

Maria Angeles Jimenez

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	Solution structure of .gamma.1-H and .gamma.1-P thionins from barley and wheat endosperm determined by proton NMR: a structural motif common to toxic arthropod proteins. <i>Biochemistry</i> , 1993, 32, 715-724.	1.2	217
2	NMR evidence of a short linear peptide that folds into a .beta.-hairpin in aqueous solution. <i>Journal of the American Chemical Society</i> , 1993, 115, 5887-5888.	6.6	203
3	NMR Solution Structure of the Isolated N-Terminal Fragment of Protein-G B1 Domain. Evidence of Trifluoroethanol Induced Native-Like .beta.-Hairpin Formation. <i>Biochemistry</i> , 1994, 33, 6004-6014.	1.2	197
4	Turn Residue Sequence Determines Î²-Hairpin Conformation in Designed Peptides. <i>Journal of the American Chemical Society</i> , 1997, 119, 175-183.	6.6	166
5	De novo design of a monomeric threeâ€stranded antiparallel Î²â€sheet. <i>Protein Science</i> , 1999, 8, 854-865.	3.1	126
6	Conformational investigation of designed short linear peptides able to fold into Î²-hairpin structures in aqueous solution. <i>Folding & Design</i> , 1996, 1, 133-144.	4.5	89
7	Conformational Analysis of Peptides Corresponding to Î²-Hairpins and a Î²-Sheet that Represent the Entire Sequence of the Î±-Spectrin SH3 Domain. <i>Journal of Molecular Biology</i> , 1996, 255, 507-521.	2.0	84
8	Tryptophan residues: Scarce in proteins but strong stabilizers of Î²â€hairpin peptides. <i>Biopolymers</i> , 2010, 94, 779-790.	1.2	81
9	1 H NMR and CD evidence of the folding of the isolated ribonuclease 50-61 fragment. <i>FEBS Letters</i> , 1987, 221, 320-324.	1.3	79
10	NMR Spectroscopy Reveals that RNase A is Chiefly Denatured in 40% Acetic Acid: Implications for Oligomer Formation by 3D Domain Swapping. <i>Journal of the American Chemical Society</i> , 2010, 132, 1621-1630.	6.6	69
11	CD and 1H-NMR studies on the conformational properties of peptide fragments from the C-terminal domain of thermolysin. <i>FEBS Journal</i> , 1993, 211, 569-581.	0.2	66
12	Thermodynamic parameters for the helix-coil thermal transition of ribonuclease-S-peptide and derivatives from 1H-nmr data. <i>Biopolymers</i> , 1986, 25, 1031-1053.	1.2	65
13	Factors involved in the stability of isolated Î²-sheets: Turn sequence, Î²-sheet twisting, and hydrophobic surface burial. <i>Protein Science</i> , 2004, 13, 1134-1147.	3.1	65
14	Crossâ€strand sideâ€chain interactions versus turn conformation in Î²â€hairpins. <i>Protein Science</i> , 1997, 6, 2548-2560.	3.1	65
15	A tyrosine-containing motif mediates ER retention of CD3-epsilon and adopts a helix-turn structure.. <i>EMBO Journal</i> , 1995, 14, 2257-2268.	3.5	63
16	The turn sequence directs Î²â€strand alignment in designed Î²â€hairpins. <i>Protein Science</i> , 1999, 8, 2234-2244.	3.1	63
17	Structural Dissection of Crotalicidin, a Rattlesnake Venom Cathelicidin, Retrieves a Fragment with Antimicrobial and Antitumor Activity. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 8553-8563.	2.9	63
18	Non-native local interactions in protein folding and stability: introducing a helical tendency in the all Î²-sheet Î±-spectrin SH3 domain. <i>Journal of Molecular Biology</i> , 1997, 268, 760-778.	2.0	60

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19	IBTM-Containing Gramicidin S Analogues: Evidence for IBTM as a Suitable Type II- β -Turn Mimetic ^{1,2} . Journal of the American Chemical Society, 1997, 119, 10579-10586.	6.6	57
