

Gabriel Cornilescu

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

69

papers

7,766

citations

28

h-index

74

g-index

74

ext. papers

8,316

ext. citations

7.6

avg, IF

5.82

L-index

#	Paper	IF	Citations
69	Protein backbone angle restraints from searching a database for chemical shift and sequence homology. <i>Journal of Biomolecular NMR</i> , 1999 , 13, 289-302	3	2724
68	TALOS+: a hybrid method for predicting protein backbone torsion angles from NMR chemical shifts. <i>Journal of Biomolecular NMR</i> , 2009 , 44, 213-23	3	1994
67	Validation of Protein Structure from Anisotropic Carbonyl Chemical Shifts in a Dilute Liquid Crystalline Phase. <i>Journal of the American Chemical Society</i> , 1998 , 120, 6836-6837	16.4	797
66	Identification of the Hydrogen Bonding Network in a Protein by Scalar Couplings. <i>Journal of the American Chemical Society</i> , 1999 , 121, 2949-2950	16.4	217
65	Measurement of Proton, Nitrogen, and Carbonyl Chemical Shielding Anisotropies in a Protein Dissolved in a Dilute Liquid Crystalline Phase. <i>Journal of the American Chemical Society</i> , 2000 , 122, 10143-10154	16.4	188
64	Correlation between $^3\text{HJNCD}$ and Hydrogen Bond Length in Proteins. <i>Journal of the American Chemical Society</i> , 1999 , 121, 6275-6279	16.4	157
63	U2-U6 RNA folding reveals a group II intron-like domain and a four-helix junction. <i>Nature Structural and Molecular Biology</i> , 2004 , 11, 1237-42	17.6	115
62	Structural basis for SRY-dependent 46-X,Y sex reversal: modulation of DNA bending by a naturally occurring point mutation. <i>Journal of Molecular Biology</i> , 2001 , 312, 481-99	6.5	114
61	Structural basis for the photoconversion of a phytochrome to the activated Pfr form. <i>Nature</i> , 2010 , 463, 250-4	50.4	106
60	Solution structure of a late embryogenesis abundant protein (LEA14) from <i>Arabidopsis thaliana</i> , a cellular stress-related protein. <i>Protein Science</i> , 2005 , 14, 2601-9	6.3	84
59	Site-specific backbone amide (^{15}N) chemical shift anisotropy tensors in a small protein from liquid crystal and cross-correlated relaxation measurements. <i>Journal of the American Chemical Society</i> , 2010 , 132, 4295-309	16.4	69
58	Cyanochromes are blue/green light photoreversible photoreceptors defined by a stable double cysteine linkage to a phycoviolobilin-type chromophore. <i>Journal of Biological Chemistry</i> , 2009 , 284, 29757-72	5.4	67
57	Solution structure of the phosphoryl transfer complex between the cytoplasmic A domain of the mannitol transporter IIMannitol and HPr of the <i>Escherichia coli</i> phosphotransferase system. <i>Journal of Biological Chemistry</i> , 2002 , 277, 42289-98	5.4	58
56	Structural analysis of the N-terminal domain of the human T-cell leukemia virus capsid protein. <i>Journal of Molecular Biology</i> , 2001 , 306, 783-97	6.5	55
55	The impact of hydrogen bonding on amide ^1H chemical shift anisotropy studied by cross-correlated relaxation and liquid crystal NMR spectroscopy. <i>Journal of the American Chemical Society</i> , 2010 , 132, 10866-75	16.4	53
54	Comparison of cell-based and cell-free protocols for producing target proteins from the <i>Arabidopsis thaliana</i> genome for structural studies. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 59, 633-43	4.2	52
53	Solution structure of a cyanobacterial phytochrome GAF domain in the red-light-absorbing ground state. <i>Journal of Molecular Biology</i> , 2008 , 383, 403-13	6.5	50

