

Arturo Muga

List of Publications by Year in descending order

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97
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3,888
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136950

32
h-index

133252

59
g-index

99
all docs

99
docs citations

99
times ranked

3926
citing authors

#	ARTICLE	IF	CITATIONS
1	All-or-none amyloid disassembly via chaperone-triggered fibril unzipping favors clearance of β -synuclein toxic species. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	15
2	Unzipping the Secrets of Amyloid Disassembly by the Human Disaggregase. Cells, 2021, 10, 2745.	4.1	4
3	Truncation-Driven Lateral Association of β -Synuclein Hinders Amyloid Clearance by the Hsp70-Based Disaggregase. International Journal of Molecular Sciences, 2021, 22, 12983.	4.1	4
4	Extraction and Refolding Determinants of Chaperone-Driven Aggregated Protein Reactivation. Journal of Molecular Biology, 2020, 432, 3239-3250.	4.2	3
5	Structural insights into the ability of nucleoplasmin to assemble and chaperone histone octamers for DNA deposition. Scientific Reports, 2019, 9, 9487.	3.3	8
6	The Complex Phosphorylation Patterns that Regulate the Activity of Hsp70 and Its Cochaperones. International Journal of Molecular Sciences, 2019, 20, 4122.	4.1	18
7	Structural and functional insights on the roles of molecular chaperones in the mistargeting and aggregation phenotypes associated with primary hyperoxaluria type I. Advances in Protein Chemistry and Structural Biology, 2019, 114, 119-152.	2.3	14
8	Regulation of Human Hsc70 ATPase and Chaperone Activities by Apg2: Role of the Acidic Subdomain. Journal of Molecular Biology, 2019, 431, 444-461.	4.2	16
9	Activation of the DnaK-ClpB Complex is Regulated by the Properties of the Bound Substrate. Scientific Reports, 2018, 8, 5796.	3.3	14
10	Label-Free, Multiplexed, Single-Molecule Analysis of Protein-DNA Complexes with Nanopores. ACS Nano, 2017, 11, 5815-5825.	14.6	37
11	A Quantitative Characterization of Nucleoplasmin/Histone Complexes Reveals Chaperone Versatility. Scientific Reports, 2016, 6, 32114.	3.3	17
12	Crowding Modulates the Conformation, Affinity, and Activity of the Components of the Bacterial Disaggregase Machinery. Journal of Molecular Biology, 2016, 428, 2474-2487.	4.2	3
13	Sedimentation Equilibrium Analysis of ClpB Self-Association in Diluted and Crowded Solutions. Methods in Enzymology, 2015, 562, 135-160.	1.0	6
14	Chaperone-assisted protein aggregate reactivation: Different solutions for the same problem. Archives of Biochemistry and Biophysics, 2015, 580, 121-134.	3.0	34
15	ClpB dynamics is driven by its ATPase cycle and regulated by the DnaK system and substrate proteins. Biochemical Journal, 2015, 466, 561-570.	3.7	20
16	Modulation of the Chaperone DnaK Allosterism by the Nucleotide Exchange Factor GrpE. Journal of Biological Chemistry, 2015, 290, 10083-10092.	3.4	20
17	The intrinsically disordered distal face of nucleoplasmin recognizes distinct oligomerization states of histones. Nucleic Acids Research, 2014, 42, 1311-1325.	14.5	17
18	Crowding Activates ClpB and Enhances Its Association with DnaK for Efficient Protein Aggregate Reactivation. Biophysical Journal, 2014, 106, 2017-2027.	0.5	15

