

# 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  
g-index

58  
all docs

58  
docs citations

58  
times ranked

1351  
citing authors

#	ARTICLE	IF	CITATIONS
1	The folding transition state between SH3 domains is conformationally restricted and evolutionarily conserved. , 1999, 6, 1010-1016.		311
2	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
3	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
4	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
5	Thermodynamic analysis of the chemotactic protein from <i>Escherichia coli</i> , CheY. <i>Biochemistry</i> , 1993, 32, 12906-12921.	1.2	61
6	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
7	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
8	Thermodynamic Analysis of $\Delta\epsilon$ -spectrin SH3 and Two of Its Circular Permutants with Different Loop Lengths: Discerning the Reasons for Rapid Folding in Proteins. <i>Biochemistry</i> , 1999, 38, 549-559.	1.2	55
9	A Calorimetric Study of the Thermal Stability of Barstar and Its Interaction with Barnase. <i>Biochemistry</i> , 1995, 34, 5224-5233.	1.2	49
10	AS-48: a circular protein with an extremely stable globular structure. <i>FEBS Letters</i> , 2001, 505, 379-382.	1.3	36
11	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
12	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
13	Thermodynamic and structural characterization of Asn and Ala residues in the disallowed $\Delta\epsilon^2$ region of the Ramachandran plot. <i>Protein Science</i> , 2000, 9, 2322-2328.	3.1	32
14	Role of Interfacial Water Molecules in Proline-rich Ligand Recognition by the Src Homology 3 Domain of Abl. <i>Journal of Biological Chemistry</i> , 2010, 285, 2823-2833.	1.6	30
15	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
16	An Oligomeric Equilibrium Intermediate as the Precursory Nucleus of Globular and Fibrillar Supramacromolecular Assemblies in a PDZ Domain. <i>Biophysical Journal</i> , 2010, 99, 263-272.	0.2	28
17	Novel conformational aspects of the third PDZ domain of the neuronal post-synaptic density-95 protein revealed from two 1.4 Å... X-ray structures. <i>Journal of Structural Biology</i> , 2010, 170, 565-569.	1.3	21
18	Thermodynamic Characterization of the Folding Equilibrium of the Human Nedd4-WW4 Domain: At the Frontiers of Cooperative Folding. <i>Biochemistry</i> , 2009, 48, 8712-8720.	1.2	20

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19	Post-Translational Modifications Modulate Ligand Recognition by the Third PDZ Domain of the MAGUK Protein PSD-95. <i>PLoS ONE</i> , 2014, 9, e90030.	1.1	19
20	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
21	Structure of human TSG101 UEV domain. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 458-464.	2.5	17
22	Analysis of the Thermodynamics of Binding of an SH3 Domain to Proline-rich Peptides using a Chimeric Fusion Protein. <i>Journal of Molecular Biology</i> , 2008, 377, 117-135.	2.0	17
23	Alteration of the C-Terminal Ligand Specificity of the Erbin PDZ Domain by Allosteric Mutational Effects. <i>Journal of Molecular Biology</i> , 2014, 426, 3500-3508.	2.0	17
24	The high-resolution NMR structure of a single-chain chimeric protein mimicking a SH3-peptide complex. <i>FEBS Letters</i> , 2007, 581, 687-692.	1.3	16
25	A comparative analysis of the folding and misfolding pathways of the third PDZ domain of PSD95 investigated under different pH conditions. <i>Biophysical Chemistry</i> , 2011, 158, 104-110.	1.5	15
26	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
27	pH dependence of the hydrogen exchange in the SH3 domain of $\beta$ -spectrin. <i>FEBS Letters</i> , 2002, 514, 295-299.	1.3	13
28	Ultrafast folding kinetics of WW domains reveal how the amino acid sequence determines the speed limit to protein folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 8137-8142.	3.3	13
29	A binding event converted into a folding event. <i>FEBS Letters</i> , 2003, 553, 328-332.	1.3	12
30	Understanding the contribution of disulfide bridges to the folding and misfolding of an anti- $\beta$ -sheet scFv. <i>Protein Science</i> , 2017, 26, 1138-1149.	3.1	12
31	The Interconversion between a Flexible $\beta$ -Sheet and a Fibril $\beta$ -Arrangement Constitutes the Main Conformational Event during Misfolding of PSD95-PDZ3 Domain. <i>Biophysical Journal</i> , 2012, 103, 738-747.	0.2	11
32	A thermodynamic study of the third PDZ domain of MAGUK neuronal protein PSD-95 reveals a complex three-state folding behavior. <i>Biophysical Chemistry</i> , 2014, 185, 1-7.	1.5	11
33	Protein Folding Cooperativity and Thermodynamic Barriers of the Simplest $\beta$ -Sheet Fold: A Survey of WW Domains. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11058-11071.	1.2	11
34	Conformational changes in the third PDZ domain of the neuronal postsynaptic density protein 95. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 381-391.	1.1	11
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. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 646-652.	2.5	10
36	PDZ/PDZ interaction between PSD-95 and nNOS neuronal proteins. <i>Journal of Molecular Recognition</i> , 2020, 33, e2826.	1.1	10