52	Dynamic structural changes underpin photoconversion of a blue/green cyanobacteriochrome between its dark and photoactivated states. <i>Journal of Biological Chemistry</i> , 2014 , 289, 3055-65	5.4	49
51	Characterization of two thermostable cyanobacterial phytochromes reveals global movements in the chromophore-binding domain during photoconversion. <i>Journal of Biological Chemistry</i> , 2008 , 283, 21251-66	5.4	46
50	Highly Stable, Amide-Bridged Autoinducing Peptide Analogues that Strongly Inhibit the AgrC Quorum Sensing Receptor in <i>Staphylococcus aureus</i> . <i>Angewandte Chemie - International Edition</i> , 2016 , 55, 8913-7	16.4	45
49	Solution structure of the iron-sulfur cluster cochaperone HscB and its binding surface for the iron-sulfur assembly scaffold protein IscU. <i>Biochemistry</i> , 2008 , 47, 9394-404	3.2	38
48	Activation of nanoscale allosteric protein domain motion revealed by neutron spin echo spectroscopy. <i>Biophysical Journal</i> , 2010 , 99, 3473-82	2.9	37
47	Integrative NMR for biomolecular research. <i>Journal of Biomolecular NMR</i> , 2016 , 64, 307-32	3	36
46	Structural Basis for a Novel Interaction between the NS1 Protein Derived from the 1918 Influenza Virus and RIG-I. <i>Structure</i> , 2015 , 23, 2001-10	5.2	35
45	Structural characterization of native autoinducing peptides and abiotic analogues reveals key features essential for activation and inhibition of an AgrC quorum sensing receptor in <i>Staphylococcus aureus</i> . <i>Journal of the American Chemical Society</i> , 2013 , 135, 18436-44	16.4	35
44	Structural Analysis of Multi-Helical RNAs by NMR-SAXS/WAXS: Application to the U4/U6 di-snRNA. <i>Journal of Molecular Biology</i> , 2016 , 428, 777-789	6.5	33
43	Characterization of structural elements in native autoinducing peptides and non-native analogues that permit the differential modulation of AgrC-type quorum sensing receptors in <i>Staphylococcus aureus</i> . <i>Organic and Biomolecular Chemistry</i> , 2016 , 14, 113-21	3.9	33
42	Structure and thermodynamics of a conserved U2 snRNA domain from yeast and human. <i>Rna</i> , 2007 , 13, 328-38	5.8	31
41	Simplified AIP-II Peptidomimetics Are Potent Inhibitors of <i>Staphylococcus aureus</i> AgrC Quorum Sensing Receptors. <i>ChemBioChem</i> , 2017 , 18, 413-423	3.8	27
40	Large Variations in One-Bond $^{13}\text{C}\text{-}^{13}\text{C}$ Couplings in Polypeptides Correlate with Backbone Conformation. <i>Journal of the American Chemical Society</i> , 2000 , 122, 2168-2171	16.4	26
39	The AUDANA algorithm for automated protein 3D structure determination from NMR NOE data. <i>Journal of Biomolecular NMR</i> , 2016 , 65, 51-7	3	24
38	Global shape mimicry of tRNA within a viral internal ribosome entry site mediates translational reading frame selection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E6446-55	11.5	20
37	Impact of Strand Number on Parallel β -Sheet Stability. <i>Angewandte Chemie - International Edition</i> , 2015 , 54, 14336-9	16.4	20
36	Chemical Genomics, Structure Elucidation, and in Vivo Studies of the Marine-Derived Anticlotrostridial Ecteinaamycin. <i>ACS Chemical Biology</i> , 2017 , 12, 2287-2295	4.9	19
35	NMR structure of the mengovirus Leader protein zinc-finger domain. <i>FEBS Letters</i> , 2008 , 582, 896-900	3.8	19