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19	Screening and Evaluation of Small Organic Molecules as ClpB Inhibitors and Potential Antimicrobials. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 7177-7189.	6.4	18
20	Structural Insights into the Chaperone Activity of the 40-kDa Heat Shock Protein DnaJ. <i>Journal of Biological Chemistry</i> , 2013, 288, 15065-15074.	3.4	21
21	The Effect of Amyloidogenic Peptides on Bacterial Aging Correlates with Their Intrinsic Aggregation Propensity. <i>Journal of Molecular Biology</i> , 2012, 421, 270-281.	4.2	27
22	A dynamic model of long-range conformational adaptations triggered by nucleotide binding in GroEL-GroES. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2333-2346.	2.6	6
23	A Quantitative Analysis of the Effect of Nucleotides and the M Domain on the Association Equilibrium of ClpB. <i>Biochemistry</i> , 2011, 50, 1991-2003.	2.5	22
24	Allosteric Communication between the Nucleotide Binding Domains of Caseinolytic Peptidase B. <i>Journal of Biological Chemistry</i> , 2011, 286, 25547-25555.	3.4	22
25	Conformational Sampling and Nucleotide-Dependent Transitions of the GroEL Subunit Probed by Unbiased Molecular Dynamics Simulations. <i>PLoS Computational Biology</i> , 2011, 7, e1002004.	3.2	27
26	Nucleotide utilization requirements that render ClpB active as a chaperone. <i>FEBS Letters</i> , 2010, 584, 929-934.	2.8	29
27	Nucleoplasmin Binds Histone H2A-H2B Dimers through Its Distal Face*. <i>Journal of Biological Chemistry</i> , 2010, 285, 33771-33778.	3.4	29
28	Role of DnaJ G/F-rich Domain in Conformational Recognition and Binding of Protein Substrates*. <i>Journal of Biological Chemistry</i> , 2010, 285, 34231-34239.	3.4	66
29	Energetics of Nucleotide-Induced DnaK Conformational States. <i>Biochemistry</i> , 2010, 49, 1338-1345.	2.5	23
30	DnaK-mediated association of ClpB to protein aggregates. A bichaperone network at the aggregate surface. <i>FEBS Letters</i> , 2009, 583, 2991-2996.	2.8	63
31	A Mechanism for Histone Chaperoning Activity of Nucleoplasmin: Thermodynamic and Structural Models. <i>Journal of Molecular Biology</i> , 2009, 393, 448-463.	4.2	44
32	Linking New Paradigms in Protein Chemistry to Reversible Membrane-Protein Interactions. <i>Current Protein and Peptide Science</i> , 2009, 10, 339-359.	1.4	43
33	The structure of CCT-Hsc70NBD suggests a mechanism for Hsp70 delivery of substrates to the chaperonin. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 858-864.	8.2	85
34	Activation of Nucleoplasmin, an Oligomeric Histone Chaperone, Challenges Its Stability ^{<sup></sup>} . <i>Biochemistry</i> , 2008, 47, 13897-13906.	2.5	22
35	Thermodynamic Characterization of Nucleoplasmin Unfolding: Interplay between Function and Stability. <i>Biochemistry</i> , 2008, 47, 7954-7962.	2.5	11
36	DnaJ Recruits DnaK to Protein Aggregates. <i>Journal of Biological Chemistry</i> , 2008, 283, 1381-1390.	3.4	47

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37	Thermal Adaptation of Heat Shock Proteins. <i>Current Protein and Peptide Science</i> , 2008, 9, 552-566.	1.4	23
38	Phosphorylation of Both Nucleoplasmin Domains Is Required for Activation of Its Chromatin Decondensation Activity. <i>Journal of Biological Chemistry</i> , 2007, 282, 21213-21221.	3.4	32
39	GrpE N-terminal Domain Contributes to the Interaction with DnaK and Modulates the Dynamics of the Chaperone Substrate Binding Domain. <i>Journal of Molecular Biology</i> , 2007, 374, 1054-1064.	4.2	19
40	Thermal Adaptation of the Yeast Mitochondrial Hsp70 System is Regulated by the Reversible Unfolding of its Nucleotide Exchange Factor. <i>Journal of Molecular Biology</i> , 2006, 358, 1367-1377.	4.2	36
41	Crystal structure of the temperature-sensitive and allosteric-defective chaperonin GroELE461K. <i>Journal of Structural Biology</i> , 2006, 155, 482-492.	2.8	13
42	The allosteric transition in DnaK probed by infrared difference spectroscopy. Concerted ATP-induced rearrangement of the substrate binding domain. <i>Protein Science</i> , 2006, 15, 223-233.	7.6	21
43	Ionic Contacts at DnaK Substrate Binding Domain Involved in the Allosteric Regulation of Lid Dynamics. <i>Journal of Biological Chemistry</i> , 2006, 281, 7479-7488.	3.4	37
44	Ionic interactions at both inter-ring contact sites of GroEL are involved in transmission of the allosteric signal: A time-resolved infrared difference study. <i>Protein Science</i> , 2005, 14, 2267-2274.	7.6	8
45	Conformational properties of bacterial DnaK and yeast mitochondrial Hsp70. <i>FEBS Journal</i> , 2005, 272, 3184-3196.	4.7	16
46	Nucleoplasmin-Mediated Unfolding of Chromatin Involves the Displacement of Linker-Associated Chromatin Proteins. <i>Biochemistry</i> , 2005, 44, 8274-8281.	2.5	25
47	The Lid Subdomain of DnaK Is Required for the Stabilization of the Substrate-binding Site. <i>Journal of Biological Chemistry</i> , 2004, 279, 19600-19606.	3.4	37
48	Nucleoplasmin: a nuclear chaperone. <i>Biochemistry and Cell Biology</i> , 2004, 82, 437-445.	2.0	47
49	Activation Mechanism of the Nuclear Chaperone Nucleoplasmin: Role of the Core Domain. <i>Journal of Molecular Biology</i> , 2003, 334, 585-593.	4.2	34
50	Interdomain interaction through helices A and B of DnaK peptide binding domain. <i>FEBS Letters</i> , 2003, 533, 119-123.	2.8	69
51	Calcium-dependent conformational changes of membrane-bound Ebola fusion peptide drive vesicle fusion. <i>FEBS Letters</i> , 2003, 535, 23-28.	2.8	21
52	The Interaction of Peripheral Proteins and Membranes Studied with $\hat{\pm}$ -Lactalbumin and Phospholipid Bilayers of Various Compositions. <i>Journal of Biological Chemistry</i> , 2003, 278, 21790-21797.	3.4	59
53	Platelet-derived Growth Factor (PDGF)-C, a PDGF Family Member with a Vascular Endothelial Growth Factor-like Structure. <i>Journal of Biological Chemistry</i> , 2003, 278, 17114-17120.	3.4	33
54	GroEL Stability and Function. <i>Journal of Biological Chemistry</i> , 2003, 278, 32083-32090.	3.4	24

