

Jose Luis Neira

List of Publications by Year in descending order

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168
papers

3,794
citations

134610

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169
all docs

169
docs citations

169
times ranked

3928
citing authors

#	ARTICLE	IF	CITATIONS
1	Biochemical and biophysical characterization of PADI4 supports its involvement in cancer. Archives of Biochemistry and Biophysics, 2022, 717, 109125.	1.4	12
2	Human Enzyme PADI4 Binds to the Nuclear Carrier Importin β 3. Cells, 2022, 11, 2166.	1.8	7
3	The muscle-relaxing C-terminal peptide from troponin I populates a nascent helix, facilitating binding to tropomyosin with a potent therapeutic effect. Journal of Biological Chemistry, 2021, 296, 100228.	1.6	5
4	Investigation of action pattern of a novel chondroitin sulfate/dermatan sulfate 4-O-sulfatase. Biochemical Journal, 2021, 478, 281-298.	1.7	2
5	Intrinsically disordered protein NUPR1 binds to the armadillo-repeat domain of Plakophilin 1. International Journal of Biological Macromolecules, 2021, 170, 549-560.	3.6	4
6	The Histidine Phosphocarrier Kinase/Phosphorylase from Bacillus Subtilis Is an Oligomer in Solution with a High Thermal Stability. International Journal of Molecular Sciences, 2021, 22, 3231.	1.8	4
7	The isolated GTPase-activating-protein-related domain of neurofibromin-1 has a low conformational stability in solution. Archives of Biochemistry and Biophysics, 2021, 700, 108767.	1.4	2
8	Crowding Effects on the Structure and Dynamics of the Intrinsically Disordered Nuclear Chromatin Protein NUPR1. Frontiers in Molecular Biosciences, 2021, 8, 684622.	1.6	17
9	The armadillo-repeat domain of plakophilin 1 binds the C-terminal sterile alpha motif (SAM) of p73. Biochimica Et Biophysica Acta - General Subjects, 2021, 1865, 129914.	1.1	3
10	The nuclear localization sequence of the epigenetic factor RYBP binds to human importin β 3. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2021, 1869, 140670.	1.1	6
11	NUPR1 inhibitor ZZW-115 induces ferroptosis in a mitochondria-dependent manner. Cell Death Discovery, 2021, 7, 269.	2.0	33
12	An N-terminal half fragment of the histidine phosphocarrier protein, HPr, is disordered but binds to HPr partners and shows antibacterial properties. Biochimica Et Biophysica Acta - General Subjects, 2021, 1865, 130015.	1.1	4
13	Design of Inhibitors of the Intrinsically Disordered Protein NUPR1: Balance between Drug Affinity and Target Function. Biomolecules, 2021, 11, 1453.	1.8	15
14	Discrimination of sulfated isomers of chondroitin sulfate disaccharides by HILIC-MS. Analytical and Bioanalytical Chemistry, 2021, 413, 7107-7117.	1.9	2
15	Residual Helicity at the Active Site of the Histidine Phosphocarrier, HPr, Modulates Binding Affinity to Its Natural Partners. International Journal of Molecular Sciences, 2021, 22, 10805.	1.8	2
16	A single evolutionarily divergent mutation determines the different FAD α binding affinities of human and rat NQO1 due to site α -specific phosphorylation. FEBS Letters, 2021, 596, 29.	1.3	2
17	Targeting intrinsically disordered proteins involved in cancer. Cellular and Molecular Life Sciences, 2020, 77, 1695-1707.	2.4	74
18	A Phosphorylation-Induced Switch in the Nuclear Localization Sequence of the Intrinsically Disordered NUPR1 Hampers Binding to Importin. Biomolecules, 2020, 10, 1313.	1.8	13

