Gabriel Cornilescu

List of Publications by Year
in descending order

70	8,703	159358 30	85405 71
papers	citations	h-index	g-index

74	74	74	9346
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Protein backbone angle restraints from searching a database for chemical shift and sequence homology. Journal of Biomolecular NMR, 1999, 13, 289-302.	1.6	2,825
2	TALOS+: a hybrid method for predicting protein backbone torsion angles from NMR chemical shifts. Journal of Biomolecular NMR, 2009, 44, 213-223.	1.6	2,305
3	Validation of Protein Structure from Anisotropic Carbonyl Chemical Shifts in a Dilute Liquid Crystalline Phase. Journal of the American Chemical Society, 1998, 120, 6836-6837.	6.6	880
4	Identification of the Hydrogen Bonding Network in a Protein by Scalar Couplings. Journal of the American Chemical Society, 1999, 121, 2949-2950.	6.6	234
5	Measurement of Proton, Nitrogen, and Carbonyl Chemical Shielding Anisotropies in a Protein Dissolved in a Dilute Liquid Crystalline Phase. Journal of the American Chemical Society, 2000, 122, 10143-10154.	6.6	208
6	Correlation between3hJNCâ€˜and Hydrogen Bond Length in Proteins. Journal of the American Chemical Society, 1999, 121, 6275-6279.	6.6	165
7	Structural Basis for SRY-dependent 46-X,Y Sex Reversal: Modulation of DNA Bending by a Naturally Occurring Point Mutation. Journal of Molecular Biology, 2001, 312, 481-499.	2.0	132
8	U2â€“U6 RNA folding reveals a group II intron-like domain and a four-helix junction. Nature Structural and Molecular Biology, 2004, 11, 1237-1242.	3.6	123
9	Structural basis for the photoconversion of a phytochrome to the activated Pfr form. Nature, 2010, 463, 250-254.	13.7	118
10	Solution structure of a late embryogenesis abundant protein (LEA14) fromArabidopsis thaliana, a cellular stress-related protein. Protein Science, 2005, 14, 2601-2609.	3.1	104
11	Site-Specific Backbone Amide ¹⁵N Chemical Shift Anisotropy Tensors in a Small Protein from Liquid Crystal and Cross-Correlated Relaxation Measurements. Journal of the American Chemical Society, 2010, 132, 4295-4309.	6.6	79
12	Cyanochromes Are Blue/Green Light Photoreversible Photoreceptors Defined by a Stable Double Cysteine Linkage to a Phycoviolobilin-type Chromophore. Journal of Biological Chemistry, 2009, 284, 29757-29772.	1.6	75
13	The Impact of Hydrogen Bonding on Amide ¹H Chemical Shift Anisotropy Studied by Cross-Correlated Relaxation and Liquid Crystal NMR Spectroscopy. Journal of the American Chemical Society, 2010, 132, 10866-10875.	6.6	64
14	Solution Structure of the Phosphoryl Transfer Complex between the Cytoplasmic A Domain of the Mannitol Transporter IIMannitol and HPr of the Escherichia coliPhosphotransferase System. Journal of Biological Chemistry, 2002, 277, 42289-42298.	1.6	61
15	Highly Stable, Amideâ€Bridged Autoinducing Peptide Analogues that Strongly Inhibit the AgrC Quorum Sensing Receptor in Staphylococcus aureus. Angewandte Chemie - International Edition, 2016, 55, 8913-8917.	7.2	59
16	Structural analysis of the N-terminal domain of the human T-cell leukemia virus capsid protein. Journal of Molecular Biology, 2001, 306, 783-797.	2.0	58
17	Comparison of cell-based and cell-free protocols for producing target proteins from the Arabidopsis thaliana genome for structural studies. Proteins: Structure, Function and Bioinformatics, 2005, 59, 633-643.	1.5	56
18	Dynamic Structural Changes Underpin Photoconversion of a Blue/Green Cyanobacteriochrome between Its Dark and Photoactivated States. Journal of Biological Chemistry, 2014, 289, 3055-3065.	1.6	55

