Fabio C L Almeida

List of Publications by Year
in descending order

115 papers	2,926 citations	168829 31 h-index	223390 49 g-index
119 all docs	119 docs citations	119 times ranked	4586 citing authors

#	Article	IF	Citations
1	15N, 13C, and 1H resonance assignments of Jarastatin: a disintegrin of Bothrops jararaca. Biomolecular NMR Assignments, 2022, 16, 37-40.	0.4	4
2	Insights into the specificity for the interaction of the promiscuous SARS-CoV-2 nucleocapsid protein N-terminal domain with deoxyribonucleic acids. International Journal of Biological Macromolecules, 2022, 203, 466-480.	3.6	16
3	The interaction of dengue virus capsid protein with negatively charged interfaces drives the in vitro assembly of nucleocapsid-like particles. PLoS ONE, 2022, 17, e0264643.	1.1	5
4	Searching for drug leads targeted to the hydrophobic cleft of dengue virus capsid protein. Journal of Enzyme Inhibition and Medicinal Chemistry, 2022, 37, 287-298.	2.5	1
5	The Câ€terminal extension of <scp>VgrG4</scp> from <scp>Klebsiella pneumoniae</scp> remodels host cell microfilaments. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1655-1668.	1.5	3
6	Deciphering the Path of S-nitrosation of Human Thioredoxin: Evidence of an Internal NO Transfer and Implication for the Cellular Responses to NO. Antioxidants, 2022, 11, 1236.	2.2	2
7	Effect of antihistamine-containing syrup on salivary metabolites: an in vitro and in vivo study. Brazilian Oral Research, 2021, 35, e032.	0.6	0
8	1H, 15N and 13C resonance assignments of the N-terminal domain of the nucleocapsid protein from the endemic human coronavirus HKU1. Biomolecular NMR Assignments, 2021, 15, 153-157.	0.4	2
9	1H, 15N and 13C backbone and sideâ€chain assignments of reduced and S-nitrosated C62only mutant of human thioredoxin. Biomolecular NMR Assignments, 2021, 15, 261-265.	0.4	1
10	Unique structural features of flavivirusesâ€™ capsid proteins: new insights on structure-function relationship. Current Opinion in Virology, 2021, 47, 106-112.	2.6	5
11	The 1H, 15N, and 13C resonance assignments of the N-terminal domain of the nucleocapsid protein from the Middle East respiratory syndrome coronavirus. Biomolecular NMR Assignments, 2021, 15, 341-345.	0.4	0
12	Large-Scale Recombinant Production of the SARS-CoV-2 Proteome for High-Throughput and Structural Biology Applications. Frontiers in Molecular Biosciences, 2021, 8, 653148.	1.6	29
13	Dynamics of the SARS-CoV-2 nucleoprotein N-terminal domain triggers RNA duplex destabilization. Biophysical Journal, 2021, 120, 2814-2827.	0.2	12
14	Protein Surface Interactionsâ€”Theoretical and Experimental Studies. Frontiers in Molecular Biosciences, 2021, 8, 706002.	1.6	9
15	1H, 15N, and 13C resonance assignments of the SH3-like tandem domain of human KIN protein. Biomolecular NMR Assignments, 2021, 15, 449-453.	0.4	0
16	A systematic structural comparison of all solved small proteins deposited in PDB. The effect of disulfide bonds in protein fold. Computational and Structural Biotechnology Journal, 2021, 19, 6255-6262.	1.9	2
17	Structure-Function Relationship of the Disintegrin Family: Sequence Signature and Integrin Interaction. Frontiers in Molecular Biosciences, 2021, 8, 783301.	1.6	19
18	Nuclear magnetic resonance solution structure of Pisum sativum defensin 2 provides evidence for the presence of hydrophobic surfaceâ€clusters. Proteins: Structure, Function and Bioinformatics, 2020, 88, 242-246.	1.5	12

