

Maria J Macias

List of Publications by Year in descending order

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66
papers

5,013
citations

186265

28
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114465

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73
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docs citations

73
times ranked

8795
citing authors

#	ARTICLE	IF	CITATIONS
1	HTSDSF Explorer, A Novel Tool to Analyze High-throughput DSF Screenings. <i>Journal of Molecular Biology</i> , 2022, 434, 167372.	4.2	12
2	Conformational ensemble of the TNF-derived peptide solnatide in solution. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2082-2090.	4.1	5
3	Controlling oncogenic KRAS signaling pathways with a Palladium-responsive peptide. <i>Communications Chemistry</i> , 2022, 5, .	4.5	1
4	Unveiling the dimer/monomer propensities of Smad MH1-DNA complexes. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 632-646.	4.1	6
5	Structures of the germline-specific Deadhead and thioredoxin T proteins from <i>Drosophila melanogaster</i> reveal unique features among thioredoxins. <i>IUCr</i> , 2021, 8, 281-294.	2.2	4
6	Structure-based design of a Cortistatin analogue with immunomodulatory activity in models of inflammatory bowel disease. <i>Nature Communications</i> , 2021, 12, 1869.	12.8	16
7	Conformational landscape of multidomain SMAD proteins. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5210-5224.	4.1	9
8	Synthesis of Stable Cholesteryl-Polyethylene Glycol-Peptide Conjugates with Non-Disperse Polyethylene Glycol Lengths. <i>ACS Omega</i> , 2020, 5, 5508-5519.	3.5	3
9	Binding site plasticity in viral PPxY Late domain recognition by the third WW domain of human NEDD4. <i>Scientific Reports</i> , 2019, 9, 15076.	3.3	12
10	Structural basis for distinct roles of SMAD2 and SMAD3 in FOXH1 pioneer-directed TGF- β 2 signaling. <i>Genes and Development</i> , 2019, 33, 1506-1524.	5.9	61
11	TGIF1 homeodomain interacts with Smad MH1 domain and represses TGF- β 2 signaling. <i>Nucleic Acids Research</i> , 2018, 46, 9220-9235.	14.5	37
12	The synthesis of an EDTA-like chelating peptidomimetic building block suitable for solid-phase peptide synthesis. <i>Chemical Communications</i> , 2017, 53, 2634-2636.	4.1	1
13	Structural basis for genome wide recognition of 5-bp GC motifs by SMAD transcription factors. <i>Nature Communications</i> , 2017, 8, 2070.	12.8	81
14	Peptide aromatic interactions modulated by fluorinated residues: Synthesis, structure and biological activity of Somatostatin analogs containing 3-(3,5-difluorophenyl)-alanine. <i>Scientific Reports</i> , 2016, 6, 27285.	3.3	10
15	ADP-ribose-derived nuclear ATP synthesis by NUDIX5 is required for chromatin remodeling. <i>Science</i> , 2016, 352, 1221-1225.	12.6	141
16	Structural Analysis of the Pin1-CPEB1 interaction and its potential role in CPEB1 degradation. <i>Scientific Reports</i> , 2015, 5, 14990.	3.3	14
17	Addition of HOBt improves the conversion of thioester-Amine chemical ligation. <i>Biopolymers</i> , 2015, 104, 693-702.	2.4	1
18	Structure of the N-terminal domain of the protein Expansion: an 'Expansion' to the Smad MH2 fold. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 844-853.	2.5	7

