

Jose C Martinez

List of Publications by Year in descending order

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58
papers

1,873
citations

430442

18
h-index

301761

39
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58
all docs

58
docs citations

58
times ranked

1351
citing authors

#	ARTICLE	IF	CITATIONS
1	Blocking PSD95&PDZ3's amyloidogenesis through point mutations that inhibit high&temperature reversible oligomerization (RO). FEBS Journal, 2022, 289, 3205-3216.	2.2	2
2	Phage display identification of nanomolar ligands for human NEDD4-WW3: Energetic and dynamic implications for the development of broad-spectrum antivirals. International Journal of Biological Macromolecules, 2022, 207, 308-323.	3.6	3
3	Understanding binding affinity and specificity of modular protein domains: A focus in ligand design for the polyproline-binding families. Advances in Protein Chemistry and Structural Biology, 2022, 130, 161-188.	1.0	0
4	Reverse Engineering Analysis of the High-Temperature Reversible Oligomerization and Amyloidogenicity of PSD95-PDZ3. Molecules, 2022, 27, 2813.	1.7	2
5	A Thermodynamic Analysis of the Binding Specificity between Four Human PDZ Domains and Eight Host, Viral and Designed Ligands. Biomolecules, 2021, 11, 1071.	1.8	1
6	Stability, conformational plasticity, oligomerization behaviour and equilibrium unfolding intermediates of the Ebola virus matrix protein VP40. Journal of Biomolecular Structure and Dynamics, 2020, 38, 4289-4303.	2.0	5
7	PDZ/PDZ interaction between PSD&95 and nNOS neuronal proteins. Journal of Molecular Recognition, 2020, 33, e2826.	1.1	10
8	Lysozyme crystals dyed with bromophenol blue: where has the dye gone?. Acta Crystallographica Section D: Structural Biology, 2020, 76, 845-856.	1.1	2
9	Thermodynamic Analysis of Point Mutations Inhibiting High-Temperature Reversible Oligomerization of PDZ3. Biophysical Journal, 2020, 119, 1391-1401.	0.2	6
10	The effect of an engineered ATCUN motif on the structure and biophysical properties of the SH3 domain of c-Src tyrosine kinase. Journal of Biological Inorganic Chemistry, 2020, 25, 621-634.	1.1	1
11	Conformational changes in the third PDZ domain of the neuronal postsynaptic density protein 95. Acta Crystallographica Section D: Structural Biology, 2019, 75, 381-391.	1.1	11
12	Ultrafast folding kinetics of WW domains reveal how the amino acid sequence determines the speed limit to protein folding. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8137-8142.	3.3	13
13	Approaching the thermodynamic view of protein folding through the reproduction of Anfinsen's experiment by undergraduate physical biochemistry students. Biochemistry and Molecular Biology Education, 2018, 46, 262-269.	0.5	0
14	Protein Folding Cooperativity and Thermodynamic Barriers of the Simplest β^2 -Sheet Fold: A Survey of WW Domains. Journal of Physical Chemistry B, 2018, 122, 11058-11071.	1.2	11
15	Understanding the contribution of disulfide bridges to the folding and misfolding of an anti- β^2 scFv. Protein Science, 2017, 26, 1138-1149.	3.1	12
16	Towards the improvement in stability of an anti- β^2 single-chain variable fragment, scFv-h3D6, as a way to enhance its therapeutic potential. Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis, 2017, 24, 167-175.	1.4	8
17	Chapter 12. Biocalorimetry: Differential Scanning Calorimetry of Protein Solutions. , 2017, , 315-335.		0
18	Common features in the unfolding and misfolding of PDZ domains and beyond: the modulatory effect of domain swapping and extra-elements. Scientific Reports, 2016, 6, 19242.	1.6	9

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19	Post-Translational Modifications Modulate Ligand Recognition by the Third PDZ Domain of the MAGUK Protein PSD-95. PLoS ONE, 2014, 9, e90030.	1.1	19
20	A thermodynamic study of the third PDZ domain of MAGUK neuronal protein PSD-95 reveals a complex three-state folding behavior. Biophysical Chemistry, 2014, 185, 1-7.	1.5	11
21	Alteration of the C-Terminal Ligand Specificity of the Erbin PDZ Domain by Allosteric Mutational Effects. Journal of Molecular Biology, 2014, 426, 3500-3508.	2.0	17
22	The Impact of Extra-Domain Structures and Post-Translational Modifications in the Folding/Misfolding Behaviour of the Third PDZ Domain of MAGUK Neuronal Protein PSD-95. PLoS ONE, 2014, 9, e98124.	1.1	8
23	The Interconversion between a Flexible β^2 -Sheet and a Fibril β^2 -Arrangement Constitutes the Main Conformational Event during Misfolding of PSD95-PDZ3 Domain. Biophysical Journal, 2012, 103, 738-747.	0.2	11
24	Thermodynamic Impact of Embedded Water Molecules in the Unfolding of Human CD2BP2-GYF Domain. Journal of Physical Chemistry B, 2012, 116, 7168-7175.	1.2	5
25	Understanding the polymorphic behaviour of a mutant of the β^1 -spectrin SH3 domain by means of two 1.1 \AA ... resolution structures. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 189-196.	2.5	7
26	A comparative analysis of the folding and misfolding pathways of the third PDZ domain of PSD95 investigated under different pH conditions. Biophysical Chemistry, 2011, 158, 104-110.	1.5	15
27	An Oligomeric Equilibrium Intermediate as the Precursory Nucleus of Globular and Fibrillar Supramacromolecular Assemblies in a PDZ Domain. Biophysical Journal, 2010, 99, 263-272.	0.2	28
28	Role of Interfacial Water Molecules in Proline-rich Ligand Recognition by the Src Homology 3 Domain of Abl. Journal of Biological Chemistry, 2010, 285, 2823-2833.	1.6	30
29	Novel conformational aspects of the third PDZ domain of the neuronal post-synaptic density-95 protein revealed from two 1.4 \AA ... X-ray structures. Journal of Structural Biology, 2010, 170, 565-569.	1.3	21
30	Evaluation of folding co-operativity of a chimeric protein based on the molecular recognition between polyproline ligands and SH3 domains. Protein Engineering, Design and Selection, 2009, 22, 597-606.	1.0	4
31	Thermodynamic Characterization of the Folding Equilibrium of the Human Nedd4-WW4 Domain: At the Frontiers of Cooperative Folding. Biochemistry, 2009, 48, 8712-8720.	1.2	20
32	An Error Analysis for Two-State Protein-Folding Kinetic Parameters and $\Delta\ddagger$ -Values: Progress toward Precision by Exploring pH Dependencies on Leffler Plots. Biophysical Journal, 2008, 94, 4393-4404.	0.2	3
33	Analysis of the Thermodynamics of Binding of an SH3 Domain to Proline-rich Peptides using a Chimeric Fusion Protein. Journal of Molecular Biology, 2008, 377, 117-135.	2.0	17
34	The high-resolution NMR structure of a single-chain chimeric protein mimicking a SH3-peptide complex. FEBS Letters, 2007, 581, 687-692.	1.3	16
35	Crystallization by capillary counter-diffusion and structure determination of the N114A mutant of the SH3 domain of Abl tyrosine kinase complexed with a high-affinity peptide ligand. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 646-652.	2.5	10
36	Structure of human TSG101 UEV domain. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 458-464.	2.5	17