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19	Biophysical and Dynamic Characterization of Fine-Tuned Binding of the Human Respiratory Syncytial Virus M2-1 Core Domain to Long RNAs. Journal of Virology, 2020, 94, .	1.5	3
20	The dynamics of free and phosphopeptide-bound Grb2-SH2 reveals two dynamically independent subdomains and an encounter complex with fuzzy interactions. Scientific Reports, 2020, 10, 13040.	1.6	11
21	Backbone assignment of ribose-5-phosphate isomerase of Mycobacterium tuberculosis (MtRpiB). Biomolecular NMR Assignments, 2020, 14, 119-122.	0.4	1
22	Retinoic Acid Binding Leads to CRABP2 Rigidification and Dimerization. Biochemistry, 2019, 58, 4183-4194.	1.2	7
23	Solution NMR investigation on the structure and function of the isolated J-domain from Sis1: Evidence of transient inter-domain interactions in the full-length protein. Archives of Biochemistry and Biophysics, 2019, 669, 71-79.	1.4	7
24	NMR structure determination of Ixolaris and factor X(a) interaction reveals a noncanonical mechanism of Kunitz inhibition. Blood, 2019, 134, 699-708.	0.6	10
25	Dynamics of Zika Virus Capsid Protein in Solution: The Properties and Exposure of the Hydrophobic Cleft Are Controlled by the Î±-Helix 1 Sequence. Biochemistry, 2019, 58, 2488-2498.	1.2	14
26	NMR assignment of free 1H, 15N and 13C-Grb2-SH2 domain. Biomolecular NMR Assignments, 2019, 13, 295-298.	0.4	5
27	Backbone and side chain 1H, 15N and 13C assignments of a putative peptidyl prolyl cisâ€“trans isomerase FKBP12 from Mycobacterium tuberculosis. Biomolecular NMR Assignments, 2019, 13, 239-243.	0.4	0
28	Fast NMR method to probe solvent accessibility and disordered regions in proteins. Scientific Reports, 2019, 9, 1647.	1.6	12
29	Regioselective Acylation of Levoglucosan Catalyzed by Candida Antarctica (CaLB) Lipase Immobilized on Epoxy Resin. Sustainability, 2019, 11, 6044.	1.6	8
30	Osteoarthritic Synovial Fluid Modulates Cell Phenotype and Metabolic BehaviorIn Vitro. Stem Cells International, 2019, 2019, 1-14.	1.2	99
31	¹H NMR metabolomics reveals increased glutaminolysis upon overexpression of NSD3s or Pdp3 in Saccharomyces cerevisiae. Journal of Cellular Biochemistry, 2019, 120, 5377-5385.	1.2	5
32	Monitoring asparaginase activity. Lancet Oncology, The, 2018, 19, e574.	5.1	3
33	Oligomeric transition and dynamics of RNA binding by the HuR RRM1 domain in solution. Journal of Biomolecular NMR, 2018, 72, 179-192.	1.6	11
34	Conformational Dynamics of a Cysteine-Stabilized Plant Defensin Reveals an Evolutionary Mechanism to Expose Hydrophobic Residues. Biochemistry, 2018, 57, 5797-5806.	1.2	15
35	Structural basis for cross-reactivity and conformation fluctuation of the major beech pollen allergen Fag s 1. Scientific Reports, 2018, 8, 10512.	1.6	17
36	1H, 15N and 13C resonance assignments of the J-domain of co-chaperone Sis1 from Saccharomyces cerevisiae. Biomolecular NMR Assignments, 2018, 12, 279-281.	0.4	2

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37	Structure and membrane interactions of the homodimeric antibiotic peptide homotarsinin. Scientific Reports, 2017, 7, 40854.	1.6	24
38	Salivary metabolic profile of children and adolescents after hemodialysis. Metabolomics, 2017, 13, 1.	1.4	20
39	1H, 13C and 15N chemical shift assignments of Saccharomyces cerevisiae type 1 thioredoxin in the oxidized state by solution NMR spectroscopy. Biomolecular NMR Assignments, 2017, 11, 221-224.	0.4	1
40	Structural and Dynamic Insights of the Interaction between Tritrpticin and Micelles: An NMR Study. Biophysical Journal, 2016, 111, 2676-2688.	0.2	19
41	DIADECOMP: A new approach to analyze decompositions from projection spectroscopy. Journal of Magnetic Resonance, 2016, 273, 1-8.	1.2	1
42	Salivary Metabolite Fingerprint of Type 1 Diabetes in Young Children. Journal of Proteome Research, 2016, 15, 2491-2499.	1.8	38
43	Antibody Binding Modulates Conformational Exchange in Domain III of Dengue Virus E Protein. Journal of Virology, 2016, 90, 1802-1811.	1.5	13
44	1H, 13C and 15N resonance assignments and second structure information of Fag s 1: Fagales allergen from Fagus sylvatica. Biomolecular NMR Assignments, 2016, 10, 45-48.	0.4	2
45	Biophysical Studies on BEX3, the p75NTR-Associated Cell Death Executor, Reveal a High-Order Oligomer with Partially Folded Regions. PLoS ONE, 2015, 10, e0137916.	1.1	8
46	1H, 15N and 13C resonance assignments of the RRM1 domain of the key post-transcriptional regulator HuR. Biomolecular NMR Assignments, 2015, 9, 281-284.	0.4	4
47	Longitudinal evaluation of salivary profile from children with dental caries before and after treatment. Metabolomics, 2015, 11, 583-593.	1.4	32
48	Dissection of the Water Cavity of Yeast Thioredoxin 1: The Effect of a Hydrophobic Residue in the Cavity. Biochemistry, 2015, 54, 2429-2442.	1.2	10
49	Structures of the reduced and oxidized state of the mutant D24A of yeast thioredoxin 1: insights into the mechanism for the closing of the water cavity. Journal of Biomolecular NMR, 2015, 63, 417-423.	1.6	3
50	Understanding Dengue Virus Capsid Protein Disordered N-Terminus and pep14-23-Based Inhibition. ACS Chemical Biology, 2015, 10, 517-526.	1.6	45
51	A Cross-Reactive Human Single-Chain Antibody for Detection of Major Fish Allergens, Parvalbumins, and Identification of a Major IgE-Binding Epitope. PLoS ONE, 2015, 10, e0142625.	1.1	12
52	Dengue virus capsid protein interacts specifically with very low-density lipoproteins. Nanomedicine: Nanotechnology, Biology, and Medicine, 2014, 10, 247-255.	1.7	59
53	Peptide:lipid ratio and membrane surface charge determine the mechanism of action of the antimicrobial peptide BP100. Conformational and functional studies. Biochimica Et Biophysica Acta - Biomembranes, 2014, 1838, 1985-1999.	1.4	93
54	Solution and high-pressure NMR studies of the structure, dynamics, and stability of the cross-reactive allergenic cod parvalbumin Gad m 1. Proteins: Structure, Function and Bioinformatics, 2014, 82, 3032-3042.	1.5	22