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19	Structural determinants of Smad function in TGF- β^2 signaling. Trends in Biochemical Sciences, 2015, 40, 296-308.	7.5	297
20	Preventing fibril formation of a protein by selective mutation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13549-13554.	7.1	17
21	Identification of novel non-canonical RNA-binding sites in Gemin5 involved in internal initiation of translation. Nucleic Acids Research, 2014, 42, 5742-5754.	14.5	47
22	RNA recognition and self-association of CPEB4 is mediated by its tandem RRM domains. Nucleic Acids Research, 2014, 42, 10185-10195.	14.5	10
23	Folding kinetics of WW domains with the united residue force field for bridging microscopic motions and experimental measurements. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18243-18248.	7.1	36
24	Structural Basis of the Activation and Degradation Mechanisms of the E3 Ubiquitin Ligase Nedd4L. Structure, 2014, 22, 1446-1457.	3.3	54
25	A tetradecapeptide somatostatin dicarba-analog: Synthesis, structural impact and biological activity. Bioorganic and Medicinal Chemistry Letters, 2014, 24, 103-107.	2.2	23
26	Insights into Structure-Activity Relationships of Somatostatin Analogs Containing Mesitylalanine. Molecules, 2013, 18, 14564-14584.	3.8	12
27	The FF4 and FF5 Domains of Transcription Elongation Regulator 1 (TCERG1) Target Proteins to the Periphery of Speckles. Journal of Biological Chemistry, 2012, 287, 17789-17800.	3.4	12
28	Structural Basis for the Versatile Interactions of Smad7 with Regulator WW Domains in TGF- β^2 Pathways. Structure, 2012, 20, 1726-1736.	3.3	93
29	Innenrücktitelbild: Fine-tuning the π - π Aromatic Interactions in Peptides: Somatostatin Analogues Containing Mesityl Alanine (Angew. Chem. 8/2012). Angewandte Chemie, 2012, 124, 2015-2015.	2.0	0
30	Fine-tuning the π - π Aromatic Interactions in Peptides: Somatostatin Analogues Containing Mesityl Alanine. Angewandte Chemie - International Edition, 2012, 51, 1820-1825.	13.8	19
31	Inside Back Cover: Fine-tuning the π - π Aromatic Interactions in Peptides: Somatostatin Analogues Containing Mesityl Alanine (Angew. Chem. Int. Ed. 8/2012). Angewandte Chemie - International Edition, 2012, 51, 1977-1977.	13.8	0
32	DOR/Tp53inp2 and Tp53inp1 Constitute a Metazoan Gene Family Encoding Dual Regulators of Autophagy and Transcription. PLoS ONE, 2012, 7, e34034.	2.5	51
33	SSTR1 and SSTR3 Selective Somatostatin Analogues. ChemBioChem, 2011, 12, 625-632.	2.6	14
34	A Smad action turnover switch operated by WW domain readers of a phosphoserine code. Genes and Development, 2011, 25, 1275-1288.	5.9	207
35	Solution structure of the fourth FF domain of yeast Prp40 splicing factor. Proteins: Structure, Function and Bioinformatics, 2009, 77, 1000-1003.	2.6	8
36	Nuclear CDKs Drive Smad Transcriptional Activation and Turnover in BMP and TGF- β^2 Pathways. Cell, 2009, 139, 757-769.	28.9	627