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19	The Parologue of the Intrinsically Disordered Nuclear Protein 1 Has a Nuclear Localization Sequence that Binds to Human Importin β 3. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7428.	1.8	7
20	Intrinsically disordered proteins in biology: One for all, all for one. <i>Archives of Biochemistry and Biophysics</i> , 2020, 684, 108328.	1.4	4
21	The isolated armadillo-repeat domain of Plakophilin 1 is a monomer in solution with a low conformational stability. <i>Journal of Structural Biology</i> , 2020, 211, 107569.	1.3	7
22	Dynamics of the intrinsically disordered inhibitor IF7 of glutamine synthetase in isolation and in complex with its partner. <i>Archives of Biochemistry and Biophysics</i> , 2020, 683, 108303.	1.4	1
23	High-throughput screening for intrinsically disordered proteins by using biophysical methods. , 2020, , 359-387.		2
24	Human importin β 3 and its N-terminal truncated form, without the importin- β 2-binding domain, are oligomeric species with a low conformational stability in solution. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129609.	1.1	11
25	ZZW-115-dependent inhibition of NUPR1 nuclear translocation sensitizes cancer cells to genotoxic agents. <i>JCI Insight</i> , 2020, 5, .	2.3	24
26	Dynamics of the intrinsically disordered protein NUPR1 in isolation and in its fuzzy complexes with DNA and prothymosin β . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019, 1867, 140252.	1.1	8
27	Kinetic and thermodynamic effects of phosphorylation on p53 binding to MDM2. <i>Scientific Reports</i> , 2019, 9, 693.	1.6	25
28	The isolated C-terminal nuclear localization sequence of the breast cancer metastasis suppressor 1 is disordered. <i>Archives of Biochemistry and Biophysics</i> , 2019, 664, 95-101.	1.4	10
29	Dendrimers as Competitors of Protein-Protein Interactions of the Intrinsically Disordered Nuclear Chromatin Protein NUPR1. <i>Biomacromolecules</i> , 2019, 20, 2567-2576.	2.6	11
30	A group II intron-encoded protein interacts with the cellular replicative machinery through the β 2-sliding clamp. <i>Nucleic Acids Research</i> , 2019, 47, 7605-7617.	6.5	10
31	Designing and repurposing drugs to target intrinsically disordered proteins for cancer treatment: using NUPR1 as a paradigm. <i>Molecular and Cellular Oncology</i> , 2019, 6, e1612678.	0.3	10
32	The C-terminal SAM domain of p73 binds to the N terminus of MDM2. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019, 1863, 760-770.	1.1	11
33	Targeting the Stress-Induced Protein NUPR1 to Treat Pancreatic Adenocarcinoma. <i>Cells</i> , 2019, 8, 1453.	1.8	28
34	Phosphorylation compromises FAD binding and intracellular stability of wild-type and cancer-associated NQO1: Insights into flavo-proteome stability. <i>International Journal of Biological Macromolecules</i> , 2019, 125, 1275-1288.	3.6	15
35	Ligand-based design identifies a potent NUPR1 inhibitor exerting anticancer activity via necroptosis. <i>Journal of Clinical Investigation</i> , 2019, 129, 2500-2513.	3.9	68
36	The histidine phosphocarrier protein, HPr, binds to the highly thermostable regulator of sigma D protein, Rsd, and its isolated helical fragments. <i>Archives of Biochemistry and Biophysics</i> , 2018, 639, 26-37.	1.4	7