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55	Bet v 1 â€“ a Trojan horse for small ligands boosting allergic sensitization?. Clinical and Experimental Allergy, 2014, 44, 1083-1093.	1.4	38
56	Hydration and Conformational Equilibrium in Yeast Thioredoxin 1: Implication for H+Exchange. Biochemistry, 2014, 53, 2890-2902.	1.2	9
57	PHD domain from human SHPRH. Journal of Biomolecular NMR, 2013, 56, 393-399.	1.6	6
58	1H, 13C and 15N resonance assignments and second structure information of Gad m 1: a Î²-parvalbumin allergen from Atlantic cod (Gadus morhua). Biomolecular NMR Assignments, 2013, 7, 133-136.	0.4	3
59	Salivary metabolite signatures of children with and without dental caries lesions. Metabolomics, 2013, 9, 657-666.	1.4	58
60	Structural Basis for the Interaction of Human Î²-Defensin 6 and Its Putative Chemokine Receptor CCR2 and Breast Cancer Microvesicles. Journal of Molecular Biology, 2013, 425, 4479-4495.	2.0	29
61	Structural meta-analysis of regular human insulin in pharmaceutical formulations. European Journal of Pharmaceutics and Biopharmaceutics, 2013, 85, 1112-1121.	2.0	44
62	Modeling the Interaction of Dodecylphosphocholine Micelles with the Anticoccidial Peptide PW2 Guided by NMR Data. Molecules, 2013, 18, 10056-10080.	1.7	7
63	Revealing the Properties of Plant Defensins through Dynamics. Molecules, 2013, 18, 11311-11326.	1.7	18
64	An Overview on Protein Structure Determination by NMR: Historical and Future Perspectives of the use of Distance Geometry Methods. , 2013, , 377-412.		7
65	The disordered N-terminal region of dengue virus capsid protein contains a lipid-droplet-binding motif. Biochemical Journal, 2012, 444, 405-415.	1.7	83
66	Heat stability of Proteobacterial PII protein facilitate purification using a single chromatography step. Protein Expression and Purification, 2012, 81, 83-88.	0.6	22
67	Herpes simplex type 1 activates glycolysis through engagement of the enzyme 6-phosphofructo-1-kinase (PFK-1). Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2012, 1822, 1198-1206.	1.8	78
68	Moniliophthora perniciosa Necrosis- and Ethylene-Inducing Protein 2 (MpNep2) as a Metastable Dimer in Solution: Structural and Functional Implications. PLoS ONE, 2012, 7, e45620.	1.1	27
69	Identification of Regions Involved in Substrate Binding and Dimer Stabilization within the Central Domains of Yeast Hsp40 Sis1. PLoS ONE, 2012, 7, e50927.	1.1	28
70	Thermodynamic and Structural Characterization of Zwitterionic Micelles of the Membrane Protein Solubilizing Amidosulfobetaine Surfactants ASB-14 and ASB-16. Langmuir, 2011, 27, 8248-8256.	1.6	24
71	Portrayal of Complex Dynamic Properties of Sugarcane Defensin 5 by NMR: Multiple Motions Associated with Membrane Interaction. Structure, 2011, 19, 26-36.	1.6	50
72	Mapping the Interactions between a Major Pollen Allergen and Human IgE Antibodies. Structure, 2010, 18, 1011-1021.	1.6	48

