69 | A Self-Sequestered Calmodulin-like Ca ²⁺ Sensor of Mitochondrial SCaMC Carrier and Its Implication to Ca ²⁺ -Dependent ATP-Mg/Pi Transport. <i>Structure</i> , 2014, 22, 209-217. | 3.3 | 28 |
| 70 | HIV-1 fusion inhibitors targeting the membrane-proximal external region of Env spikes. <i>Nature Chemical Biology</i> , 2020, 16, 529-537. | 8.0 | 28 |
| 71 | A View into the Blind Spot: Solution NMR Provides New Insights into Signal Transduction Across the Lipid Bilayer. <i>Structure</i> , 2010, 18, 1559-1569. | 3.3 | 27 |
| 72 | Structure and multistate function of the transmembrane electron transporter CcdA. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 809-814. | 8.2 | 27 |

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|----|---|------|-----------|
| 73 | Comparing the structure and dynamics of phospholamban pentamer in its unphosphorylated and pseudo-phosphorylated states. <i>Protein Science</i> , 2007, 16, 1977-1983. | 7.6 | 25 |
| 74 | Implementation of the prolyl hydroxylase inhibitor Roxadustat (FG4592) and its main metabolites into routine doping controls. <i>Drug Testing and Analysis</i> , 2017, 9, 1768-1778. | 2.6 | 25 |
| 75 | Stability and Water Accessibility of the Trimeric Membrane Anchors of the HIV-1 Envelope Spikes. <i>Journal of the American Chemical Society</i> , 2017, 139, 18432-18435. | 13.7 | 25 |
| 76 | A Trimeric Hydrophobic Zipper Mediates the Intramembrane Assembly of SARS-CoV-2 Spike. <i>Journal of the American Chemical Society</i> , 2021, 143, 8543-8546. | 13.7 | 24 |
| 77 | Genotype-specific differences in structural features of hepatitis C virus (HCV) p7 membrane protein. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015, 1848, 1383-1392. | 2.6 | 23 |
| 78 | An amphipathic Bax core dimer forms part of the apoptotic pore wall in the mitochondrial membrane. <i>EMBO Journal</i> , 2021, 40, e106438. | 7.8 | 23 |
| 79 | The present and future of solution NMR in investigating the structure and dynamics of channels and transporters. <i>Current Opinion in Structural Biology</i> , 2013, 23, 547-554. | 5.7 | 20 |
| 80 | Protein structure similarity from Principle Component Correlation analysis. <i>BMC Bioinformatics</i> , 2006, 7, 40. | 2.6 | 19 |
| 81 | Nonuniform sampling and maximum entropy reconstruction applied to the accurate measurement of residual dipolar couplings. <i>Journal of Magnetic Resonance</i> , 2007, 186, 201-211. | 2.1 | 19 |
| 82 | Molecular Basis of MgATP Selectivity of the Mitochondrial SCaMC Carrier. <i>Structure</i> , 2015, 23, 1394-1403. | 3.3 | 19 |
| 83 | Transverse relaxation dispersion of the p7 membrane channel from hepatitis C virus reveals conformational breathing. <i>Journal of Biomolecular NMR</i> , 2015, 61, 369-378. | 2.8 | 19 |
| 84 | The Diversity and Similarity of Transmembrane Trimerization of TNF Receptors. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 569684. | 3.7 | 19 |
| 85 | Structure and Evolutionary Analysis of a Non-biological ATP-binding Protein. <i>Journal of Molecular Biology</i> , 2007, 371, 501-513. | 4.2 | 18 |
| 86 | Structure of the transmembrane domain of HIV-1 envelope glycoprotein. <i>FEBS Journal</i> , 2017, 284, 1171-1177. | 4.7 | 18 |
| 87 | Oral Hypoxia-Inducible Factor Prolyl Hydroxylase Inhibitor Roxadustat (FG4592) for Treatment of Anemia in Chronic Kidney Disease: A Placebo-Controlled Study of Pharmacokinetic and Pharmacodynamic Profiles in Hemodialysis Patients. <i>Journal of Clinical Pharmacology</i> , 2020, 60, 1432-1440. | 2.0 | 18 |
| 88 | The Unusual Transmembrane Partition of the Hexameric Channel of the Hepatitis C Virus. <i>Structure</i> , 2018, 26, 627-634.e4. | 3.3 | 17 |
| 89 | Mapping Conformational Heterogeneity of Mitochondrial Nucleotide Transporter in Uninhibited States. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 2436-2441. | 13.8 | 15 |
| 90 | A functional NMR for membrane proteins: dynamics, ligand binding, and allosteric modulation. <i>Protein Science</i> , 2016, 25, 959-973. | 7.6 | 14 |

