

Jose Manuel PÃ©rez-Cañadillas

List of Publications by Year in descending order

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27
papers

1,151
citations

516710

16
h-index

580821

25
g-index

29
all docs

29
docs citations

29
times ranked

1380
citing authors

#	ARTICLE	IF	CITATIONS
1	Solution structure of p53 core domain: Structural basis for its instability. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 2109-2114.	7.1	157
2	Recognition of GU-rich polyadenylation regulatory elements by human CstF-64 protein. EMBO Journal, 2003, 22, 2821-2830.	7.8	133
3	Core domain interactions in full-length p53 in solution. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 2115-2119.	7.1	91
4	Grabbing the message: structural basis of mRNA 3'UTR recognition by Hrp1. EMBO Journal, 2006, 25, 3167-3178.	7.8	79
5	NMR Solution Structure of Murine CCL20/MIP-3 β , a Chemokine That Specifically Chemoattracts Immature Dendritic Cells and Lymphocytes through Its Highly Specific Interaction with the β 2-Chemokine Receptor CCR6. Journal of Biological Chemistry, 2001, 276, 28372-28379.	3.4	77
6	Exploring the Use of Conformationally Locked Aminoglycosides as a New Strategy to Overcome Bacterial Resistance. Journal of the American Chemical Society, 2006, 128, 100-116.	13.7	73
7	Characterization of pKa Values and Titration Shifts in the Cytotoxic Ribonuclease β -Sarcin by NMR. Relationship between Electrostatic Interactions, Structure, and Catalytic Function. Biochemistry, 1998, 37, 15865-15876.	2.5	72
8	The highly refined solution structure of the cytotoxic ribonuclease β -sarcin reveals the structural requirements for substrate recognition and ribonucleolytic activity. Edited by M. F. Summers. Journal of Molecular Biology, 2000, 299, 1061-1073.	4.2	66
9	Protein and RNA Dynamics Play Key Roles in Determining the Specific Recognition of GU-rich Polyadenylation Regulatory Elements by Human Cstf-64 Protein. Journal of Molecular Biology, 2005, 347, 719-733.	4.2	57
10	NMR Structure of the β -Hemoglobin Stabilizing Protein. Journal of Biological Chemistry, 2004, 279, 34963-34970.	3.4	52
11	The C-terminal Domains of Vertebrate CstF-64 and Its Yeast Orthologue Rna15 Form a New Structure Critical for mRNA 3'-End Processing. Journal of Biological Chemistry, 2007, 282, 2101-2115.	3.4	50
12	Role of histidine-50, glutamic acid-96, and histidine-137 in the ribonucleolytic mechanism of the ribotoxin β -sarcin. , 1999, 37, 474-484.		47
13	Assignment of the contribution of the tryptophan residues to the spectroscopic and functional properties of the ribotoxin β -sarcin. Proteins: Structure, Function and Bioinformatics, 2000, 41, 350-361.	2.6	29
14	Solution structure and dynamics of ribonuclease Sa. Proteins: Structure, Function and Bioinformatics, 2001, 44, 200-211.	2.6	28
15	Gbp2 interacts with THO/TREX through a novel type of RRM domain. Nucleic Acids Research, 2016, 44, 437-448.	14.5	26
16	Backbone dynamics of the cytotoxic ribonuclease alpha-sarcin by 15N NMR relaxation methods. Journal of Biomolecular NMR, 2002, 24, 301-316.	2.8	17
17	Dissecting Structural and Electrostatic Interactions of Charged Groups in β -Sarcin. An NMR Study of Some Mutants Involving the Catalytic Residues. Biochemistry, 2003, 42, 13122-13133.	2.5	17
18	Leucine 145 of the ribotoxin β -sarcin plays a key role for determining the specificity of the ribosome-inactivating activity of the protein. Protein Science, 2003, 12, 161-169.	7.6	16

#	ARTICLE	IF	CITATIONS
19	The structure of transcription termination factor Nrd1 reveals an original mode for GUAA recognition. <i>Nucleic Acids Research</i> , 2017, 45, 10293-10305.	14.5	12
20	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, 5970-5981.	3.3	11
21	Pub1p C-Terminal RRM Domain Interacts with Tif4631p through a Conserved Region Neighbouring the Pab1p Binding Site. <i>PLoS ONE</i> , 2011, 6, e24481.	2.5	10
22	NMR structure note: PHD domain from death inducer obliterator protein and its interaction with H3K4me3. <i>Journal of Biomolecular NMR</i> , 2013, 56, 183-190.	2.8	9
23	Two Singular Types of CCCH Tandem Zinc Finger in Nab2p Contribute to Polyadenosine RNA Recognition. <i>Structure</i> , 2013, 21, 1800-1811.	3.3	7
24	The RBS1 domain of Gemin5 is intrinsically unstructured and interacts with RNA through conserved Arg and aromatic residues. <i>RNA Biology</i> , 2021, 18, 496-506.	3.1	7
25	Mip6 binds directly to the Mex67 UBA domain to maintain low levels of Msn2/4 stress-dependent mRNAs. <i>EMBO Reports</i> , 2019, 20, e47964.	4.5	6
26	Structural basis of Nrd1-Nab3 heterodimerization. <i>Life Science Alliance</i> , 2022, 5, e202101252.	2.8	2
27	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, .	3.3	0