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73	Conformational selection, dynamic restriction and the hydrophobic effect coupled to stabilization of the BIR3 domain of the human X-linked inhibitor of apoptosis protein by the tetrapeptide AVPI. Biophysical Chemistry, 2010, 152, 99-108.	1.5	5
74	Novel Zn2+-binding Sites in Human Transthyretin. Journal of Biological Chemistry, 2010, 285, 31731-31741.	1.6	42
75	From combinatorial peptide selection to drug prototype (I): Targeting the vascular endothelial growth factor receptor pathway. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5112-5117.	3.3	62
76	Backbone dynamics of the antifungal Psd1 pea defensin and its correlation with membrane interaction by NMR spectroscopy. Biochimica Et Biophysica Acta - Biomembranes, 2010, 1798, 105-113.	1.4	82
77	Ferromagnetic Levan Composite: An Affinity Matrix to Purify Lectin. Journal of Biomedicine and Biotechnology, 2009, 2009, 1-6.	3.0	20
78	Sequence-specific 1H, 15N and 13C resonance assignments of Art v 1: a proline-rich allergen of Artemisia vulgaris pollen. Biomolecular NMR Assignments, 2009, 3, 103-106.	0.4	5
79	Interaction of the Dengue Virus Fusion Peptide with Membranes Assessed by NMR: The Essential Role of the Envelope Protein Trp101 for Membrane Fusion. Journal of Molecular Biology, 2009, 392, 736-746.	2.0	45
80	Structure and Membrane Interactions of the Antibiotic Peptide Dermadistinctin K by Multidimensional Solution and Oriented 15N and 31P Solid-State NMR Spectroscopy. Biophysical Journal, 2009, 96, 2194-2203.	0.2	41
81	Inhibition of energy-producing pathways of HepG2 cells by 3-bromopyruvate1. Biochemical Journal, 2009, 417, 717-726.	1.7	155
82	NMR solution structure of the reduced form of thioredoxin 1 from Sacharomyces cerevisiae. Proteins: Structure, Function and Bioinformatics, 2008, 70, 584-587.	1.5	21
83	Evolutionary relationship between defensins in the Poaceae family strengthened by the characterization of new sugarcane defensins. Plant Molecular Biology, 2008, 68, 321-335.	2.0	28
84	Spectroscopic characterization of a truncated hemoglobin from the nitrogen-fixing bacterium Herbaspirillum seropedicae. Journal of Biological Inorganic Chemistry, 2008, 13, 1085-1096.	1.1	8
85	A minor Î²â€structured conformation is the active state of a fusion peptide of vesicular stomatitis virus glycoprotein. Journal of Peptide Science, 2008, 14, 429-435.	0.8	3
86	Solution NMR structures of the antimicrobial peptides phylloseptin-1, -2, and -3 and biological activity: The role of charges and hydrogen bonding interactions in stabilizing helix conformations. Peptides, 2008, 29, 1633-1644.	1.2	59
87	A Ligand Peptide Motif Selected from a Cancer Patient Is a Receptor-Interacting Site within Human Interleukin-11. PLoS ONE, 2008, 3, e3452.	1.1	31
88	Structure of the Ebola Fusion Peptide in a Membrane-mimetic Environment and the Interaction with Lipid Rafts. Journal of Biological Chemistry, 2007, 282, 27306-27314.	1.6	43
89	Structural biology of membrane-acting peptides: Conformational plasticity of anticoccidial peptide PW2 probed by solution NMR. Biochimica Et Biophysica Acta - Biomembranes, 2007, 1768, 3182-3192.	1.4	10
90	NMR solution structure of the reduced form of thioredoxin 2 from Saccharomyces cerevisiae. Journal of Biomolecular NMR, 2007, 38, 99-104.	1.6	18