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19	Solution Structure of a Cyanobacterial Phytochrome GAF Domain in the Red-Light-Absorbing Ground State. Journal of Molecular Biology, 2008, 383, 403-413.	2.0	53
20	Characterization of Two Thermostable Cyanobacterial Phytochromes Reveals Global Movements in the Chromophore-binding Domain during Photoconversion. Journal of Biological Chemistry, 2008, 283, 21251-21266.	1.6	51
21	Structural Characterization of Native Autoinducing Peptides and Abiotic Analogues Reveals Key Features Essential for Activation and Inhibition of an AgrC Quorum Sensing Receptor in Staphylococcus aureus. Journal of the American Chemical Society, 2013, 135, 18436-18444.	6.6	49
22	Structural Basis for a Novel Interaction between the NS1 Protein Derived from the 1918 Influenza Virus and RIG-I. Structure, 2015, 23, 2001-2010.	1.6	47
23	Integrative NMR for biomolecular research. Journal of Biomolecular NMR, 2016, 64, 307-332.	1.6	47
24	Structural Analysis of Multi-Helical RNAs by NMRâ€“SAXS/WAXS: Application to the U4/U6 di-snRNA. Journal of Molecular Biology, 2016, 428, 777-789.	2.0	45
25	Characterization of structural elements in native autoinducing peptides and non-native analogues that permit the differential modulation of AgrC-type quorum sensing receptors in Staphylococcus aureus. Organic and Biomolecular Chemistry, 2016, 14, 113-121.	1.5	43
26	Solution Structure of the Ironâ^'Sulfur Cluster Cochaperone HscB and Its Binding Surface for the Ironâ^'Sulfur Assembly Scaffold Protein IscU. Biochemistry, 2008, 47, 9394-9404.	1.2	42
27	Simplified AIPâ€‖ Peptidomimetics Are Potent Inhibitors of Staphylococcus aureus AgrC Quorum Sensing Receptors. ChemBioChem, 2017, 18, 413-423.	1.3	42
28	Structure and thermodynamics of a conserved U2 snRNA domain from yeast and human. Rna, 2007, 13, 328-338.	1.6	40
29	Activation of Nanoscale Allosteric Protein Domain Motion Revealed by Neutron Spin Echo Spectroscopy. Biophysical Journal, 2010, 99, 3473-3482.	0.2	40
30	The AUDANA algorithm for automated protein 3D structure determination from NMR NOE data. Journal of Biomolecular NMR, 2016, 65, 51-57.	1.6	36
31	Designing cyclic competence-stimulating peptide (CSP) analogs with pan-group quorum-sensing inhibition activity in Streptococcus pneumoniae. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1689-1699.	3.3	31
32	Broadening the functionality of a J-protein/Hsp70 molecular chaperone system. PLoS Genetics, 2017, 13, e1007084.	1.5	30
33	Large Variations in One-Bond 13CÎ±â^'13CÎ² J Couplings in Polypeptides Correlate with Backbone Conformation. Journal of the American Chemical Society, 2000, 122, 2168-2171.	6.6	26
34	Mechanism of Histone H3K4me3 Recognition by the Plant Homeodomain of Inhibitor of Growth 3. Journal of Biological Chemistry, 2016, 291, 18326-18341.	1.6	26
35	Impact of Strand Number on Parallel Î²â€Sheet Stability. Angewandte Chemie - International Edition, 2015, 54, 14336-14339.	7.2	25
36	Global shape mimicry of tRNA within a viral internal ribosome entry site mediates translational reading frame selection. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6446-55.	3.3	24

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37	Progressive Stereo Locking (PSL): A Residual Dipolar Coupling Based Force Field Method for Determining the Relative Configuration of Natural Products and Other Small Molecules. ACS Chemical Biology, 2017, 12, 2157-2163.	1.6	24
38	Chemical Genomics, Structure Elucidation, and in Vivo Studies of the Marine-Derived Anticlostridial Ecteinamycin. ACS Chemical Biology, 2017, 12, 2287-2295.	1.6	24
39	NMR structure of the mengovirus Leader protein zincâ€finger domain. FEBS Letters, 2008, 582, 896-900.	1.3	23
40	Solution structure of a small protein containing a fluorinated side chain in the core. Protein Science, 2006, 16, 14-19.	3.1	20
41	Brazzein, a Small, Sweet Protein: Effects of Mutations on its Structure, Dynamics and Functional Properties. Chemical Senses, 2005, 30, i90-i91.	1.1	19
42	Structure and Function of the PriC DNA Replication Restart Protein. Journal of Biological Chemistry, 2016, 291, 18384-18396.	1.6	17
43	Structural Characterization of Competence-Stimulating Peptide Analogues Reveals Key Features for ComD1 and ComD2 Receptor Binding in Streptococcus pneumoniae. Biochemistry, 2018, 57, 5359-5369.	1.2	17
44	The BRPF1 bromodomain is a molecular reader of di-acetyllysine. Current Research in Structural Biology, 2020, 2, 104-115.	1.1	16
45	Temperatureâ€dependent conformational change affecting Tyr11 and sweetness loops of brazzein. Proteins: Structure, Function and Bioinformatics, 2013, 81, 919-925.	1.5	15
46	Structural Insights into the Recognition of Mono- and Diacetylated Histones by the ATAD2B Bromodomain. Journal of Medicinal Chemistry, 2020, 63, 12799-12813.	2.9	15
47	Highly Stable, Amideâ€Bridged Autoinducing Peptide Analogues that Strongly Inhibit the AgrC Quorum Sensing Receptor in Staphylococcus aureus. Angewandte Chemie, 2016, 128, 9059-9063.	1.6	14
48	Insights into the Cross Talk between Effector and Allosteric Lobes of KRAS from Methyl Conformational Dynamics. Journal of the American Chemical Society, 2022, 144, 4196-4205.	6.6	14
49	Letter to the Editor: Solution Structure of a Homodimeric Hypothetical Protein, At5g22580, a Structural Genomics Target from Arabidopsis Thaliana. Journal of Biomolecular NMR, 2004, 29, 387-390.	1.6	13
50	HIFI-C: a robust and fast method for determining NMR couplings from adaptive 3D to 2D projections. Journal of Biomolecular NMR, 2007, 38, 341-351.	1.6	13
51	Structural and Dynamics Studies of the D54A Mutant of Human T Cell Leukemia Virus-1 Capsid Protein. Journal of Biological Chemistry, 2005, 280, 6792-6801.	1.6	12
52	Solution structures of Mengovirus Leader protein, its phosphorylated derivatives, and in complex with nuclear transport regulatory protein, RanGTPase. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15792-15797.	3.3	12
53	Probabilistic validation of protein NMR chemical shift assignments. Journal of Biomolecular NMR, 2016, 64, 17-25.	1.6	11
54	Function and solution structure of the Arabidopsis thaliana RALF8 peptide. Protein Science, 2019, 28, 1115-1126.	3.1	10

