

Nina Pastor

List of Publications by Year in descending order

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70
papers

981
citations

623734

14
h-index

501196

28
g-index

71
all docs

71
docs citations

71
times ranked

1460
citing authors

#	ARTICLE	IF	CITATIONS
1	Recombinant C-Terminal Domains from Scorpine-like Peptides Inhibit the Plasmodium berghei Ookinete Development In Vitro. International Journal of Peptide Research and Therapeutics, 2021, 27, 817-829.	1.9	3
2	Clinical Manifestations, Mutational Analysis, and Immunological Phenotype in Patients with RAG1/2 Mutations: First Cases Series from Mexico and Description of Two Novel Mutations. Journal of Clinical Immunology, 2021, 41, 1291-1302.	3.8	2
3	Colombian Scorpion Centruroides margaritatus: Purification and Characterization of a Gamma Potassium Toxin with Full-Block Activity on the hERG1 Channel. Toxins, 2021, 13, 407.	3.4	8
4	Effect of the Substituent and Amino Group Position on the Lipase-Catalyzed Resolution of β -Amino Esters: A Molecular Docking Study Shedding Light on Candida antarctica lipase B Enantioselectivity. European Journal of Organic Chemistry, 2021, 2021, 4790-4802.	2.4	4
5	The TATA-binding Protein DNA-binding domain of eukaryotic parasites is a potentially druggable target. Chemical Biology and Drug Design, 2020, 95, 130-149.	3.2	4
6	Identification of an α -MoRF in the Intrinsically Disordered Region of the Escargot Transcription Factor. ACS Omega, 2020, 5, 18331-18341.	3.5	0
7	Exploring the Role of Phenylalanine Residues in Modulating the Flexibility and Topography of the Active Site in the Peroxygenase Variant PaDa-I. International Journal of Molecular Sciences, 2020, 21, 5734.	4.1	8
8	Revealing the Structural Contributions to Thermal Adaptation of the TATA-Box Binding Protein: Molecular Dynamics and QSPR Analyses. Journal of Chemical Information and Modeling, 2020, 60, 866-879.	5.4	2
9	1,4-Disubstituted 1,2,3-triazole GABA Analogues: Synthesis, In Vitro Evaluation, Quantum QSAR and Molecular Docking against Pseudomonas fluorescens GABA-AT. ChemistrySelect, 2020, 5, 1071-1079.	1.5	2
10	Site-Specific Interactions with Copper Promote Amyloid Fibril Formation for β 6aJL2-R24G. ACS Omega, 2020, 5, 7085-7095.	3.5	5
11	Isatin derivatives as DNA minor groove-binding agents: a structural and theoretical study. Structural Chemistry, 2020, 31, 1289-1307.	2.0	6
12	FRET-based analysis and molecular modeling of the human GPN-loop GTPases 1 and 3 heterodimer unveils a dominant negative protein complex. FEBS Journal, 2019, 286, 4797-4818.	4.7	7
13	In silico analysis of missense mutations in exons 1-5 of the F9 gene that cause hemophilia B. BMC Bioinformatics, 2019, 20, 363.	2.6	9
14	A Review on Viral Metagenomics in Extreme Environments. Frontiers in Microbiology, 2019, 10, 2403.	3.5	54
15	Different Dynamics in β 6aJL2 Proteins Associated with AL Amyloidosis, a Conformational Disease. International Journal of Molecular Sciences, 2019, 20, 4078.	4.1	4
16	In silico structure-based design of GABA B receptor agonists using a combination of docking and QSAR. Chemical Biology and Drug Design, 2019, 94, 1782-1798.	3.2	7
17	The human adenovirus type 5 E1B 55kDa protein interacts with RNA promoting timely DNA replication and viral late mRNA metabolism. PLoS ONE, 2019, 14, e0214882.	2.5	4
18	Localized conformational changes trigger the pH-induced fibrillogenesis of an amyloidogenic light chain protein. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 1656-1666.	2.4	8