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37	Amphipathic helical peptides hamper protein-protein interactions of the intrinsically disordered chromatin nuclear protein 1 (NUPR1). <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 1283-1295.	1.1	22
38	Inactivation of NUPR1 promotes cell death by coupling ER-stress responses with necrosis. <i>Scientific Reports</i> , 2018, 8, 16999.	1.6	44
39	The C Terminus of the Ribosomal-Associated Protein LrtA is an Intrinsically Disordered Oligomer. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3902.	1.8	2
40	The Cyanobacterial Ribosomal-Associated Protein LrtA from <i>Synechocystis</i> sp. PCC 6803 Is an Oligomeric Protein in Solution with Chameleonic Sequence Properties. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1857.	1.8	5
41	The chromatin nuclear protein NUPR1L is intrinsically disordered and binds to the same proteins as its paralogue. <i>Biochemical Journal</i> , 2018, 475, 2271-2291.	1.7	9
42	Identification of a Drug Targeting an Intrinsically Disordered Protein Involved in Pancreatic Adenocarcinoma. <i>Scientific Reports</i> , 2017, 7, 39732.	1.6	101
43	The isolated, twenty-three-residue-long, N-terminal region of the glutamine synthetase inactivating factor binds to its target. <i>Biophysical Chemistry</i> , 2017, 228, 1-9.	1.5	1
44	Intrinsically disordered inhibitor of glutamine synthetase is a functional protein with random-coil-like $\langle r^2 \rangle / \langle r^2 \rangle_{\text{coil}}$ values. <i>Protein Science</i> , 2017, 26, 1105-1115.	3.1	6
45	Trifluoroethanol-induced conformational transition of the C-terminal sterile alpha motif (SAM) of human p73. <i>Archives of Biochemistry and Biophysics</i> , 2017, 619, 1-9.	1.4	2
46	Site-to-site interdomain communication may mediate different loss-of-function mechanisms in a cancer-associated NQO1 polymorphism. <i>Scientific Reports</i> , 2017, 7, 44532.	1.6	35
47	Enhanced vulnerability of human proteins towards disease-associated inactivation through divergent evolution. <i>Human Molecular Genetics</i> , 2017, 26, 3531-3544.	1.4	34
48	Intrinsically disordered chromatin protein NUPR1 binds to the C-terminal region of Polycomb RING1B. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E6332-E6341.	3.3	39
49	An introduction to the special issue on biomolecular NMR. <i>Archives of Biochemistry and Biophysics</i> , 2017, 628, 1-2.	1.4	0
50	The PipX Protein, When Not Bound to Its Targets, Has Its Signaling C-Terminal Helix in a Flexed Conformation. <i>Biochemistry</i> , 2017, 56, 3211-3224.	1.2	8
51	Determinants of the pKa values of ionizable residues in an intrinsically disordered protein. <i>Archives of Biochemistry and Biophysics</i> , 2016, 598, 18-27.	1.4	32
52	The Monomeric Species of the Regulatory Domain of Tyrosine Hydroxylase Has a Low Conformational Stability. <i>Biochemistry</i> , 2016, 55, 3418-3431.	1.2	29
53	Dissecting the Binding between Glutamine Synthetase and Its Two Natively Unfolded Protein Inhibitors. <i>Biochemistry</i> , 2016, 55, 3370-3382.	1.2	14
54	The chondroitin sulfate/dermatan sulfate 4-O-endosulfatase from marine bacterium <i>Vibrio</i> sp FC509 is a dimeric species: Biophysical characterization of an endosulfatase. <i>Biochimie</i> , 2016, 131, 85-95.	1.3	9

