Gabriel Cornilescu

List of Publications by Year in Descending Order

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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	Coordination of Di-Acetylated Histone Ligands by the ATAD2 Bromodomain. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	3
68	The BRPF1 bromodomain is a molecular reader of di-acetyllysine. *Current Research in Structural Biology*, **2020**, 2, 104-115	2.8	5
67	Designing cyclic competence-stimulating peptide (CSP) analogs with pan-group quorum-sensing inhibition activity in. *Proceedings of the National Academy of Sciences of the United States of America* , **2020**, 117, 1689-1699	11.5	15
66	Conformational Switch to a βTurn in a Staphylococcal Quorum Sensing Signal Peptide Causes a Dramatic Increase in Potency. *Journal of the American Chemical Society*, **2020**, 142, 750-761	16.4	6
65	Structural Insights into the Recognition of Mono- and Diacetylated Histones by the ATAD2B Bromodomain. *Journal of Medicinal Chemistry*, **2020**, 63, 12799-12813	8.3	5
64	Structure and evolution of the 4-helix bundle domain of Zuotin, a J-domain protein co-chaperone of Hsp70. *PLoS ONE*, **2019**, 14, e0217098	3.7	2
63	Function and solution structure of the Arabidopsis thaliana RALF8 peptide. *Protein Science*, **2019**, 28, 1115-1126	6.3	5
62	Conformational flexibility in the enterovirus RNA replication platform. *Rna*, **2019**, 25, 376-387	5.8	5
61	Structural Characterization of Competence-Stimulating Peptide Analogues Reveals Key Features for ComD1 and ComD2 Receptor Binding in Streptococcus pneumoniae. *Biochemistry*, **2018**, 57, 5359-5369	3.2	14
60	Structure of RNA Stem Loop B from the Picornavirus Replication Platform. *Biochemistry*, **2017**, 56, 2549-2557	3.2	5
59	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	4.9	16
58	Simplified AIP-II Peptidomimetics Are Potent Inhibitors of Staphylococcus aureus AgrC Quorum Sensing Receptors. *ChemBioChem*, **2017**, 18, 413-423	3.8	27
57	Chemical Genomics, Structure Elucidation, and in Vivo Studies of the Marine-Derived Anticlostridial Ecteinamycin. *ACS Chemical Biology*, **2017**, 12, 2287-2295	4.9	19
56	Broadening the functionality of a J-protein/Hsp70 molecular chaperone system. *PLoS Genetics*, **2017**, 13, e1007084	6	19
55	NMR Structures and Dynamics in a Prohead RNA Loop that Binds Metal Ions. *Journal of Physical Chemistry Letters*, **2016**, 7, 3841-3846	6.4	3
54	Structure and Function of the PriC DNA Replication Restart Protein. *Journal of Biological Chemistry*, **2016**, 291, 18384-96	5.4	11
53	Mechanism of Histone H3K4me3 Recognition by the Plant Homeodomain of Inhibitor of Growth 3. *Journal of Biological Chemistry*, **2016**, 291, 18326-41	5.4	18

52	Probabilistic validation of protein NMR chemical shift assignments. *Journal of Biomolecular NMR*, **2016**, 64, 17-25	3	8
51	Structural Analysis of Multi-Helical RNAs by NMR-SAXS/WAXS: Application to the U4/U6 di-snRNA. *Journal of Molecular Biology*, **2016**, 428, 777-789	6.5	33
50	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, 113-21	3.9	33
49	Highly Stable, Amide-Bridged Autoinducing Peptide Analogues that Strongly Inhibit the AgrC Quorum Sensing Receptor in Staphylococcus aureus. *Angewandte Chemie*, **2016**, 128, 9059-9063	3.6	10
48	Highly Stable, Amide-Bridged Autoinducing Peptide Analogues that Strongly Inhibit the AgrC Quorum Sensing Receptor in Staphylococcus aureus. *Angewandte Chemie - International Edition*, **2016**, 55, 8913-7	16.4	45
47	Integrative NMR for biomolecular research. *Journal of Biomolecular NMR*, **2016**, 64, 307-32	3	36
46	The AUDANA algorithm for automated protein 3D structure determination from NMR NOE data. *Journal of Biomolecular NMR*, **2016**, 65, 51-7	3	24
45	NMRFAM-SDF: a protein structure determination framework. *Journal of Biomolecular NMR*, **2015**, 62, 481-95	3	4
44	Structural Basis for a Novel Interaction between the NS1 Protein Derived from the 1918 Influenza Virus and RIG-I. *Structure*, **2015**, 23, 2001-10	5.2	35
43	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	11.5	20
42	Impact of Strand Number on Parallel β-Sheet Stability. *Angewandte Chemie*, **2015**, 127, 14544-14547	3.6	5
41	Impact of Strand Number on Parallel β-Sheet Stability. *Angewandte Chemie - International Edition*, **2015**, 54, 14336-9	16.4	20
40	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, 15792-7	11.5	7
39	Dynamic structural changes underpin photoconversion of a blue/green cyanobacteriochrome between its dark and photoactivated states. *Journal of Biological Chemistry*, **2014**, 289, 3055-65	5.4	49
38	Temperature-dependent conformational change affecting Tyr11 and sweetness loops of brazzein. *Proteins: Structure, Function and Bioinformatics*, **2013**, 81, 919-25	4.2	10
37	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, 18436-44	16.4	35
36	Structural basis for the photoconversion of a phytochrome to the activated Pfr form. *Nature*, **2010**, 463, 250-4	50.4	106
35	Activation of nanoscale allosteric protein domain motion revealed by neutron spin echo spectroscopy. *Biophysical Journal*, **2010**, 99, 3473-82	2.9	37