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37	Kinetic analysis and modelling of the allosteric behaviour of liver and muscle glycogen phosphorylases. <i>Journal of Molecular Recognition</i> , 2006, 19, 451-457.	1.1	6
38	Binding curves by continuous gradient flow-mix calorimetry. <i>Thermochimica Acta</i> , 2005, 437, 140-144.	1.2	0
39	Thermodynamic Dissection of the Binding Energetics of Proline-rich Peptides to the Abl-SH3 Domain: Implications for Rational Ligand Design. <i>Journal of Molecular Biology</i> , 2004, 336, 527-537.	2.0	59
40	A Miniprotein Scaffold Used to Assemble the Polyproline II Binding Epitope Recognized by SH3 Domains. <i>Journal of Molecular Biology</i> , 2004, 342, 355-365.	2.0	33
41	A Thermodynamic and Kinetic Analysis of the Folding Pathway of an SH3 Domain Entropically Stabilised by a Redesigned Hydrophobic Core. <i>Journal of Molecular Biology</i> , 2003, 328, 221-233.	2.0	33
42	Structural cooperativity in the SH3 domain studied by site-directed mutagenesis and amide hydrogen exchange. <i>FEBS Letters</i> , 2003, 539, 125-130.	1.3	17
43	A binding event converted into a folding event. <i>FEBS Letters</i> , 2003, 553, 328-332.	1.3	12
44	pH dependence of the hydrogen exchange in the SH3 domain of Î±-spectrin. <i>FEBS Letters</i> , 2002, 514, 295-299.	1.3	13
45	The denaturation of circular enterocin AS-48 by urea and guanidinium hydrochloride. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2002, 1598, 98-107.	1.1	28
46	AS-48: a circular protein with an extremely stable globular structure. <i>FEBS Letters</i> , 2001, 505, 379-382.	1.3	36
47	Thermodynamic analysis of helix-engineered forms of the activation domain of human procarboxypeptidase A2. <i>FEBS Journal</i> , 2000, 267, 5891-5899.	0.2	13
48	Thermodynamic and structural characterization of Asn and Ala residues in the disallowed IIâ€² region of the Ramachandran plot. <i>Protein Science</i> , 2000, 9, 2322-2328.	3.1	32
49	The folding transition state between SH3 domains is conformationally restricted and evolutionarily conserved. , 1999, 6, 1010-1016.		311
50	Thermodynamic Analysis of Î±-spectrin SH3 and Two of Its Circular Permutants with Different Loop Lengths:â€” Discerning the Reasons for Rapid Folding in Proteins,. <i>Biochemistry</i> , 1999, 38, 549-559.	1.2	55
51	Obligatory steps in protein folding and the conformational diversity of the transition state. <i>Nature Structural and Molecular Biology</i> , 1998, 5, 721-729.	3.6	231
52	The DSC data analysis for small, single-domain proteins. Application to the SH3 domain. <i>Reactive and Functional Polymers</i> , 1998, 36, 221-225.	2.0	7
53	Structure of the transition state in the folding process of human procarboxypeptidase A2 activation domain. <i>Journal of Molecular Biology</i> , 1998, 283, 1027-1036.	2.0	165
54	A Calorimetric Study of the Thermal Stability of Barstar and Its Interaction with Barnase. <i>Biochemistry</i> , 1995, 34, 5224-5233.	1.2	49

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55	A Calorimetric Study of the Thermal Stability of Barnase and Its Interaction with 3'GMP. <i>Biochemistry</i> , 1994, 33, 3919-3926.	1.2	55
56	Thermodynamic and Kinetic Analysis of the SH3 Domain of Spectrin Shows a Two-State Folding Transition. <i>Biochemistry</i> , 1994, 33, 2142-2150.	1.2	294
57	Thermodynamic analysis of the chemotactic protein from <i>Escherichia coli</i> , CheY. <i>Biochemistry</i> , 1993, 32, 12906-12921.	1.2	61
58	Isothermal Titration Calorimetry: Thermodynamic Analysis of the Binding Thermograms of Molecular Recognition Events by Using Equilibrium Models. , 0, , .		8