20	¹³ C(α) and ¹³ C(β) chemical shifts as a tool to delineate beta-hairpin structures in peptides. Journal of Biomolecular NMR, 2001, 19, 331-345.	1.6	57
21	DNA-induced β -Helical Structure in the NH ₂ -terminal Domain of Histone H1. Journal of Biological Chemistry, 2001, 276, 46429-46435.	1.6	57
22	Structure of Stable Protein Folding Intermediates by Equilibrium β -Analysis: The Apoflavodoxin Thermal Intermediate. Journal of Molecular Biology, 2004, 344, 239-255.	2.0	55
23	Context-Dependence of the Contribution of Disulfide Bonds to β -Hairpin Stability. Chemistry - A European Journal, 2008, 14, 488-499.	1.7	55
24	Interactions Responsible for the pH Dependence of the beta-Hairpin Conformational Population Formed by a Designed Linear Peptide. FEBS Journal, 1995, 233, 283-292.	0.2	54
25	Three-Dimensional Structure of Acidic Fibroblast Growth Factor in Solution: Effects of Binding to a Heparin Functional Analog. Journal of Molecular Biology, 1996, 264, 162-178.	2.0	53
26	Thermodynamic Analysis of β -Hairpin-Forming Peptides from the Thermal Dependence of ¹ H NMR Chemical Shifts. Journal of the American Chemical Society, 2002, 124, 14903-14909.	6.6	51
27	A study of the NH NMR signals of Gly-Gly-X-Ala tetrapeptides in H ₂ O at low temperature.. Journal of Molecular Structure, 1986, 143, 435-438.	1.8	49
28	Periodic properties of proton conformational shifts in isolated protein helices. An experimental study. FEBS Journal, 1992, 207, 39-49.	0.2	49
29	Solution structure of acidic fibroblast growth factor bound to 1,3,6-naphthalenetrisulfonate: A minimal model for the anti-tumoral action of suramins and suradistas 1 Edited by P. E. Wright. Journal of Molecular Biology, 1998, 281, 899-915.	2.0	49
30	¹ H-NMR Assignment and Solution Structure of Human Acidic Fibroblast Growth Factor Activated by Inositol Hexasulfate. Journal of Molecular Biology, 1994, 242, 81-98.	2.0	47
31	Position effect of cross-strand side-chain interactions on β -hairpin formation. Protein Science, 2000, 9, 2151-2160.	3.1	47
32	NMR chemical shifts: a tool to characterize distortions of peptide and protein helices. Journal of the American Chemical Society, 1992, 114, 9676-9677.	6.6	46
33	β -Hairpin formation in aqueous solution and in the presence of trifluoroethanol: A ¹ H and ¹³ C nuclear magnetic resonance conformational study of designed peptides. Biopolymers, 2005, 79, 150-162.	1.2	46
34	Therapeutic Index of Gramicidin S is Strongly Modulated by β -Phenylalanine Analogues at the β -Turn. Journal of Medicinal Chemistry, 2009, 52, 664-674.	2.9	46
35	¹ H NMR Structural Characterization of a Nonmitogenic, Vasodilatory, Ischemia-Protector and Neuromodulatory Acidic Fibroblast Growth Factor. Biochemistry, 2000, 39, 4982-4993.	1.2	41
36	The Long and Short Flavodoxins. Journal of Biological Chemistry, 2004, 279, 47177-47183.	1.6	39

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37	A helix-turn motif in the C-terminal domain of histone H1. <i>Protein Science</i> , 2000, 9, 627-636.	3.1	38
38	Sequence Inversion and Phenylalanine Surrogates at the $\hat{1}^2$ -Turn Enhance the Antibiotic Activity of Gramicidin S. <i>Journal of Medicinal Chemistry</i> , 2010, 53, 4119-4129.	2.9	38
39	First-in-class inhibitor of the T cell receptor for the treatment of autoimmune diseases. <i>Science Translational Medicine</i> , 2016, 8, 370ra184.	5.8	38
40	The Atomic Structure of the HIV-1 gp41 Transmembrane Domain and Its Connection to the Immunogenic Membrane-proximal External Region. <i>Journal of Biological Chemistry</i> , 2015, 290, 12999-13015.	1.6	37