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37	Common features in the unfolding and misfolding of PDZ domains and beyond: the modulatory effect of domain swapping and extra-elements. <i>Scientific Reports</i> , 2016, 6, 19242.	1.6	9
38	Isothermal Titration Calorimetry: Thermodynamic Analysis of the Binding Thermograms of Molecular Recognition Events by Using Equilibrium Models. , 0, , .		8
39	Towards the improvement in stability of an anti-A $\beta$ 2 single-chain variable fragment, scFv-h3D6, as a way to enhance its therapeutic potential. <i>Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis</i> , 2017, 24, 167-175.	1.4	8
40	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. <i>PLoS ONE</i> , 2014, 9, e98124.	1.1	8
41	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
42	Understanding the polymorphic behaviour of a mutant of the $\beta$ -spectrin SH3 domain by means of two 1.1Å resolution structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 189-196.	2.5	7
43	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
44	Thermodynamic Analysis of Point Mutations Inhibiting High-Temperature Reversible Oligomerization of PDZ3. <i>Biophysical Journal</i> , 2020, 119, 1391-1401.	0.2	6
45	Thermodynamic Impact of Embedded Water Molecules in the Unfolding of Human CD2BP2-GYF Domain. <i>Journal of Physical Chemistry B</i> , 2012, 116, 7168-7175.	1.2	5
46	Stability, conformational plasticity, oligomerization behaviour and equilibrium unfolding intermediates of the Ebola virus matrix protein VP40. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 4289-4303.	2.0	5
47	Evaluation of folding co-operativity of a chimeric protein based on the molecular recognition between polyproline ligands and SH3 domains. <i>Protein Engineering, Design and Selection</i> , 2009, 22, 597-606.	1.0	4
48	An Error Analysis for Two-State Protein-Folding Kinetic Parameters and $\Delta\Delta G^\ddagger$ -Values: Progress toward Precision by Exploring pH Dependencies on Leffler Plots. <i>Biophysical Journal</i> , 2008, 94, 4393-4404.	0.2	3
49	Phage display identification of nanomolar ligands for human NEDD4-WW3: Energetic and dynamic implications for the development of broad-spectrum antivirals. <i>International Journal of Biological Macromolecules</i> , 2022, 207, 308-323.	3.6	3
50	Lysozyme crystals dyed with bromophenol blue: where has the dye gone?. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 845-856.	1.1	2
51	Blocking PSD95-PDZ3's amyloidogenesis through point mutations that inhibit high-temperature reversible oligomerization (RO). <i>FEBS Journal</i> , 2022, 289, 3205-3216.	2.2	2
52	Reverse Engineering Analysis of the High-Temperature Reversible Oligomerization and Amyloidogenicity of PSD95-PDZ3. <i>Molecules</i> , 2022, 27, 2813.	1.7	2
53	The effect of an engineered ATCUN motif on the structure and biophysical properties of the SH3 domain of c-Src tyrosine kinase. <i>Journal of Biological Inorganic Chemistry</i> , 2020, 25, 621-634.	1.1	1
54	A Thermodynamic Analysis of the Binding Specificity between Four Human PDZ Domains and Eight Host, Viral and Designed Ligands. <i>Biomolecules</i> , 2021, 11, 1071.	1.8	1

#	ARTICLE	IF	CITATIONS
55	Binding curves by continuous gradient flow-mix calorimetry. <i>Thermochimica Acta</i> , 2005, 437, 140-144.	1.2	0
56	Approaching the thermodynamic view of protein folding through the reproduction of Anfinsen's experiment by undergraduate physical biochemistry students. <i>Biochemistry and Molecular Biology Education</i> , 2018, 46, 262-269.	0.5	0
57	Chapter 12. Biocalorimetry: Differential Scanning Calorimetry of Protein Solutions. , 2017, , 315-335.		0
58	Understanding binding affinity and specificity of modular protein domains: A focus in ligand design for the polyproline-binding families. <i>Advances in Protein Chemistry and Structural Biology</i> , 2022, 130, 161-188.	1.0	0