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55	Human COA3 Is an Oligomeric Highly Flexible Protein in Solution. <i>Biochemistry</i> , 2016, 55, 6209-6220.	1.2	4
56	Cysteine Mutational Studies Provide Insight into a Thiol-Based Redox Switch Mechanism of Metal and DNA Binding in FurA from <i>Anabaena</i> sp. PCC 7120. <i>Antioxidants and Redox Signaling</i> , 2016, 24, 173-185.	2.5	16
57	Functional Characterization of Nupr1L, A Novel p53-Regulated Isoform of the High-Mobility Group (HMG)-Related Protumoral Protein Nupr1. <i>Journal of Cellular Physiology</i> , 2015, 230, 2936-2950.	2.0	14
58	Biophysical Analysis of the MHR Motif in Folding and Domain Swapping of the HIV Capsid Protein C-Terminal Domain. <i>Biophysical Journal</i> , 2015, 108, 338-349.	0.2	3
59	The Carboxy-Terminal Domain of Erb1 Is a Seven-Bladed Å-Propeller that Binds RNA. <i>PLoS ONE</i> , 2015, 10, e0123463.	1.1	10
60	Biochemical and mutational studies of allantoinase from <i>Bacillus licheniformis</i> CECT 20T. <i>Biochimie</i> , 2014, 99, 178-188.	1.3	8
61	The isolated N terminus of Ring1B is a well-folded, monomeric fragment with native-like structure. <i>Protein Engineering, Design and Selection</i> , 2014, 27, 1-11.	1.0	2
62	Structural dissection of the C-terminal sterile alpha motif (SAM) of human p73. <i>Archives of Biochemistry and Biophysics</i> , 2014, 558, 133-142.	1.4	10
63	Evidence supporting the existence of a NUPR1-like family of helix-loop-helix chromatin proteins related to, yet distinct from, AT hook-containing HMG proteins. <i>Journal of Molecular Modeling</i> , 2014, 20, 2357.	0.8	15
64	Electrostatic Effects in the Folding of the SH3 Domain of the c-Src Tyrosine Kinase: pH-Dependence in 3D-Domain Swapping and Amyloid Formation. <i>PLoS ONE</i> , 2014, 9, e113224.	1.1	22
65	Falling Down: Landscape and Kinetics of One-Dimensional Protein Folding. <i>Structure</i> , 2013, 21, 1905-1907.	1.6	2
66	Protein folding and stability: A Prague cemetery. <i>Archives of Biochemistry and Biophysics</i> , 2013, 531, 1-3.	1.4	3
67	NMR as a tool to identify and characterize protein folding intermediates. <i>Archives of Biochemistry and Biophysics</i> , 2013, 531, 90-99.	1.4	17
68	BRMS151-98 and BRMS151-84 Are Crystal Oligomeric Coiled Coils with Different Oligomerization States, Which Behave as Disordered Protein Fragments in Solution. <i>Journal of Molecular Biology</i> , 2013, 425, 2147-2163.	2.0	5
69	Nuclear Magnetic Resonance Spectroscopy to Study Virus Structure. <i>Sub-Cellular Biochemistry</i> , 2013, 68, 145-176.	1.0	1
70	Fluorescence, Circular Dichroism and Mass Spectrometry as Tools to Study Virus Structure. <i>Sub-Cellular Biochemistry</i> , 2013, 68, 177-202.	1.0	7
71	The Histidine-Phosphocarrier Protein of the Phosphoenolpyruvate: Sugar Phosphotransferase System of <i>Bacillus sphaericus</i> Self-Associates. <i>PLoS ONE</i> , 2013, 8, e69307.	1.1	8
72	Deciphering the Binding between Nupr1 and MSL1 and Their DNA-Repairing Activity. <i>PLoS ONE</i> , 2013, 8, e78101.	1.1	33