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19	Replacement of oxidizable residues predicted by QM-MM simulation of a fungal laccase generates variants with higher operational stability. <i>Journal of Inorganic Biochemistry</i> , 2018, 178, 125-133.	3.5	8
20	QSAR and Molecular Docking Studies of the Inhibitory Activity of Novel Heterocyclic GABA Analogues over GABA-AT. <i>Molecules</i> , 2018, 23, 2984.	3.8	7
21	Novel-Substituted Heterocyclic GABA Analogues. Enzymatic Activity against the GABA-AT Enzyme from <i>Pseudomonas fluorescens</i> and In Silico Molecular Modeling. <i>Molecules</i> , 2018, 23, 1128.	3.8	6
22	Analysis of the Binding of Expansin Exl1, from <i>Pectobacterium carotovorum</i> , to Plant Xylem and Comparison to EXLX1 from <i>Bacillus subtilis</i> . <i>ACS Omega</i> , 2018, 3, 7008-7018.	3.5	11
23	Synthetic peptide antigens derived from long-chain alpha-neurotoxins: Immunogenicity effect against elapid venoms. <i>Peptides</i> , 2017, 88, 80-86.	2.4	11
24	STRUCTURE-FUNCTION STUDIES OF THE ALPHA PHEROMONE RECEPTOR FROM YEAST. <i>TIP Revista Especializada En Ciencias Químico-Biológicas</i> , 2017, 20, 16-26.	0.3	6
25	A family 13 thioesterase isolated from an activated sludge metagenome: insights into aromatic compounds metabolism. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1222-1237.	2.6	6
26	Convergent mechanisms favor fast amyloid formation in two lambda 6a Ig light chain mutants. <i>Biopolymers</i> , 2017, 107, e23027.	2.4	7
27	Two novel mutations in ZAP70 gene that result in human immunodeficiency. <i>Clinical Immunology</i> , 2017, 183, 278-284.	3.2	9
28	Dissecting the protein architecture of DNA-binding transcription factors in bacteria and archaea. <i>Microbiology (United Kingdom)</i> , 2017, 163, 1167-1178.	1.8	13
29	Early expression of the receptor for advanced glycation end products in a toxic model produced by 6-hydroxydopamine in the rat striatum. <i>Chemico-Biological Interactions</i> , 2016, 249, 10-18.	4.0	8
30	Chasing Unfolding Intermediates of IG Light Chains with Residual Structures that Could Fit in an Amyloid Core. <i>Biophysical Journal</i> , 2015, 108, 45a.	0.5	0
31	Information flow and protein dynamics: the interplay between nuclear magnetic resonance spectroscopy and molecular dynamics simulations. <i>Frontiers in Plant Science</i> , 2015, 6, 306.	3.6	14
32	Electrostatic analysis of bacterial expansins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 215-223.	2.6	21
33	Identification of a novel carbohydrate esterase from <i>Bjerkandera adusta</i> : Structural and function predictions through bioinformatics analysis and molecular modeling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 533-546.	2.6	6
34	Inhibition of Light Chain 6aJL2-R24G Amyloid Fiber Formation Associated with Light Chain Amyloidosis. <i>Biochemistry</i> , 2015, 54, 4978-4986.	2.5	14
35	Modeling the Interaction between Quinolate and the Receptor for Advanced Glycation End Products (RAGE): Relevance for Early Neuropathological Processes. <i>PLoS ONE</i> , 2015, 10, e0120221.	2.5	17
36	A novel TctA citrate transporter from an activated sludge metagenome: Structural and mechanistic predictions for the TTT family. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1756-1764.	2.6	9

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37	The Subdomains of the Tata-Binding Protein Display Discordant Strategies to Adapt to Temperature. <i>Biophysical Journal</i> , 2014, 106, 52a.	0.5	0
38	Looks can be Deceiving: a Single Mutation on an Ig Domain Alters Dynamics while Conserving Structure. Implications for A β , a Misfolding Disease. <i>Biophysical Journal</i> , 2014, 106, 258a.	0.5	0
39	PcExl1 a Novel Acid Expansin-Like Protein from the Plant Pathogen <i>Pectobacterium carotovorum</i> , Binds Cell Walls Differently to BsEXLX1. <i>PLoS ONE</i> , 2014, 9, e95638.	2.5	34
40	Why Would a Monomeric Ig Domain Form Amyloid Fibers?. <i>Biophysical Journal</i> , 2013, 104, 370a.	0.5	0
41	Soybean dihydrolipoamide dehydrogenase (ferric leghemoglobin reductase 2) interacts with and reduces ferric rice non-symbiotic hemoglobin 1. <i>Sciencejet</i> , 2013, 2, .	1.0	2
42	Exploring the Effect of Mutations on the Conformational Landscape of Amyloidogenic Antibody Fragments. <i>Biophysical Journal</i> , 2012, 102, 455a.	0.5	0
43	Exploration of the Conformational Landscape of an Amyloidogenic Ig Domain. <i>Biophysical Journal</i> , 2011, 100, 211a.	0.5	0
44	Segmental motions of rat thymidylate synthase leading to half-site behavior. <i>Biopolymers</i> , 2010, 93, 549-559.	2.4	7
45	Amyloid Fiber Precursors in Native and Denaturing MD Simulations of an IG Light Chain Domain. <i>Biophysical Journal</i> , 2010, 98, 200a.	0.5	1
46	On the consequences of placing amino groups at the TBP-DNA interface. Does TATA really matter?. <i>Journal of Molecular Recognition</i> , 2009, 22, 453-464.	2.1	4
47	TBP Carries Out Specific DNA Binding Involving Information From Both Grooves. <i>Biophysical Journal</i> , 2009, 96, 64a.	0.5	0
48	Thermal Adaptation Strategies used by TBP. <i>Biophysical Journal</i> , 2009, 96, 331a.	0.5	2
49	Computer-Based Screening of Functional Conformers of Proteins. <i>PLoS Computational Biology</i> , 2008, 4, e1000009.	3.2	4
50	Use of In Silico (Computer) Methods to Predict and Analyze the Tertiary Structure of Plant Hemoglobins. <i>Methods in Enzymology</i> , 2008, 436, 393-410.	1.0	10
51	Human frataxin: iron and ferrochelatase binding surface. <i>Chemical Communications</i> , 2007, , 1798-1800.	4.1	65
52	The Structure and Function of Frataxin. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2006, 41, 269-291.	5.2	139
53	Model of the TBP-TFIIB Complex from <i>Plasmodium falciparum</i> : Interface Analysis and Perspectives as a New Target for Antimalarial Design. <i>Archives of Medical Research</i> , 2005, 36, 317-330.	3.3	7
54	Role of a spatial distribution of IP3 receptors in the Ca ²⁺ dynamics of the <i>Xenopus</i> embryo at the mid-blastula transition stage. <i>Developmental Dynamics</i> , 2005, 232, 301-312.	1.8	6