34	Broadening the functionality of a J-protein/Hsp70 molecular chaperone system. <i>PLoS Genetics</i> , 2017 , 13, e1007084	6	19
33	Mechanism of Histone H3K4me3 Recognition by the Plant Homeodomain of Inhibitor of Growth 3. <i>Journal of Biological Chemistry</i> , 2016 , 291, 18326-41	5.4	18
32	Solution structure of a small protein containing a fluorinated side chain in the core. <i>Protein Science</i> , 2007 , 16, 14-9	6.3	17
31	Progressive Stereo Locking (PSL): A Residual Dipolar Coupling Based Force Field Method for Determining the Relative Configuration of Natural Products and Other Small Molecules. <i>ACS Chemical Biology</i> , 2017 , 12, 2157-2163	4.9	16
30	Designing cyclic competence-stimulating peptide (CSP) analogs with pan-group quorum-sensing inhibition activity in. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 1689-1699	11.5	15
29	Structural Characterization of Competence-Stimulating Peptide Analogues Reveals Key Features for ComD1 and ComD2 Receptor Binding in <i>Streptococcus pneumoniae</i> . <i>Biochemistry</i> , 2018 , 57, 5359-5369	2.2	14
28	Brazzein, a small, sweet protein: effects of mutations on its structure, dynamics and functional properties. <i>Chemical Senses</i> , 2005 , 30 Suppl 1, i90-1	4.8	14
27	HIFI-C: a robust and fast method for determining NMR couplings from adaptive 3D to 2D projections. <i>Journal of Biomolecular NMR</i> , 2007 , 38, 341-51	3	12
26	Structural and dynamics studies of the D54A mutant of human T cell leukemia virus-1 capsid protein. <i>Journal of Biological Chemistry</i> , 2005 , 280, 6792-801	5.4	12
25	Structure and Function of the PriC DNA Replication Restart Protein. <i>Journal of Biological Chemistry</i> , 2016 , 291, 18384-96	5.4	11
24	Solution structure of a homodimeric hypothetical protein, At5g22580, a structural genomics target from <i>Arabidopsis thaliana</i> . <i>Journal of Biomolecular NMR</i> , 2004 , 29, 387-90	3	11
23	Temperature-dependent conformational change affecting Tyr11 and sweetness loops of brazzein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013 , 81, 919-25	4.2	10
22	Highly Stable, Amide-Bridged Autoinducing Peptide Analogues that Strongly Inhibit the AgrC Quorum Sensing Receptor in <i>Staphylococcus aureus</i> . <i>Angewandte Chemie</i> , 2016 , 128, 9059-9063	3.6	10
21	One-sample approach to determine the relative orientations of proteins in ternary and binary complexes from residual dipolar coupling measurements. <i>Journal of the American Chemical Society</i> , 2009 , 131, 14138-9	16.4	9
20	Solution structure of a single-domain thiosulfate sulfurtransferase from <i>Arabidopsis thaliana</i> . <i>Protein Science</i> , 2006 , 15, 2836-41	6.3	9
19	Probabilistic validation of protein NMR chemical shift assignments. <i>Journal of Biomolecular NMR</i> , 2016 , 64, 17-25	3	8
18	Solution structures of Mengovirus Leader protein, its phosphorylated derivatives, and in complex with nuclear transport regulatory protein, RanGTPase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 15792-7	11.5	7
17	Structural dependencies of protein backbone 2JNCScouplings. <i>Protein Science</i> , 2008 , 17, 768-76	6.3	7

16	Backbone (15)N relaxation analysis of the N-terminal domain of the HTLV-I capsid protein and comparison with the capsid protein of HIV-1. <i>Protein Science</i> , 2003 , 12, 973-81	6.3	7
15	X-ray structure of Arabidopsis At1g77680, 12-oxophytodienoate reductase isoform 1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61, 206-8	4.2	7
14	Conformational Switch to a β Turn in a Staphylococcal Quorum Sensing Signal Peptide Causes a Dramatic Increase in Potency. <i>Journal of the American Chemical Society</i> , 2020 , 142, 750-761	16.4	6
13	Structure of RNA Stem Loop B from the Picornavirus Replication Platform. <i>Biochemistry</i> , 2017 , 56, 2549-2557	3.5	5
12	Function and solution structure of the Arabidopsis thaliana RALF8 peptide. <i>Protein Science</i> , 2019 , 28, 1115-1126	6.3	5
11	The BRPF1 bromodomain is a molecular reader of di-acetyllysine. <i>Current Research in Structural Biology</i> , 2020 , 2, 104-115	2.8	5
10	Impact of Strand Number on Parallel β Sheet Stability. <i>Angewandte Chemie</i> , 2015 , 127, 14544-14547	3.6	5
9	Structural Insights into the Recognition of Mono- and Diacetylated Histones by the ATAD2B Bromodomain. <i>Journal of Medicinal Chemistry</i> , 2020 , 63, 12799-12813	8.3	5
8	Conformational flexibility in the enterovirus RNA replication platform. <i>Rna</i> , 2019 , 25, 376-387	5.8	5
7	NMRFAM-SDF: a protein structure determination framework. <i>Journal of Biomolecular NMR</i> , 2015 , 62, 481-95	3	4
6	How Sweet It Is: Detailed Molecular and Functional Studies of Brazzein, a Sweet Protein and Its Analogs. <i>ACS Symposium Series</i> , 2008 , 560-572	0.4	4
5	Resonance assignments for the two N-terminal RNA recognition motifs (RRM) of the <i>S. cerevisiae</i> pre-mRNA processing protein Prp24. <i>Journal of Biomolecular NMR</i> , 2006 , 36 Suppl 1, 58	3	4
4	NMR Structures and Dynamics in a Prohead RNA Loop that Binds Metal Ions. <i>Journal of Physical Chemistry Letters</i> , 2016 , 7, 3841-3846	6.4	3
3	Coordination of Di-Acetylated Histone Ligands by the ATAD2 Bromodomain. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	3
2	Structure and evolution of the 4-helix bundle domain of Zuotin, a J-domain protein co-chaperone of Hsp70. <i>PLoS ONE</i> , 2019 , 14, e0217098	3.7	2
1	Robust nomenclature and software for enhanced reproducibility in molecular modeling of small molecules		2