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55	Conformational Switch to a Î²-Turn in a Staphylococcal Quorum Sensing Signal Peptide Causes a Dramatic Increase in Potency. Journal of the American Chemical Society, 2020, 142, 750-761.	6.6	10
56	X-ray structure of Arabidopsis At1g77680, 12-oxophytodienoate reductase isoform 1. Proteins: Structure, Function and Bioinformatics, 2005, 61, 206-208.	1.5	9
57	Solution structure of a single-domain thiosulfate sulfurtransferase fromArabidopsis thaliana. Protein Science, 2006, 15, 2836-2841.	3.1	9
58	One-Sample Approach to Determine the Relative Orientations of Proteins in Ternary and Binary Complexes from Residual Dipolar Coupling Measurements. Journal of the American Chemical Society, 2009, 131, 14138-14139.	6.6	9
59	Conformational flexibility in the enterovirus RNA replication platform. Rna, 2019, 25, 376-387.	1.6	9
60	Coordination of Di-Acetylated Histone Ligands by the ATAD2 Bromodomain. International Journal of Molecular Sciences, 2021, 22, 9128.	1.8	9
61	Structure and evolution of the 4-helix bundle domain of Zuotin, a J-domain protein co-chaperone of Hsp70. PLoS ONE, 2019, 14, e0217098.	1.1	8
62	Backbone15N relaxation analysis of the N-terminal domain of the HTLV-I capsid protein and comparison with the capsid protein of HIV-1. Protein Science, 2003, 12, 973-981.	3.1	7
63	Structural dependencies of protein backbone ²J_{NCâ€²} couplings. Protein Science, 2008, 17, 768-776.	3.1	7
64	Structure of RNA Stem Loop B from the Picornavirus Replication Platform. Biochemistry, 2017, 56, 2549-2557.	1.2	7
65	Resonance assignments for the two N-terminal RNA recognition motifs (RRM) of the S. cerevisiae Pre-mRNA Processing Protein Prp24. Journal of Biomolecular NMR, 2006, 36, 58-58.	1.6	5
66	How Sweet It Is: Detailed Molecular and Functional Studies of Brazzein, a Sweet Protein and Its Analogs. ACS Symposium Series, 2008, , 560-572.	0.5	5
67	NMRFAM-SDF: a protein structure determination framework. Journal of Biomolecular NMR, 2015, 62, 481-495.	1.6	4
68	NMR Structures and Dynamics in a Prohead RNA Loop that Binds Metal Ions. Journal of Physical Chemistry Letters, 2016, 7, 3841-3846.	2.1	4
69	Solution structure and dynamics of the mitochondrialâ€targeted GTPase â€activating protein (GAP) VopE by an integrated NMR / SAXS approach. Protein Science, 2022, , .	3.1	2
70	Solution Structure Determination of Arabidopsis Thaliana RALF8 Illustrates the use of Cutting-Edge Software Developed at the National Magnetic Resonance Facility at Madison. Biophysical Journal, 2020, 118, 62a.	0.2	0