41	Helix-Stabilizing Nonpolar Interactions between Tyrosine and Leucine in Aqueous and TFE Solutions: \hat{A} 2D-1H NMR and CD Studies in Alanine-Lysine Peptides. <i>Biochemistry</i> , 1998, 37, 17318-17330.	1.2	36
42	Disulfide Bonds versus Trp...Trp Pairs in Irregular $\hat{1}^2$ -Hairpins: NMR Structure of Vammin Loop $\hat{3}$ Derived Peptides as a Case Study. <i>ChemBioChem</i> , 2009, 10, 902-910.	1.3	36
43	Structural analysis of peptides encompassing all $\hat{1}^{\pm}$ -helices of three $\hat{1}^{\pm}/\hat{1}^2$ parallel proteins: Che-Y, flavodoxin and P21-Ras: Implications for $\hat{1}^{\pm}$ -Helix stability and the folding of $\hat{1}^{\pm}/\hat{1}^2$ parallel proteins. <i>Journal of Molecular Biology</i> , 1995, 247, 648-669.	2.0	35
44	Cooperative Stabilization of a Molten Globule Apoflavodoxin Fragment. <i>Biochemistry</i> , 1998, 37, 10589-10596.	1.2	34
45	Design, NMR characterization and activity of a 21-residue peptide fragment of bacteriocin AS-48 containing its putative membrane interacting region. <i>Journal of Peptide Science</i> , 2005, 11, 29-36.	0.8	34
46	Helicity of $\hat{1}^{\pm}$ (404-451) and $\hat{1}^2$ (394-445) tubulin C-terminal recombinant peptides. <i>Protein Science</i> , 1999, 8, 788-799.	3.1	34
47	Structural basis for broad neutralization of HIV-1 through the molecular recognition of 10E8 helical epitope at the membrane interface. <i>Scientific Reports</i> , 2016, 6, 38177.	1.6	34
48	Tendamistat (12-26) fragment. NMR characterization of isolated beta-turn folding intermediates. <i>FEBS Journal</i> , 1991, 200, 345-351.	0.2	33
49	Acylated flavonol sophorotriosides from pea shoots. <i>Phytochemistry</i> , 1995, 39, 1443-1446.	1.4	33
50	Alanine scan and 2 H NMR analysis of the membrane-active peptide BP100 point to a distinct carpet mechanism of action. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016, 1858, 1328-1338.	1.4	32
51	1H-NMR assignment and folding of the isolated ribonuclease 21-42 fragment. <i>FEBS Journal</i> , 1988, 175, 101-109.	0.2	31
52	Structural and functional study of a conserved region in the uncoupling protein UCP1: the three matrix loops are involved in the control of transport 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1999, 292, 137-149.	2.0	31
53	A bacterial antirepressor with SH3 domain topology mimics operator DNA in sequestering the repressor DNA recognition helix. <i>Nucleic Acids Research</i> , 2010, 38, 5226-5241.	6.5	30
54	NMR Solution Structure of the C-Terminal Fragment 255-316 of Thermolysin: A Dimer Formed by Subunits Having the Native Structure. <i>Biochemistry</i> , 1994, 33, 14834-14847.	1.2	29

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55	<i>De novo</i> Design of Monomeric β^2 -Hairpin and β^2 -Sheet Peptides. , 2006, 340, 27-52.		29
56	Influence of the Bifunctional Chelator on the Pharmacokinetic Properties of $^{99m}\text{Tc}(\text{CO})_3$ -Labeled Cyclic β^2 -Melanocyte Stimulating Hormone Analog. Journal of Medicinal Chemistry, 2013, 56, 1961-1973.	2.9	29
57	An inducible helix-Gly-Gly-helix motif in the N-terminal domain of histone H1e: A CD and NMR study. Protein Science, 2009, 11, 214-220.	3.1	28
58	Solvent polarity-dependent structural refolding: A CD and NMR study of a 15 residue peptide. Proteins: Structure, Function and Bioinformatics, 1995, 23, 196-203.	1.5	27
59	Helical peptides from VEGF and Vammin hotspots for modulating the VEGF-VEGFR interaction. Organic and Biomolecular Chemistry, 2013, 11, 1896.	1.5	27