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91	Effect of micelle interface on the binding of anticoccidial PW2 peptide. Journal of Biomolecular NMR, 2007, 39, 315-322.	1.6	11
92	Prediction of the amount of secondary structure of proteins using unassigned NMR spectra: a tool for target selection in structural proteomics. Genetics and Molecular Biology, 2006, 29, 762-770.	0.6	6
93	In-Cell NMR Spectroscopy: Inhibition of Autologous Protein Expression Reduces Escherichia coli Lysis. Cell Biochemistry and Biophysics, 2006, 44, 497-502.	0.9	20
94	1 H, 13 C and 15 N Resonance Assignments for the Reduced Forms of Thioredoxin 1 and 2 fromÂS. cerevisiae. Journal of Biomolecular NMR, 2006, 36, 35-35.	1.6	5
95	Implications of Protein Conformational Diversity for Binding and Development of New Biological Active Compounds. Current Medicinal Chemistry, 2006, 13, 3697-3703.	1.2	43
96	Structure of a Membrane-binding Domain from a Non-enveloped Animal Virus. Journal of Biological Chemistry, 2006, 281, 29278-29286.	1.6	25
97	Structural Basis for the Interaction of a Vascular Endothelial Growth Factor Mimic Peptide Motif and Its Corresponding Receptors. Chemistry and Biology, 2005, 12, 1075-1083.	6.2	40
98	Study of the effect of the peptide loading and solvent system in SPPS by HRMAS-NMR. Journal of Peptide Science, 2005, 11, 556-563.	0.8	9
99	Controlling Î²-Amyloid Oligomerization by the Use of Naphthalene Sulfonates. Journal of Biological Chemistry, 2005, 280, 34747-34754.	1.6	60
100	Letter to Editor: Solution structure of the HPV-16 E2 DNA binding domain, a transcriptional regulator with a dimeric Î²-barrel fold. Journal of Biomolecular NMR, 2004, 30, 211-214.	1.6	25
101	The bZIP Region of the Plant Transcription Factor Opaque-2 Forms Stable Homodimers in Solution and Retains Its Helical Structure upon Subunit Dissociationâ€. Biochemistry, 2004, 43, 4862-4868.	1.2	12
102	Correlation between conformation and antibody binding: NMR structure of cross-reactive peptides fromT. cruzi, human andL. braziliensis. FEBS Letters, 2004, 560, 134-140.	1.3	14
103	Conversion of Wild-type p53 Core Domain into a Conformation that Mimics a Hot-spot Mutant. Journal of Molecular Biology, 2003, 333, 443-451.	2.0	41
104	High-throughput screening of structural proteomics targets using NMR. FEBS Letters, 2003, 552, 207-213.	1.3	33
105	Structural Studies of MS2 Bacteriophage Virus Particle Disassembly by Nuclear Magnetic Resonance Relaxation Measurements. Biophysical Journal, 2003, 84, 3894-3903.	0.2	8
106	Production of the active antifungal Pisum sativum defensin 1 (Psd1) in Pichia pastoris: overcoming the inefficiency of the STE13 protease. Protein Expression and Purification, 2003, 31, 115-122.	0.6	87
107	NMR Structure of PW2 Bound to SDS Micelles. Journal of Biological Chemistry, 2002, 277, 36351-36356.	1.6	32
108	Solution structure of Pisum sativum defensin 1 by high resolution NMR: plant defensins, identical backbone with different mechanisms of action 1 1Edited by M. F. Summers. Journal of Molecular Biology, 2002, 315, 749-757.	2.0	135

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109	High-Risk (HPV16) Human Papillomavirus E7 Oncoprotein Is Highly Stable and Extended, with Conformational Transitions that Could Explain Its Multiple Cellular Binding Partners. Biochemistry, 2002, 41, 10510-10518.	1.2	58
110	cDNA Cloning and Heterologous Expression of Functional Cysteine-Rich Antifungal Protein Psd1 in the Yeast Pichia pastoris. Archives of Biochemistry and Biophysics, 2001, 395, 199-207.	1.4	55
111	Selectively Labeling the Heterologous Protein in Escherichia coli for NMR Studies: A Strategy to Speed Up NMR Spectroscopy. Journal of Magnetic Resonance, 2001, 148, 142-146.	1.2	26
112	Virus Maturation Targets the Protein Capsid to Concerted Disassembly and Unfolding. Journal of Biological Chemistry, 2000, 275, 16037-16043.	1.6	29
113	fd coat protein structure in membrane environments: structural dynamics of the loop between the hydrophobic trans-membrane helix and the amphipathic in-plane helix. Journal of Molecular Biology, 1997, 270, 481-495.	2.0	110
114	Measurement of1HT1ïn a Uniformly15N-Labeled Protein in Solution with Heteronuclear Two-Dimensional Spectroscopy. Journal of Magnetic Resonance, 1997, 124, 509-511.	1.2	7
115	Solvent-induced changes in the photophysical properties of N-alkylphthalimides II. Temperature and acidity effects. Journal of Photochemistry and Photobiology A: Chemistry, 1991, 58, 289-294.	2.0	14