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|-----|---|------|-----------|
| 91 | DNA-Mediated Assembly of Multispecific Antibodies for T Cell Engaging and Tumor Killing. <i>Advanced Science</i> , 2020, 7, 1900973. | 11.2 | 14 |
| 92 | The Three-Dimensional Structure of the cGMP-Dependent Protein Kinase I - Î± Leucine Zipper Domain and Its Interaction with the Myosin Binding Subunit.. <i>Blood</i> , 2004, 104, 3539-3539. | 1.4 | 14 |
| 93 | Identification of substrates of the small RNA methyltransferase Hen1 in mouse spermatogonial stem cells and analysis of its methyl-transfer domain. <i>Journal of Biological Chemistry</i> , 2018, 293, 9981-9994. | 3.4 | 13 |
| 94 | A Study on Local-Global Cooperativity in Protein Collapse. <i>Journal of Physical Chemistry B</i> , 1999, 103, 2535-2542. | 2.6 | 10 |
| 95 | Determination of the Packing Mode of the Coiled-Coil Domain of cGMP-Dependent Protein Kinase Î± in Solution Using Charge-Predicted Dipolar Couplings. <i>Journal of the American Chemical Society</i> , 2005, 127, 11918-11919. | 13.7 | 9 |
| 96 | Structural basis of interaction between the hepatitis C virus p7 channel and its blocker hexamethylene amiloride. <i>Protein and Cell</i> , 2016, 7, 300-304. | 11.0 | 9 |
| 97 | An Exhaustive Search Algorithm to Aid NMR-Based Structure Determination of Rotationally Symmetric Transmembrane Oligomers. <i>Scientific Reports</i> , 2017, 7, 17373. | 3.3 | 9 |
| 98 | Unidirectional Presentation of Membrane Proteins in Nanoparticle-Supported Liposomes. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 9866-9870. | 13.8 | 9 |
| 99 | Critical Effect of the Detergent:Protein Ratio on the Formation of the Hepatitis C Virus p7 Channel. <i>Biochemistry</i> , 2019, 58, 3834-3837. | 2.5 | 8 |
| 100 | Pharmacokinetics of Roxadustat: A Population Analysis of 2855 Dialysis- and Non-Dialysis-Dependent Patients with Chronic Kidney Disease. <i>Clinical Pharmacokinetics</i> , 2021, 60, 759-773. | 3.5 | 8 |
| 101 | NMR Model of the Entire Membrane-Interacting Region of the HIV-1 Fusion Protein and Its Perturbation of Membrane Morphology. <i>Journal of the American Chemical Society</i> , 2021, 143, 6609-6615. | 13.7 | 8 |
| 102 | Specific Lipid Binding of Membrane Proteins in Detergent Micelles Characterized by NMR and Molecular Dynamics. <i>Biochemistry</i> , 2016, 55, 5317-5320. | 2.5 | 7 |
| 103 | Reply to "Concerns with yeast mitochondrial ADP/ATP carrier's integrity in DPC" and "Dynamics and interactions of AAC3 in DPC are not functionally relevant". <i>Nature Structural and Molecular Biology</i> , 2018, 25, 749-750. | 8.2 | 6 |
| 104 | Structural Characterization of the N-Terminal Domain of the <i>Dictyostelium discoideum</i> Mitochondrial Calcium Uniporter. <i>ACS Omega</i> , 2020, 5, 6452-6460. | 3.5 | 6 |
| 105 | Developmental Compound E61 Overcomes Proteasome Inhibitor Resistance in Multiple Myeloma Cells By Targeting the Cellular Protein Folding Machinery. <i>Blood</i> , 2016, 128, 1139-1139. | 1.4 | 6 |
| 106 | Inhibitor Development against p7 Channel in Hepatitis C Virus. <i>Molecules</i> , 2021, 26, 1350. | 3.8 | 5 |
| 107 | Structural and Functional Properties of Viral Membrane Proteins. , 2018, , 147-181. | | 5 |
| 108 | Chen et al. reply. <i>Nature</i> , 2018, 562, E19-E20. | 27.8 | 5 |

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|-----|---|------|-----------|
| 109 | 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 |
| 110 | Purification, crystallization and preliminary X-ray diffraction of the N-terminal calmodulin-like domain of the human mitochondrial ATP-Mg/Picarrier S _{Ca} MC1. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 68-71. | 0.8 | 3 |
| 111 | Solution Nuclear Magnetic Resonance Spectroscopy. Methods in Molecular Biology, 2013, 955, 495-517. | 0.9 | 2 |
| 112 | Mapping Conformational Heterogeneity of Mitochondrial Nucleotide Transporter in Uninhibited States. Angewandte Chemie, 2015, 127, 2466-2471. | 2.0 | 2 |
| 113 | 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 |
| 114 | Structure and Mechanism of Influenza Proton Channels. Biophysical Journal, 2010, 98, 198a-199a. | 0.5 | 0 |
| 115 | In Silico Assessment of Bundle Architectures of HCV P7 Protein. Biophysical Journal, 2014, 106, 54a. | 0.5 | 0 |
| 116 | Transmembrane signaling: A multiplex problem with converging solutions. Progress in Biophysics and Molecular Biology, 2015, 118, 87-88. | 2.9 | 0 |
| 117 | Pore Architecture and Ion Selectivity Filter of the Mitochondrial Calcium Uniporter. Biophysical Journal, 2017, 112, 3a-4a. | 0.5 | 0 |
| 118 | Unidirectional Presentation of Membrane Proteins in Nanoparticle-Supported Liposomes. Angewandte Chemie, 2019, 131, 9971-9975. | 2.0 | 0 |
| 119 | Unidirectional Presentation of Membrane Proteins in Nanoparticle-Supported Liposomes (Angew. Chem. 29/2019). Angewandte Chemie, 2019, 131, 10114-10114. | 2.0 | 0 |
| 120 | 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 |
| 121 | Higher-order Clustering of the Transmembrane Anchor of DR5 Drives Signaling. Biophysical Journal, 2020, 118, 354a. | 0.5 | 0 |
| 122 | Multispecific Antibodies: DNA-Mediated Assembly of Multispecific Antibodies for T Cell Engaging and Tumor Killing (Adv. Sci. 2/2020). Advanced Science, 2020, 7, 2070010. | 11.2 | 0 |
| 123 | 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 |
| 124 | Higher-Order Clustering of the Transmembrane Anchor of DR5 Drives Signaling. FASEB Journal, 2019, 33, 792.3. | 0.5 | 0 |