60	Peptide group chemical shift computation. Magnetic Resonance in Chemistry, 1992, 30, 1012-1018.	1.1	26
61	Helix Stop and Start Signals in Peptides and Proteins. Journal of Molecular Biology, 1994, 242, 487-496.	2.0	26
62	Solution Structure and Interaction with Basic and Acidic Fibroblast Growth Factor of a 3-kDa Human Platelet Factor-4 Fragment with Antiangiogenic Activity. Journal of Biological Chemistry, 2001, 276, 35723-35734.	1.6	26
63	β^2 -Hairpin folding and stability: molecular dynamics simulations of designed peptides in aqueous solution. Journal of Peptide Science, 2004, 10, 546-565.	0.8	26
64	Structure and Immunogenicity of a Peptide Vaccine, Including the Complete HIV-1 gp41 2F5 Epitope. Journal of Biological Chemistry, 2014, 289, 6565-6580.	1.6	26
65	Design and Structure of an Equilibrium Protein Folding Intermediate: A Hint into Dynamical Regions of Proteins. Journal of Molecular Biology, 2010, 400, 922-934.	2.0	25
66	Anabaena pflavodoxin hydrogen exchange: On the stable exchange core of the β^2/β^2 (21345) flavodoxin-like family. Proteins: Structure, Function and Bioinformatics, 2001, 43, 476-488.	1.5	24
67	Structural basis for operator and antirepressor recognition by Myxococcus xanthus CarA repressor. Molecular Microbiology, 2007, 63, 980-994.	1.2	24
68	Folding of the presequence of yeast pAPI into an amphipathic helix determines transport of the protein from the cytosol to the vacuole. Journal of Molecular Biology, 1997, 267, 1124-1138.	2.0	22
69	Disulfide and amide-bridged cyclic peptide analogues of the VEGF81-91 fragment: Synthesis, conformational analysis and biological evaluation. Bioorganic and Medicinal Chemistry, 2011, 19, 7526-7533.	1.4	22
70	Parallel solid-phase synthesis of a small library of linear and hydrocarbon-bridged analogues of VEGF81-91: Potential biological tools for studying the VEGF/VEGFR-1 interaction. Bioorganic and Medicinal Chemistry, 2011, 19, 1978-1986.	1.4	21
71	Design and structural characterisation of monomeric water-soluble β^2 -helix and β^2 -hairpin peptides: State-of-the-art. Archives of Biochemistry and Biophysics, 2019, 661, 149-167.	1.4	21
72	Penetrating the Blood-Brain Barrier with New Peptide-Porphyrin Conjugates Having anti-HIV Activity. Bioconjugate Chemistry, 2021, 32, 1067-1077.	1.8	21

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73	Design of Monomeric Water-Soluble β^2 -Hairpin and β^2 -Sheet Peptides. <i>Methods in Molecular Biology</i> , 2014, 1216, 15-52.	0.4	21
74	Conformational properties of the isolated 1-23 fragment of human hemoglobin β -chain. <i>BBA - Proteins and Proteomics</i> , 1988, 957, 380-389.	2.1	20
75	Three-Dimensional Solution Structure and Stability of Phage 434 Cro Protein. <i>Biochemistry</i> , 1997, 36, 6424-6436.	1.2	20
76	Structural Insights into RNA Polymerase Recognition and Essential Function of <i>Myxococcus xanthus</i> CdnL. <i>PLoS ONE</i> , 2014, 9, e108946.	1.1	19
77	Helix formation by the phospholipase A238-59 fragment: Influence of chain shortening and dimerization monitored by nmr chemical shifts. <i>Biopolymers</i> , 1994, 34, 647-661.	1.2	18
78	The homologous angiogenin and ribonuclease N-terminal fragments fold into very similar helices when isolated. <i>Biochemical and Biophysical Research Communications</i> , 1992, 182, 1491-1498.	1.0	16
79	Micelle-triggered β^2 -Hairpin to β -Helix Transition in a 14-Residue Peptide from a Choline-Binding Repeat of the Pneumococcal Autolysin LytA. <i>Chemistry - A European Journal</i> , 2015, 21, 8076-8089.	1.7	16