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73	NS3 Protease from Hepatitis C Virus: Biophysical Studies on an Intrinsically Disordered Protein Domain. <i>International Journal of Molecular Sciences</i> , 2013, 14, 13282-13306.	1.8	16
74	An N-terminally Truncated Mutant of Human Chemokine CXCL14 has Biological Activity. <i>Protein and Peptide Letters</i> , 2013, 20, 955-967.	0.4	2
75	The HIV-1 Capsid Protein as a Drug Target: Recent Advances and Future Prospects. <i>Current Protein and Peptide Science</i> , 2013, 14, 658-668.	0.7	6
76	The C-terminal sterile alpha motif (SAM) domain of human p73 is a highly dynamic protein, which acquires high thermal stability through a decrease in backbone flexibility. <i>Physical Chemistry Chemical Physics</i> , 2012, 14, 10308.	1.3	9
77	Peptides as Inhibitors of the First Phosphorylation Step of the <i>Streptomyces coelicolor</i> Phosphoenolpyruvate: Sugar Phosphotransferase System. <i>Biochemistry</i> , 2012, 51, 7393-7402.	1.2	7
78	Mutation of Ser-50 and Cys-66 in Snapin Modulates Protein Structure and Stability. <i>Biochemistry</i> , 2012, 51, 3470-3484.	1.2	6
79	Stability and binding of the phosphorylated species of the N-terminal domain of enzyme I and the histidine phosphocarrier protein from the <i>Streptomyces coelicolor</i> phosphoenolpyruvate:sugar phosphotransferase system. <i>Archives of Biochemistry and Biophysics</i> , 2012, 526, 44-53.	1.4	6
80	Insights into the mechanism of activation of the phosphorylation-independent response regulator NblR. Role of residues Cys69 and Cys96. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012, 1819, 382-390.	0.9	4
81	Non-canonical residues of the marginally stable monomeric ubiquitin conjugase from goldfish are involved in binding to the C terminus of Ring 1B. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 991-1001.	1.1	1
82	Biophysical characterization of the isolated C-terminal region of the transient receptor potential vanilloid 1. <i>FEBS Letters</i> , 2012, 586, 1154-1159.	1.3	5
83	Biochemical and Mutational Studies of the <i>Bacillus cereus</i> CECT 5050T Formamidase Support the Existence of a C-E-E-K Tetrad in Several Members of the Nitrilase Superfamily. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5761-5769.	1.4	16
84	The Inactivating Factor of Glutamine Synthetase IF17 Is an Intrinsically Disordered Protein, Which Folds upon Binding to Its Target. <i>Biochemistry</i> , 2011, 50, 9767-9778.	1.2	8
85	Larger Helical Populations in Peptides Derived from the Dimerization Helix of the Capsid Protein of HIV-1 Results in Peptide Binding toward Regions Other than the "Hotspot" Interface. <i>Biomacromolecules</i> , 2011, 12, 3252-3264.	2.6	4
86	The Structure of BRMS1 Nuclear Export Signal and SNX6 Interacting Region Reveals a Hexamer Formed by Antiparallel Coiled Coils. <i>Journal of Molecular Biology</i> , 2011, 411, 1114-1127.	2.0	13
87	The isolated major homology region of the HIV capsid protein is mainly unfolded in solution and binds to the intact protein. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 1269-1278.	1.1	3
88	Nucleotide-induced conformational transitions in the CBS domain protein MJ0729 of <i>Methanocaldococcus jannaschii</i> . <i>Protein Engineering, Design and Selection</i> , 2011, 24, 161-169.	1.0	3
89	The Conformational Stability and Biophysical Properties of the Eukaryotic Thioredoxins of <i>Pisum Sativum</i> Are Not Family-Conserved. <i>PLoS ONE</i> , 2011, 6, e17068.	1.1	6
90	Rationally Designed Interfacial Peptides Are Efficient In Vitro Inhibitors of HIV-1 Capsid Assembly with Antiviral Activity. <i>PLoS ONE</i> , 2011, 6, e23877.	1.1	24

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91	The regulatory factor SipA is a highly stable β class protein with a SH3 fold. FEBS Letters, 2010, 584, 989-994.	1.3	8
92	The CBS domain protein MJ0729 of <i>Methanocaldococcus jannaschii</i> binds DNA. FEBS Letters, 2010, 584, 4485-4489.	1.3	12
93	High-recovery one-step purification of the DNA-binding protein Fur by mild guanidinium chloride treatment. Process Biochemistry, 2010, 45, 292-296.	1.8	10
94	The Bronze Age of science in Spain. EMBO Reports, 2010, 11, 12-13.	2.0	2
95	Folded and Unfolded Conformations of Proteins Involved in Pancreatic Cancer: a Layman's Guide. Scientific World Journal, The, 2010, 10, 1612-1633.	0.8	4
96	Pancreatic Cancer: Molecular, Biochemical, Chemopreventive, and Therapeutic Aspects. Scientific World Journal, The, 2010, 10, 1967-1970.	0.8	4
97	The N-terminal domain of the enzyme I is a monomeric well-folded protein with a low conformational stability and residual structure in the unfolded state. Protein Engineering, Design and Selection, 2010, 23, 729-742.	1.0	7
98	Structural characterisation of the natively unfolded enterocin EJ97. Protein Engineering, Design and Selection, 2010, 23, 507-518.	1.0	7
99	Conformational Stability of Hepatitis C Virus NS3 Protease. Biophysical Journal, 2010, 99, 3811-3820.	0.2	26
100	Insights into the Functionality of the Putative Residues Involved in Enterocin AS-48 Maturation. Applied and Environmental Microbiology, 2010, 76, 7268-7276.	1.4	27
101	The Basic Helix~Loop~Helix Region of Human Neurogenin 1 Is a Monomeric Natively Unfolded Protein Which Forms a "Fuzzy" Complex upon DNA Binding. Biochemistry, 2010, 49, 1577-1589.	1.2	36
102	Evidence of non-functional redundancy between two pea h-type thioredoxins by specificity and stability studies. Journal of Plant Physiology, 2010, 167, 423-429.	1.6	10
103	Dendrimers as Potential Inhibitors of the Dimerization of the Capsid Protein of HIV-1. Biomacromolecules, 2010, 11, 2069-2078.	2.6	41
104	Biophysical and Structural Studies on the Capsid Protein of the Human Immunodeficiency Virus Type 1: A New Drug Target?. Scientific World Journal, The, 2009, 9, 404-419.	0.8	8
105	The positively charged C-terminal region of the inactivating Shaker B peptide binds to the potassium channel KcsA. Protein Engineering, Design and Selection, 2009, 22, 341-347.	1.0	1
106	p8/nupr1 regulates DNA repair activity after double-strand gamma irradiation-induced DNA damage. Journal of Cellular Physiology, 2009, 221, 594-602.	2.0	46
107	Structure and conformational stability of a tetrameric thermostable <i>N</i> -succinylamino acid racemase. Biopolymers, 2009, 91, 757-772.	1.2	10
108	Thermodynamics of zinc binding to hepatitis C virus NS3 protease: A folding by binding event. Proteins: Structure, Function and Bioinformatics, 2009, 77, 624-636.	1.5	21

