

David Pantoja-Uceda

List of Publications by Year in descending order

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53
papers

1,297
citations

331670

21
h-index

395702

33
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59
all docs

59
docs citations

59
times ranked

1947
citing authors

#	ARTICLE	IF	CITATIONS
1	NMR assignments for the C-terminal domain of human TDP-43. <i>Biomolecular NMR Assignments</i> , 2021, 15, 177-181.	0.8	6
2	Phe-Gly motifs drive fibrillization of TDP-43's prion-like domain condensates. <i>PLoS Biology</i> , 2021, 19, e3001198.	5.6	17
3	Aromatic and aliphatic residues of the disordered region of TDP-43 are on a fast track for self-assembly. <i>Biochemical and Biophysical Research Communications</i> , 2021, 578, 110-114.	2.1	6
4	Conformational Priming of RepA-WH1 for Functional Amyloid Conversion Detected by NMR Spectroscopy. <i>Structure</i> , 2020, 28, 336-347.e4.	3.3	6
5	The isolated C-terminal nuclear localization sequence of the breast cancer metastasis suppressor 1 is disordered. <i>Archives of Biochemistry and Biophysics</i> , 2019, 664, 95-101.	3.0	10
6	Backbone assignment of cytochrome PccH, a crucial protein for microbial electrosynthesis in <i>Geobacter sulfurreducens</i> . <i>Biomolecular NMR Assignments</i> , 2019, 13, 321-326.	0.8	6
7	Solution conformation of a cohesin module and its scaffoldin linker from a prototypical cellulosome. <i>Archives of Biochemistry and Biophysics</i> , 2018, 644, 1-7.	3.0	5
8	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. <i>Journal of Biomolecular NMR</i> , 2018, 72, 139-148.	2.8	12
9	The Singular NMR Fingerprint of a Polyproline II Helical Bundle. <i>Journal of the American Chemical Society</i> , 2018, 140, 16988-17000.	13.7	30
10	Insights into the mechanism of Apoptin's exquisitely selective anti-tumor action from atomic level characterization of its conformation and dynamics. <i>Archives of Biochemistry and Biophysics</i> , 2017, 614, 53-64.	3.0	3
11	Solution structure and dynamics of the outer membrane cytochrome OmcF from <i>Geobacter sulfurreducens</i> . <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2017, 1858, 733-741.	1.0	15
12	Point mutations in the N-terminal domain of transactive response DNA-binding protein 43 kDa (TDP-43) compromise its stability, dimerization, and functions. <i>Journal of Biological Chemistry</i> , 2017, 292, 11992-12006.	3.4	66
13	De novo active sites for resurrected Precambrian enzymes. <i>Nature Communications</i> , 2017, 8, 16113.	12.8	60
14	NMR Insights into the Structure-Function Relationships in the Binding of Melanocortin Analogues to the MC1R Receptor. <i>Molecules</i> , 2017, 22, 1189.	3.8	3
15	Modular Architecture and Unique Teichoic Acid Recognition Features of Choline-Binding Protein L (Cbpl) Contributing to Pneumococcal Pathogenesis. <i>Scientific Reports</i> , 2016, 6, 38094.	3.3	32
16	Dissecting the Binding between Glutamine Synthetase and Its Two Natively Unfolded Protein Inhibitors. <i>Biochemistry</i> , 2016, 55, 3370-3382.	2.5	14
17	The TDP-43 N-terminal domain structure at high resolution. <i>FEBS Journal</i> , 2016, 283, 1242-1260.	4.7	121
18	DMSO affects Δ^2 's conformation and interactions with aggregation inhibitors as revealed by NMR. <i>RSC Advances</i> , 2015, 5, 69761-69764.	3.6	7

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19	New ¹³ C-detected experiments for the assignment of intrinsically disordered proteins. <i>Journal of Biomolecular NMR</i> , 2014, 59, 43-50.	2.8	25
20	A suite of amino acid residue type classification pulse sequences for ¹³ C-detected NMR of proteins. <i>Journal of Magnetic Resonance</i> , 2013, 234, 190-196.	2.1	7
21	Structure of a simplified ¹² I-hairpin and its ATP complex. <i>Archives of Biochemistry and Biophysics</i> , 2013, 537, 62-71.	3.0	6
22	Design, Synthesis, and Functional Evaluation of Leukocyte Function Associated Antigen-1 Antagonists in Early and Late Stages of Cancer Development. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 735-747.	6.4	21
23	Direct correlation of consecutive C ¹⁵ N groups in proteins: a method for the assignment of intrinsically disordered proteins. <i>Journal of Biomolecular NMR</i> , 2013, 57, 57-63.	2.8	28
24	Deciphering the Binding between Nupr1 and MSL1 and Their DNA-Repairing Activity. <i>PLoS ONE</i> , 2013, 8, e78101.	2.5	33
25	New amino acid residue type identification experiments valid for protonated and deuterated proteins. <i>Journal of Biomolecular NMR</i> , 2012, 54, 145-153.	2.8	17
26	NMR Structural Analysis of MC1R-Targeted Rhenium(I) Metallopeptides and Biological Evaluation of ^{99m} Tc(I) Congeners. <i>Organometallics</i> , 2012, 31, 5929-5939.	2.3	7
27	Proliferating Cell Nuclear Antigen (PCNA) Interactions in Solution Studied by NMR. <i>PLoS ONE</i> , 2012, 7, e48390.	2.5	27
28	Oxidative Folding and Structural Analyses of a Kunitz-Related Inhibitor and Its Disulfide Intermediates: Functional Implications. <i>Journal of Molecular Biology</i> , 2011, 414, 427-441.	4.2	20
29	Selective observation of Asp and Glu resonances in ¹³ CO detected experiments. <i>Magnetic Resonance in Chemistry</i> , 2011, 49, 558-561.	1.9	3
30	Simultaneous measurement of N ¹⁵ H and C ¹³ H coupling constants in proteins. <i>Magnetic Resonance in Chemistry</i> , 2010, 48, 20-24.	1.9	1
31	Solution Structure of Human Growth Arrest and DNA Damage 45 ¹ (Gadd45 ¹) and Its Interactions with Proliferating Cell Nuclear Antigen (PCNA) and Aurora A Kinase. <i>Journal of Biological Chemistry</i> , 2010, 285, 22196-22201.	3.4	25
32	Deciphering the Structural Basis That Guides the Oxidative Folding of Leech-derived Trypsin Inhibitor. <i>Journal of Biological Chemistry</i> , 2009, 284, 35612-35620.	3.4	15
33	Aliasing in reduced dimensionality NMR spectra: (3,2)D HNHA and (4,2)D HN(COCA)NH experiments as examples. <i>Journal of Biomolecular NMR</i> , 2009, 45, 351-356.	2.8	15
34	A Conserved Docking Surface on Calcineurin Mediates Interaction with Substrates and Immunosuppressants. <i>Molecular Cell</i> , 2009, 33, 616-626.	9.7	108
35	Solution structure of the rhodanese homology domain At4g01050(175-295) from <i>Arabidopsis thaliana</i> . <i>Protein Science</i> , 2009, 14, 224-230.	7.6	24
36	NMR assignment and secondary structure of human growth arrest and DNA damage ¹ protein (Gadd45 ¹). <i>Biomolecular NMR Assignments</i> , 2008, 2, 139-142.	0.8	5