80	Trypanothione reductase inhibition and anti-leishmanial activity of all-hydrocarbon stapled β -helical peptides with improved proteolytic stability. <i>European Journal of Medicinal Chemistry</i> , 2018, 149, 238-247.	2.6	16
81	Amide 1H n.m.r. study of the folding of ribonuclease C-peptide. <i>International Journal of Biological Macromolecules</i> , 1985, 7, 66-70.	3.6	15
82	Synthesis of the Blood Circulating C-terminal Fragment of Insulin-like Growth Factor (IGF)-binding Protein-4 in Its Native Conformation. <i>Journal of Biological Chemistry</i> , 2005, 280, 18899-18907.	1.6	15
83	Design and NMR conformational study of a β^2 -sheet peptide based on Betanova and WW domains. <i>Protein Science</i> , 2006, 15, 2278-2289.	3.1	15
84	The ^1H , ^{13}C , ^{15}N resonance assignment, solution structure, and residue level stability of eosinophil cationic protein/RNase 3 determined by NMR spectroscopy. <i>Biopolymers</i> , 2009, 91, 1018-1028.	1.2	14
85	Assessing the Protonation State of Drug Molecules: The Case of Aztreonam. <i>Journal of Medicinal Chemistry</i> , 2006, 49, 3235-3243.	2.9	13
86	Interaction between the N-terminal SH3 domain of Nck β and CD3 ϵ -derived peptides: Non-canonical and canonical recognition motifs. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 110-117.	1.1	13
87	Comparison of hydrocarbon-and lactam-bridged cyclic peptides as dimerization inhibitors of <i>Leishmania infantum</i> trypanothione reductase. <i>RSC Advances</i> , 2015, 5, 55784-55794.	1.7	13
88	Rationally Modified Antimicrobial Peptides from the N-Terminal Domain of Human RNase 3 Show Exceptional Serum Stability. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 11472-11482.	2.9	13
89	Folding propensities of synthetic peptide fragments covering the entire sequence of phage 434 Cro protein. <i>Protein Science</i> , 1999, 8, 1675-1688.	3.1	12
90	Insights into the determinants of β^2 -sheet stability: ^1H and ^{13}C NMR conformational investigation of three-stranded antiparallel β^2 -sheet-forming peptides. <i>Chemical Biology and Drug Design</i> , 2008, 61, 177-188.	1.2	12

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91	Structure-Function Dissection of Myxococcus xanthus CarD N-Terminal Domain, a Defining Member of the CarD_CdnL_TRCF Family of RNA Polymerase Interacting Proteins. PLoS ONE, 2015, 10, e0121322.	1.1	12
92	A CON-based NMR assignment strategy for pro-rich intrinsically disordered proteins with low signal dispersion: the C-terminal domain of histone H1.0 as a case study. Journal of Biomolecular NMR, 2018, 72, 139-148.	1.6	12
93	Cyclic amino acid linkers stabilizing key loops of brain derived neurotrophic factor. Bioorganic and Medicinal Chemistry Letters, 2012, 22, 444-448.	1.0	11
94	Effect of Phosphorylation on the Structural Behaviour of Peptides Derived from the Intrinsically Disordered C-terminal Domain of Histone H1.0. Chemistry - A European Journal, 2020, 26, 5970-5981.	1.7	11
95	Conformationally restricted PACAP27 analogues incorporating type II/II ² IBTM β -Turn Mimetics. Synthesis, NMR Structure Determination, and Binding Affinity. Bioorganic and Medicinal Chemistry, 2001, 9, 3173-3183.	1.4	10
96	Hints of Nonhierarchical Folding of Acidic Fibroblast Growth Factor. Biochemistry, 2002, 41, 1923-1933.	1.2	10
97	Structural autonomy of a β -hairpin peptide derived from the pneumococcal choline-binding protein LytA. Protein Engineering, Design and Selection, 2011, 24, 113-122.	1.0	10