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109	The capsid protein of human immunodeficiency virus: molecular recognition and design of antiviral agents. <i>FEBS Journal</i> , 2009, 276, 6097-6097.	2.2	2
110	The capsid protein of human immunodeficiency virus: designing inhibitors of capsid assembly. <i>FEBS Journal</i> , 2009, 276, 6110-6117.	2.2	26
111	Metal-triggered changes in the stability and secondary structure of a tetrameric dihydropyrimidinase: A biophysical characterization. <i>Biophysical Chemistry</i> , 2009, 139, 42-52.	1.5	13
112	The CBS Domain Protein MJ0729 of <i>Methanocaldococcus jannaschii</i> Is a Thermostable Protein with a pH-Dependent Self-Oligomerization. <i>Biochemistry</i> , 2009, 48, 2760-2776.	1.2	10
113	The Transcriptional Repressor RYBP Is a Natively Unfolded Protein Which Folds upon Binding to DNA. <i>Biochemistry</i> , 2009, 48, 1348-1360.	1.2	37
114	Discovery of Specific Flavodoxin Inhibitors as Potential Therapeutic Agents against <i>Helicobacter pylori</i> Infection. <i>ACS Chemical Biology</i> , 2009, 4, 928-938.	1.6	48
115	The family 52 β -xylosidase from <i>Geobacillus stearothermophilus</i> is a dimer: Structural and biophysical characterization of a glycoside hydrolase. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008, 1784, 1924-1934.	1.1	17
116	Structural mobility of the monomeric C-terminal domain of the HIV-1 capsid protein. <i>FEBS Journal</i> , 2008, 275, 3299-3311.	2.2	23
117	Spain should implement a model that's known to work. <i>Nature</i> , 2008, 453, 26-27.	13.7	5
118	Envelope Lipids Regulate the In Vitro Assembly of the HIV-1 Capsid. <i>Biophysical Journal</i> , 2008, 94, L08-L10.	0.2	10
119	Defining the Epitope Region of a Peptide from the <i>Streptomyces coelicolor</i> Phosphoenolpyruvate: Sugar Phosphotransferase System Able to Bind to the Enzyme I. <i>Biophysical Journal</i> , 2008, 95, 1336-1348.	0.2	11
120	Conformational Stability of <i>Helicobacter pylori</i> Flavodoxin. <i>Journal of Biological Chemistry</i> , 2008, 283, 2883-2895.	1.6	13
121	N-type Inactivation of the Potassium Channel KcsA by the Shaker B α -Peptide. <i>Journal of Biological Chemistry</i> , 2008, 283, 18076-18085.	1.6	12
122	Into the Lipid Realm: Stability and Thermodynamics of Membrane Proteins. <i>Current Protein and Peptide Science</i> , 2008, 9, 626-637.	0.7	5
123	The Helical Structure Propensity in the First Helix of the Histidine Phosphocarrier Protein of <i>Streptomyces coelicolor</i> . <i>Protein and Peptide Letters</i> , 2007, 14, 281-290.	0.4	7
124	Dynamics of Tryptophan in the Histidine-Containing Phosphocarrier Protein of <i>Streptomyces coelicolor</i> : Evidence of Multistate Equilibrium Unfolding. <i>Biochemistry</i> , 2007, 46, 7252-7260.	1.2	8
125	The Isolated C-Terminal Domain of Ring1B Is a Dimer Made of Stable, Well-Structured Monomers. <i>Biochemistry</i> , 2007, 46, 12764-12776.	1.2	46
126	Flexibility in HIV-1 Assembly Subunits: Solution Structure of the Monomeric C-Terminal Domain of the Capsid Protein. <i>Biophysical Journal</i> , 2007, 93, 1264-1276.	0.2	48