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55	Salt Bridges at the Inter-ring Interface Regulate the Thermostat of GroEL. <i>Journal of Biological Chemistry</i> , 2002, 277, 34024-34029.	3.4	21
56	Electrostatic Interactions at the C-Terminal Domain of Nucleoplasmin Modulate Its Chromatin Decondensation Activity. <i>Biochemistry</i> , 2002, 41, 6408-6413.	2.5	23
57	The binding of tyrosine hydroxylase to negatively charged lipid bilayers involves the N-terminal region of the enzyme. <i>FEBS Letters</i> , 2002, 519, 221-226.	2.8	20
58	The Membrane-bound Conformation of β -Lactalbumin Studied by NMR-monitored ^1H Exchange. <i>Journal of Molecular Biology</i> , 2002, 321, 99-110.	4.2	71
59	Effect of Asp85 replacement by Thr on the conformation, surface electric properties and stability of bacteriorhodopsin. <i>Colloids and Surfaces A: Physicochemical and Engineering Aspects</i> , 2002, 209, 193-200.	4.7	3
60	Structural and functional properties of Escherichia coli -derived nucleoplasmin. <i>FEBS Journal</i> , 2001, 268, 1739-1748.	0.2	25
61	Excluded Volume Effects on the Refolding and Assembly of an Oligomeric Protein. <i>Journal of Biological Chemistry</i> , 2001, 276, 957-964.	3.4	38
62	Exogenously incorporated ketocarotenoids in large unilamellar vesicles. Protective activity against peroxidation. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2000, 1463, 179-187.	2.6	40
63	Redox- and pH-dependent association of plastocyanin with lipid bilayers: effect on protein conformation and thermal stability. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2000, 1463, 429-438.	2.6	12
64	Protein-membrane interaction: Lipid environment modulates protein conformation. , 1999, , 343-346.		0
65	Conformational Changes Generated in GroEL during ATP Hydrolysis as Seen by Time-resolved Infrared Spectroscopy. <i>Journal of Biological Chemistry</i> , 1999, 274, 5508-5513.	3.4	24
66	ATP hydrolysis induces an intermediate conformational state in GroEL. <i>FEBS Journal</i> , 1999, 259, 347-355.	0.2	10
67	Tyrosine hydroxylase binds tetrahydrobiopterin cofactor with negative cooperativity, as shown by kinetic analyses and surface plasmon resonance detection. <i>FEBS Journal</i> , 1999, 262, 840-849.	0.2	41
68	Redox-Induced Conformational Changes in Plastocyanin: An Infrared Study. <i>Biochemistry</i> , 1999, 38, 9640-9647.	2.5	12
69	Domain structure and stability of human phenylalanine hydroxylase inferred from infrared spectroscopy. <i>FEBS Letters</i> , 1998, 422, 225-230.	2.8	40
70	GroEL under Heat-Shock. <i>Journal of Biological Chemistry</i> , 1998, 273, 32587-32594.	3.4	49
71	Effects of the Inter-ring Communication in GroEL Structural and Functional Asymmetry. <i>Journal of Biological Chemistry</i> , 1997, 272, 32925-32932.	3.4	20
72	The Effect of Phosphorylation at Ser-40 on the Structure and Thermal Stability of Tyrosine Hydroxylase. <i>Advances in Pharmacology</i> , 1997, 42, 15-18.	2.0	6