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55	The B- to A-DNA Transition and the Reorganization of Solvent at the DNA Surface. <i>Biophysical Journal</i> , 2005, 88, 3262-3275.	0.5	51
56	Solution Structural Studies of the <i>Saccharomyces cerevisiae</i> TATA Binding Protein (TBP). <i>Biochemistry</i> , 2002, 41, 9559-9571.	2.5	18
57	Interaction of the IP3-Ca ²⁺ and the FGF-MAPK signaling pathways in the <i>Xenopus laevis</i> embryo: a qualitative approach to the mesodermal induction problem. <i>Biophysical Chemistry</i> , 2002, 97, 55-72.	2.8	7
58	Calibrating nucleic acids torsional energetics in force-field: insights from model compounds. <i>Computational and Theoretical Chemistry</i> , 2001, 537, 283-305.	1.5	14
59	Protein-DNA interactions in the initiation of transcription: The Role of Flexibility and Dynamics of the TATA Recognition Sequence and the TATA Box Binding Protein. <i>Theoretical and Computational Chemistry</i> , 2001, 9, 377-407.	0.4	2
60	A detailed interpretation of OH radical footprints in a TBP-DNA complex reveals the role of dynamics in the mechanism of sequence-specific binding. Edited by I. Tinoco. <i>Journal of Molecular Biology</i> , 2000, 304, 55-68.	4.2	140
61	Binding Mechanisms of TATA Box-Binding Proteins: DNA Kinking is Stabilized by Specific Hydrogen Bonds. <i>Biophysical Journal</i> , 2000, 78, 1988-1996.	0.5	19
62	TIT for TAT: The Properties of Inosine and Adenosine in TATA Box DNA. <i>Journal of Biomolecular Structure and Dynamics</i> , 1999, 16, 787-810.	3.5	20
63	Selective Binding of the TATA Box-Binding Protein to the TATA Box-Containing Promoter: Analysis of Structural and Energetic Factors. <i>Biophysical Journal</i> , 1998, 75, 2411-2421.	0.5	19
64	Progressive DNA Bending Is Made Possible by Gradual Changes in the Torsion Angle of the Glycosyl Bond. <i>Biophysical Journal</i> , 1998, 74, 2191-2198.	0.5	12
65	How the TATA Box Selects Its Protein Partner. <i>ACS Symposium Series</i> , 1997, , 329-345.	0.5	4
66	Does TATA matter? A structural exploration of the selectivity determinants in its complexes with TATA box-binding protein. <i>Biophysical Journal</i> , 1997, 73, 640-652.	0.5	39
67	Electrostatic analysis of DNA binding properties in lysine to leucine mutants of TATA-box binding proteins. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 543-550.	2.1	7
68	On the existence of very large nonadditivities for clusters of distorted water molecules. <i>Journal of Chemical Physics</i> , 1993, 99, 7899-7906.	3.0	22
69	Molecular evolution of class A β -lactamases: phylogeny and patterns of sequence conservation. <i>Molecular Microbiology</i> , 1990, 4, 1957-1965.	2.5	15
70	Relating Protein Structure and Function Through a Bijection and Its Implications on Protein Structure Prediction. , 0, , .		1