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37	Design of a bivalent peptide with two independent elements of secondary structure able to fold autonomously. <i>Journal of Peptide Science</i> , 2008, 14, 845-854.	1.4	10
38	Amino acid type identification in NMR spectra of proteins via $\hat{1}^2$ - and $\hat{1}^3$ -carbon edited experiments. <i>Journal of Magnetic Resonance</i> , 2008, 195, 187-195.	2.1	30
39	The NMR Structure and Dynamics of the Two-Domain Tick Carboxypeptidase Inhibitor Reveal Flexibility in Its Free Form and Stiffness upon Binding to Human Carboxypeptidase B. <i>Biochemistry</i> , 2008, 47, 7066-7078.	2.5	19
40	The NMR Structures of the Major Intermediates of the Two-domain Tick Carboxypeptidase Inhibitor Reveal Symmetry in Its Folding and Unfolding Pathways. <i>Journal of Biological Chemistry</i> , 2008, 283, 27110-27120.	3.4	9
41	Molecular Basis of Histone H3K4me3 Recognition by ING4. <i>Journal of Biological Chemistry</i> , 2008, 283, 15956-15964.	3.4	71
42	Selective Pressures at a Codon-level Predict Deleterious Mutations in Human Disease Genes. <i>Journal of Molecular Biology</i> , 2006, 358, 1390-1404.	4.2	42
43	$\hat{1}^2$ -Hairpin formation in aqueous solution and in the presence of trifluoroethanol: A1H and13C nuclear magnetic resonance conformational study of designed peptides. <i>Biopolymers</i> , 2005, 79, 150-162.	2.4	46
44	Refined NMR structure of $\hat{1}^3$ -sarcin by 15N - ^1H residual dipolar couplings. <i>European Biophysics Journal</i> , 2005, 34, 1057-1065.	2.2	9
45	Solution structure of the Src homology 2 domain from the human feline sarcoma oncogene Fes. <i>Journal of Biomolecular NMR</i> , 2005, 31, 357-361.	2.8	16
46	Letter to the Editor: NMR assignment of the hypothetical ENTH-VHS domain At3g16270 from <i>Arabidopsis thaliana</i> . <i>Journal of Biomolecular NMR</i> , 2004, 29, 205-206.	2.8	18
47	Letter to the Editor: NMR assignment of the hypothetical rhodanese domain At4g01050 from <i>Arabidopsis thaliana</i> . <i>Journal of Biomolecular NMR</i> , 2004, 29, 207-208.	2.8	12
48	Letter to the Editor: NMR assignment of the SH2 domain from the human feline sarcoma oncogene FES. <i>Journal of Biomolecular NMR</i> , 2004, 30, 463-464.	2.8	13
49	Solution Structure and Stability against Digestion of rproBnlb, a Recombinant 2S Albumin from Rapeseed: A Relationship to Its Allergenic Properties. <i>Biochemistry</i> , 2004, 43, 16036-16045.	2.5	44
50	Solution Structure of a Methionine-Rich 2S Albumin from Sunflower Seeds: Relationship to Its Allergenic and Emulsifying Properties. <i>Biochemistry</i> , 2004, 43, 6976-6986.	2.5	50
51	Solution Structure of RicC3, a 2S Albumin Storage Protein from <i>Ricinus communis</i> . <i>Biochemistry</i> , 2003, 42, 13839-13847.	2.5	70
52	Solution structure of allergenic 2 S albumins. <i>Biochemical Society Transactions</i> , 2002, 30, 919-924.	3.4	24
53	Assignment of ^1H and ^{15}N resonances and secondary structure of the recombinant RicC3 of 2S albumin storage protein from <i>Ricinus communis</i> . <i>Journal of Biomolecular NMR</i> , 2002, 23, 331-332.	2.8	1