34	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, 10866-75	16.4	53
33	Site-specific backbone amide (15)N chemical shift anisotropy tensors in a small protein from liquid crystal and cross-correlated relaxation measurements. *Journal of the American Chemical Society*, **2010**, 132, 4295-309	16.4	69
32	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, 29757-72	5.4	67
31	TALOS+: a hybrid method for predicting protein backbone torsion angles from NMR chemical shifts. *Journal of Biomolecular NMR*, **2009**, 44, 213-23	3	1994
30	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, 14138-9	16.4	9
29	NMR structure of the mengovirus Leader protein zinc-finger domain. *FEBS Letters*, **2008**, 582, 896-900	3.8	19
28	Solution structure of a cyanobacterial phytochrome GAF domain in the red-light-absorbing ground state. *Journal of Molecular Biology*, **2008**, 383, 403-13	6.5	50
27	Solution structure of the iron-sulfur cluster cochaperone HscB and its binding surface for the iron-sulfur assembly scaffold protein IscU. *Biochemistry*, **2008**, 47, 9394-404	3.2	38
26	Characterization of two thermostable cyanobacterial phytochromes reveals global movements in the chromophore-binding domain during photoconversion. *Journal of Biological Chemistry*, **2008**, 283, 21251-66	5.4	46
25	How Sweet It Is: Detailed Molecular and Functional Studies of Brazzein, a Sweet Protein and Its Analogs. *ACS Symposium Series*, **2008**, 560-572	0.4	4
24	Structural dependencies of protein backbone 2JNCScouplings. *Protein Science*, **2008**, 17, 768-76	6.3	7
23	HIFI-C: a robust and fast method for determining NMR couplings from adaptive 3D to 2D projections. *Journal of Biomolecular NMR*, **2007**, 38, 341-51	3	12
22	Structure and thermodynamics of a conserved U2 snRNA domain from yeast and human. *Rna*, **2007**, 13, 328-38	5.8	31
21	Solution structure of a small protein containing a fluorinated side chain in the core. *Protein Science*, **2007**, 16, 14-9	6.3	17
20	Solution structure of a single-domain thiosulfate sulfurtransferase from Arabidopsis thaliana. *Protein Science*, **2006**, 15, 2836-41	6.3	9
19	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 Suppl 1, 58	3	4
18	Brazzein, a small, sweet protein: effects of mutations on its structure, dynamics and functional properties. *Chemical Senses*, **2005**, 30 Suppl 1, i90-1	4.8	14
17	Solution structure of a late embryogenesis abundant protein (LEA14) from Arabidopsis thaliana, a cellular stress-related protein. *Protein Science*, **2005**, 14, 2601-9	6.3	84

16	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, 633-43	4.2	52
15	X-ray structure of Arabidopsis At1g77680, 12-oxophytodienoate reductase isoform 1. *Proteins: Structure, Function and Bioinformatics*, **2005**, 61, 206-8	4.2	7
14	Structural and dynamics studies of the D54A mutant of human T cell leukemia virus-1 capsid protein. *Journal of Biological Chemistry*, **2005**, 280, 6792-801	5.4	12
13	U2-U6 RNA folding reveals a group II intron-like domain and a four-helix junction. *Nature Structural and Molecular Biology*, **2004**, 11, 1237-42	17.6	115
12	Solution structure of a homodimeric hypothetical protein, At5g22580, a structural genomics target from Arabidopsis thaliana. *Journal of Biomolecular NMR*, **2004**, 29, 387-90	3	11
11	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. *Protein Science*, **2003**, 12, 973-81	6.3	7
10	Solution structure of the phosphoryl transfer complex between the cytoplasmic A domain of the mannitol transporter IIMannitol and HPr of the Escherichia coli phosphotransferase system. *Journal of Biological Chemistry*, **2002**, 277, 42289-98	5.4	58
9	Structural analysis of the N-terminal domain of the human T-cell leukemia virus capsid protein. *Journal of Molecular Biology*, **2001**, 306, 783-97	6.5	55
8	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, 481-99	6.5	114
7	Large Variations in One-Bond 13C□13C□ Couplings in Polypeptides Correlate with Backbone Conformation. *Journal of the American Chemical Society*, **2000**, 122, 2168-2171	16.4	26
6	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	16.4	188
5	Protein backbone angle restraints from searching a database for chemical shift and sequence homology. *Journal of Biomolecular NMR*, **1999**, 13, 289-302	3	2724
4	Identification of the Hydrogen Bonding Network in a Protein by Scalar Couplings. *Journal of the American Chemical Society*, **1999**, 121, 2949-2950	16.4	217
3	Correlation between 3hJNC□and Hydrogen Bond Length in Proteins. *Journal of the American Chemical Society*, **1999**, 121, 6275-6279	16.4	157
2	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	16.4	797
1	Robust nomenclature and software for enhanced reproducibility in molecular modeling of small molecules		2