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127	Isolation and characterization of a thermostable β -xylosidase in the thermophilic bacterium <i>Geobacillus pallidus</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2007, 1774, 510-518.	1.1	23
128	Biophysical Characterization of the Enzyme I of the <i>Streptomyces coelicolor</i> Phosphoenolpyruvate: Sugar Phosphotransferase System. <i>Biophysical Journal</i> , 2006, 90, 4592-4604.	0.2	14
129	Filling Small, Empty Protein Cavities: Structural and Energetic Consequences. <i>Journal of Molecular Biology</i> , 2006, 358, 701-712.	2.0	23
130	Binding of the C-terminal domain of the HIV-1 capsid protein to lipid membranes: a biophysical characterization. <i>Biochemical Journal</i> , 2006, 394, 345-353.	1.7	10
131	Site-directed mutagenesis indicates an important role of cysteines 76 and 181 in the catalysis of hydantoin racemase from <i>Sinorhizobium meliloti</i> . <i>Protein Science</i> , 2006, 15, 2729-2738.	3.1	11
132	p8 and Prothymosin Alpha : Unity is Strength. <i>Cell Cycle</i> , 2006, 5, 829-830.	1.3	17
133	Regulation of apoptosis by the p8/prothymosin Δ complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2671-2676.	3.3	109
134	An extensive thermodynamic characterization of the dimerization domain of the HIV-1 capsid protein. <i>Protein Science</i> , 2005, 14, 2387-2404.	3.1	24
135	Structure and conformational stability of the enzyme I of <i>Streptomyces coelicolor</i> explored by FTIR and circular dichroism. <i>Biophysical Chemistry</i> , 2005, 115, 229-233.	1.5	15
136	Unfolding and Refolding in Vitro of a Tetrameric, α -Helical Membrane Protein: The Prokaryotic Potassium Channel KcsA. <i>Biochemistry</i> , 2005, 44, 14344-14352.	1.2	60
137	The Conformational Stability and Thermodynamics of Fur A (Ferric Uptake Regulator) from <i>Anabaena</i> sp. PCC 7119. <i>Biophysical Journal</i> , 2005, 89, 4188-4200.	0.2	10
138	The conformational stability of the <i>Streptomyces coelicolor</i> histidine-phosphocarrier protein. <i>FEBS Journal</i> , 2004, 271, 2165-2181.	0.2	16
139	The dimerization domain of the HIV-1 capsid protein binds a capsid protein-derived peptide: A biophysical characterization. <i>Protein Science</i> , 2004, 13, 1512-1523.	3.1	44
140	The inactivating factor of glutamine synthetase, IF7, is a α -natively unfolded protein. <i>Protein Science</i> , 2003, 12, 1443-1454.	3.1	39
141	The histidine-phosphocarrier protein of <i>Streptomyces coelicolor</i> folds by a partially folded species at low pH. <i>FEBS Journal</i> , 2003, 270, 2254-2267.	0.2	15
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