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37	NMR Structural Studies on Human p190-A RhoGAPFF1 Revealed that Domain Phosphorylation by the PDGF-Receptor Requires Its Previous Unfolding. <i>Journal of Molecular Biology</i> , 2009, 389, 230-237.	4.2	8
38	Ubiquitin Ligase Nedd4L Targets Activated Smad2/3 to Limit TGF- β Signaling. <i>Molecular Cell</i> , 2009, 36, 457-468.	9.7	306
39	Solution structure of the yeast URN1 splicing factor FF domain: Comparative analysis of charge distributions in FF domain structures of FFs and SURPs, two domains with a similar fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 1001-1009.	2.6	22
40	Structure of the Dimeric Exonuclease TREX1 in Complex with DNA Displays a Proline-rich Binding Site for WW Domains. <i>Journal of Biological Chemistry</i> , 2007, 282, 14547-14557.	3.4	45
41	Myotonia-related mutations in the distal C-terminus of ClC-1 and ClC-0 chloride channels affect the structure of a poly-proline helix. <i>Biochemical Journal</i> , 2007, 403, 79-87.	3.7	23
42	Structural Characterization of a New Binding Motif and a Novel Binding Mode in Group 2 WW Domains. <i>Journal of Molecular Biology</i> , 2007, 373, 1255-1268.	4.2	15
43	NMR Structural Studies of the ItchWW3 Domain Reveal that Phosphorylation at T30 Inhibits the Interaction with PPxY-Containing Ligands. <i>Structure</i> , 2007, 15, 473-483.	3.3	25
44	The Structure of Prp40 FF1 Domain and Its Interaction with the crn-TPR1 Motif of Clf1 Gives a New Insight into the Binding Mode of FF Domains. <i>Journal of Biological Chemistry</i> , 2006, 281, 356-364.	3.4	32
45	Phosphorylation of either Ser16 or Thr30 does not disrupt the structure of the Itch E3 ubiquitin ligase third WW domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 558-560.	2.6	4
46	Structure and dynamics of the human pleckstrin DEP domain: Distinct molecular features of a novel DEP domain subfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 354-366.	2.6	27
47	WW and SH3 domains, two different scaffolds to recognize proline-rich ligands. <i>FEBS Letters</i> , 2002, 513, 30-37.	2.8	431
48	Solution Structure and Ligand Recognition of the WW Domain Pair of the Yeast Splicing Factor Prp40. <i>Journal of Molecular Biology</i> , 2002, 324, 807-822.	4.2	73
49	Solution structures of the YAP65 WW domain and the variant L30 K in complex with the peptides GTPPPPYTVG, N-(n-octyl)-GPPPY and PLPPY and the application of peptide libraries reveal a minimal binding epitope. <i>Journal of Molecular Biology</i> , 2001, 314, 1147-1156.	4.2	106
50	SYNTHESIS AND PROPERTIES OF OLIGONUCLEOTIDES CONTAINING 8-BROMO-2'-DEOXYGUANOSINE. <i>Nucleosides, Nucleotides and Nucleic Acids</i> , 2001, 20, 251-260.	1.1	11
51	Ultrafast folding of WW domains without structured aromatic clusters in the denatured state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 13002-13007.	7.1	94
52	Structural analysis of WW domains and design of a WW prototype. <i>Nature Structural Biology</i> , 2000, 7, 375-379.	9.7	208
53	Theoretical calculations, synthesis and base pairing properties of oligonucleotides containing 8-amino-2'-deoxyadenosine. <i>Nucleic Acids Research</i> , 1999, 27, 1991-1998.	14.5	31
54	A novel NMR experiment for the sequential assignment of proline residues and proline stretches in $^{13}\text{C}/^{15}\text{N}$ -labeled proteins. <i>Journal of Biomolecular NMR</i> , 1999, 13, 381-385.	2.8	29

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55	The three-dimensional structure of the HRDC domain and implications for the Werner and Bloom syndrome proteins. <i>Structure</i> , 1999, 7, 1557-1566.	3.3	126
56	A tale of two secondary structure elements: when a β -hairpin becomes an α -helix 1 Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1999, 292, 389-401.	4.2	31
57	Specific interactions between the syntrophin PDZ domain and voltage-gated sodium channels. <i>Nature Structural Biology</i> , 1998, 5, 19-24.	9.7	217
58	Furanoeremophilanes and a bakkenolide from <i>Senecio auricula</i> var. <i>major</i> . <i>Phytochemistry</i> , 1998, 47, 57-61.	2.9	29
59	Automated NOESY interpretation with ambiguous distance restraints: the refined NMR solution structure of the pleckstrin homology domain from β -spectrin 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1997, 269, 408-422.	4.2	414
60	A small region in phosphducin inhibits G-protein beta gamma -subunit function. <i>EMBO Journal</i> , 1997, 16, 4908-4915.	7.8	36
61	Structure of the WW domain of a kinase-associated protein complexed with a proline-rich peptide. <i>Nature</i> , 1996, 382, 646-649.	27.8	426
62	Gibberellin-like activity of some tetracyclic diterpenoids from <i>Elaeoselinum</i> species and their derivatives. <i>Phytochemistry</i> , 1994, 37, 635-639.	2.9	13
63	Phenylpropanoids from <i>Pimpinella villosa</i> . <i>Phytochemistry</i> , 1994, 37, 539-542.	2.9	8
64	Structure of the pleckstrin homology domain from β -spectrin. <i>Nature</i> , 1994, 369, 675-677.	27.8	256
65	Carbon-13 nuclear magnetic resonance spectra of some tetracyclic diterpenoids isolated from <i>Elaeoselinum</i> species. <i>Phytochemical Analysis</i> , 1993, 4, 19-24.	2.4	6
66	New Kaurane Diterpenoids from the Aerial Parts of <i>Distichoselinum tenuifolium</i> . <i>Journal of Natural Products</i> , 1991, 54, 866-869.	3.0	9