98	Quantitative interpretation of the helix coil transition in RNase a S-peptide. Journal of Molecular Structure, 1986, 143, 439-444.	1.8	9
99	Dihydrofolate reductase: control of the mode of substrate binding by aspartate 26. Protein Engineering, Design and Selection, 1989, 2, 627-631.	1.0	9
100	NMR solution structure of the activation domain of human procarboxypeptidase A2. Protein Science, 2003, 12, 296-305.	3.1	9
101	Trp-Trp pairs as β -hairpin stabilisers: Hydrogen-bonded versus non-hydrogen-bonded sites. Organic and Biomolecular Chemistry, 2011, 9, 5487.	1.5	9
102	NMR structure note: N-terminal domain of Thermus thermophilus CdnL. Journal of Biomolecular NMR, 2012, 53, 355-363.	1.6	9
103	NMR structure note: PHD domain from death inducer obliterator protein and its interaction with H3K4me3. Journal of Biomolecular NMR, 2013, 56, 183-190.	1.6	9
104	Emergence of structure through protein-protein interactions and pH changes in dually predicted coiled-coil and disordered regions of centrosomal proteins. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 1808-1819.	1.1	9
105	Nuclear Overhauser effects in aqueous solution as dynamic probes in short linear peptides. FEBS Letters, 1988, 239, 83-87.	1.3	8
106	Peptides Mimicking the β 27/ β 28 Loop of HIV-1 Reverse Transcriptase p51 as Hotspot-Targeted Dimerization Inhibitors. ACS Medicinal Chemistry Letters, 2020, 11, 811-817.	1.3	8
107	Conformational study of linear and cyclic peptides corresponding to the 276-284 epitope region of HSV gD-1. Biophysical Chemistry, 2003, 103, 51-65.	1.5	7
108	Characterization of the structure and self-recognition of the human centrosomal protein NA14: implications for stability and function. Protein Engineering, Design and Selection, 2011, 24, 883-892.	1.0	7

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109	NMR Structural Analysis of MC1R-Targeted Rhenium(I) Metallopeptides and Biological Evaluation of ^{99m} Tc(I) Congeners. <i>Organometallics</i> , 2012, 31, 5929-5939.	1.1	7
110	DMSO affects α -helix's conformation and interactions with aggregation inhibitors as revealed by NMR. <i>RSC Advances</i> , 2015, 5, 69761-69764.	1.7	7
111	Roles of Amphipathicity and Hydrophobicity in the Micelle-Driven Structural Switch of a 14-mer Peptide Core from a Choline-Binding Repeat. <i>Chemistry - A European Journal</i> , 2018, 24, 5825-5839.	1.7	7
112	Turncoat Polypeptides: We Adapt to Our Environment. <i>ChemBioChem</i> , 2020, 21, 432-441.	1.3	7
113	NMR Solution Structure of the 205-316 C-Terminal Fragment of Thermolysin. An Example of Dimerization Coupled to Partial Unfolding. <i>Biochemistry</i> , 1997, 36, 11975-11983.	1.2	6
114	Structure of a simplified β -hairpin and its ATP complex. <i>Archives of Biochemistry and Biophysics</i> , 2013, 537, 62-71.	1.4	6
115	¹ H-NMR analysis of CD3- β reveals the presence of turn-helix structures around the ITAM motif in an otherwise random coil cytoplasmic tail. <i>J Biol Chem</i> , 1997, 272, 75-88.		5
116	NMR characterisation of the minimal interacting regions of centrosomal proteins 4.1R and NuMA1: effect of phosphorylation. <i>BMC Biochemistry</i> , 2010, 11, 7.	4.4	5
117	Structure-Related Roles for the Conservation of the HIV-1 Fusion Peptide Sequence Revealed by Nuclear Magnetic Resonance. <i>Biochemistry</i> , 2017, 56, 5503-5511.	1.2	5
118	¹ H, ¹³ C and ¹⁵ N assignments of CdnL, an essential protein in <i>Myxococcus xanthus</i> . <i>Biomolecular NMR Assignments</i> , 2013, 7, 51-55.	0.4	4