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73	Membrane destabilization induced by the human immunodeficiency virus type-1 fusion peptide. <i>International Journal of Peptide Research and Therapeutics</i> , 1997, 4, 365-369.	0.1	0
74	Membrane destabilization induced by the human immunodeficiency virus type-1 fusion peptide. <i>International Journal of Peptide Research and Therapeutics</i> , 1997, 4, 365-369.	0.1	0
75	Structural Requirements for the Association of Native and Partially Folded Conformations of $\hat{1}\pm$ -Lactalbumin with Model Membranes. <i>Biochemistry</i> , 1996, 35, 3892-3898.	2.5	57
76	Interaction of native and partially folded conformations of $\hat{1}\pm$ -lactalbumin with lipid bilayers: characterization of two membrane-bound states. <i>FEBS Letters</i> , 1996, 386, 21-25.	2.8	25
77	Conformational Properties and Stability of Tyrosine Hydroxylase Studied by Infrared Spectroscopy. <i>Journal of Biological Chemistry</i> , 1996, 271, 19737-19742.	3.4	79
78	Binding of Molten Globule-like Conformations to Lipid Bilayers. <i>Journal of Biological Chemistry</i> , 1995, 270, 29910-29915.	3.4	114
79	Prediction of the structure of GroES and its interaction with GroEL. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 22, 199-209.	2.6	14
80	A pathway for the thermal destabilization of bacteriorhodopsin. <i>FEBS Letters</i> , 1995, 367, 297-300.	2.8	44
81	Membrane Interaction and Conformational Properties of the Putative Fusion Peptide of PH-30, a Protein Active in Sperm-Egg Fusion. <i>Biochemistry</i> , 1994, 33, 4444-4448.	2.5	98
82	Interaction of the HIV-1 Fusion Peptide with Phospholipid Vesicles: Different Structural Requirements for Fusion and Leakage. <i>Biochemistry</i> , 1994, 33, 3201-3209.	2.5	207
83	The interaction of daunomycin with model membranes. Effect of the lipid physical state and the lipid composition. <i>FEBS Journal</i> , 1993, 213, 1269-1275.	0.2	15
84	A comparative study of the conformational properties of Escherichia coli-derived rat intestinal and liver fatty acid binding proteins. <i>BBA - Proteins and Proteomics</i> , 1993, 1162, 291-296.	2.1	26
85	Structural and Functional Studies on the Interaction of Sodium Dodecyl Sulfate with $\hat{1}^2$ -Galactosidase. <i>Archives of Biochemistry and Biophysics</i> , 1993, 300, 451-457.	3.0	86
86	Quantitative studies of the structure of proteins in solution by fourier-transform infrared spectroscopy. <i>Progress in Biophysics and Molecular Biology</i> , 1993, 59, 23-56.	2.9	764
87	Membrane binding induces destabilization of cytochrome c structure. <i>Biochemistry</i> , 1991, 30, 7219-7224.	2.5	213
88	Apocytochrome c interaction with phospholipid membranes studied by Fourier-transform infrared spectroscopy. <i>Biochemistry</i> , 1991, 30, 2629-2635.	2.5	59
89	Infrared spectroscopic studies of detergent-solubilized uncoupling protein from brown-adipose-tissue mitochondria. <i>FEBS Journal</i> , 1990, 188, 83-89.	0.2	30
90	Water penetration and phase behavior of surfactant gel phases and lipid bilayers. <i>The Journal of Physical Chemistry</i> , 1990, 94, 7265-7271.	2.9	10

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91	Structural studies with the uveopathogenic peptide M derived from retinal S-antigen. <i>Biochemistry</i> , 1990, 29, 2925-2930.	2.5	48
92	Solubilization of sarcoplasmic reticulum membranes by sodium dodecylsulphate. <i>FEBS Letters</i> , 1990, 269, 324-327.	2.8	5
93	Fourier-transform infrared studies on cation binding to native and modified purple membranes. <i>Biochemistry</i> , 1989, 28, 8940-8945.	2.5	23
94	An infrared spectroscopic study of \hat{I}^2 -galactosidase structure in aqueous solutions. <i>FEBS Letters</i> , 1989, 252, 118-120.	2.8	52
95	Interaction of SDS with \hat{I}^2 -galactosidase. A FT-IR study of the influence of detergent concentration and temperature.. <i>Journal of Molecular Structure</i> , 1988, 175, 67-72.	3.6	3
96	The structure of proteins in aqueous solutions: An assessment of triose phosphate isomerase structure by fourier-transform infrared spectroscopy. <i>Biochemical and Biophysical Research Communications</i> , 1988, 152, 69-75.	2.1	34
97	Influence of temperature on the conformation of membrane proteins as seen by FT-IR. <i>Journal of Molecular Structure</i> , 1986, 143, 465-468.	3.6	3