119	Structural Insights into β -arrestin/CB1 Receptor Interaction: NMR and CD Studies on Model Peptides. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8111.	1.8	4
120	Editorial: Peptides Targeting Protein-Protein Interactions: Methods and Applications. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 780106.	1.6	4
121	Separation and identification of ribonuclease S-peptide methyl esters by ion-exchange high-performance liquid chromatography and ¹ H nuclear magnetic resonance spectroscopy. <i>Journal of Chromatography A</i> , 1986, 360, 288-292.	1.8	3
122	Solution structure of the isolated ribonuclease C-terminal 112-124 fragment. <i>BBA - Proteins and Proteomics</i> , 1990, 1038, 322-329.	2.1	3
123	¹ H, ¹³ C and ¹⁵ N backbone and side chain resonance assignments of the C-terminal domain of CdnL from <i>Myxococcus xanthus</i> . <i>Biomolecular NMR Assignments</i> , 2009, 3, 9-12.	0.4	3
124	NMR Insights into the Structure-Function Relationships in the Binding of Melanocortin Analogues to the MC1R Receptor. <i>Molecules</i> , 2017, 22, 1189.	1.7	3
125	Peptides in biology and biomedicine: Walking towards the future. <i>Archives of Biochemistry and Biophysics</i> , 2019, 665, 20-22.	1.4	3
126	Pescador: the PEptides in Solution Conformation Database: Online Resource. <i>Journal of Biomolecular NMR</i> , 2002, 23, 85-102.	1.6	2

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127	¹ H, ¹³ C and ¹⁵ N backbone and side chain resonance assignments of a <i>Myxococcus xanthus</i> anti-repressor with no known sequence homologues. <i>Biomolecular NMR Assignments</i> , 2009, 3, 37-40.	0.4	2
128	Structural insight into the XTACC3/XMAP215 interaction from CD and NMR studies on model peptides. <i>Biopolymers</i> , 2017, 107, e23039.	1.2	2
129	DD04107-Derived neuronal exocytosis inhibitor peptides: Evidences for synaptotagmin-1 as a putative target. <i>Bioorganic Chemistry</i> , 2021, 115, 105231.	2.0	2
130	Structural basis of Nrd1–Nab3 heterodimerization. <i>Life Science Alliance</i> , 2022, 5, e202101252.	1.3	2
131	Solution structure of the hypothetical protein TA0095 from <i>Thermoplasma acidophilum</i> : A novel superfamily with a two-layer sandwich architecture. <i>Protein Science</i> , 2007, 16, 2278-2286.	3.1	1
132	Insights Into the Micelle-Induced ¹² C-Hairpin-to- ¹³ C-Helix Transition of a LytA-Derived Peptide by Photo-CIDNP Spectroscopy. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6666.	1.8	1
133	Inter-hairpin linker sequences determine the structure of the ¹² C- ¹³ C-solenoid fold: a “bottom-up” study of pneumococcal LytA choline-binding module. <i>International Journal of Biological Macromolecules</i> , 2021, 190, 679-692.	3.6	1
134	The Gp41 Sequence Connecting Mper and Tm Domains Constitutes a Distinct HIV-1 “Fusion Peptide” Targeted by Neutralizing Antibodies. <i>Biophysical Journal</i> , 2014, 106, 708a-709a.	0.2	0
135	Frontispiece: Micelle-Triggered ¹² C-Hairpin to ¹³ C-Helix Transition in a 14-Residue Peptide from a Choline-Binding Repeat of the Pneumococcal Autolysin LytA. <i>Chemistry - A European Journal</i> , 2015, 21, n/a-n/a.	1.7	0
136	Mode of Action of Antimicrobial Peptides: Long and Short Amphipathic Alpha-Helices Use Different Mechanisms. <i>Biophysical Journal</i> , 2017, 112, 381a.	0.2	0
137	Frontispiece: Effect of Phosphorylation on the Structural Behaviour of Peptides Derived from the Intrinsically Disordered C-terminal Domain of Histone H1.0. <i>Chemistry - A European Journal</i> , 2020, 26, .	1.7	0
138	PACAP27 Analogues Incorporating Type II/III ¹² C-Turn Mimetics. , 2001, , 632-633.		0