

Jose Luis Neira

List of Publications by Year in descending order

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papers

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citations

117625

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docs citations

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times ranked

3487
citing authors

#	ARTICLE	IF	CITATIONS
1	Towards a complete description of the structural and dynamic properties of the denatured state of barnase and the role of residual structure in folding 1 Edited by B. Honig. Journal of Molecular Biology, 2000, 296, 1257-1282.	4.2	171
2	High-resolution Three-dimensional Structure of Ribonuclease A in Solution by Nuclear Magnetic Resonance Spectroscopy. Journal of Molecular Biology, 1993, 229, 722-734.	4.2	155
3	Human p8 Is a HMG-I/Y-like Protein with DNA Binding Activity Enhanced by Phosphorylation. Journal of Biological Chemistry, 2001, 276, 2742-2751.	3.4	110
4	Regulation of apoptosis by the p8/prothymosin $\hat{\Delta}$ complex. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 2671-2676.	7.1	109
5	Identification of a Drug Targeting an Intrinsically Disordered Protein Involved in Pancreatic Adenocarcinoma. Scientific Reports, 2017, 7, 39732.	3.3	101
6	An N-terminal fragment of barnase has residual helical structure similar to that in a refolding intermediate. Journal of Molecular Biology, 1992, 224, 749-758.	4.2	93
7	Hydrogen exchange in chymotrypsin inhibitor 2 probed by denaturants and temperature. Journal of Molecular Biology, 1997, 270, 89-98.	4.2	89
8	Binding of the C-terminal Sterile $\hat{\Delta}$ Motif (SAM) Domain of Human p73 to Lipid Membranes. Journal of Biological Chemistry, 2003, 278, 46878-46885.	3.4	78
9	Targeting intrinsically disordered proteins involved in cancer. Cellular and Molecular Life Sciences, 2020, 77, 1695-1707.	5.4	74
10	Search for Nucleation Sites in Smaller Fragments of Chymotrypsin Inhibitor 2. Journal of Molecular Biology, 1995, 254, 289-304.	4.2	72
11	Exploring the Folding Funnel of a Polypeptide Chain by Biophysical Studies on Protein Fragments. Journal of Molecular Biology, 1999, 285, 1309-1333.	4.2	71
12	Sequential $^1\text{H-NMR}$ assignment and solution structure of bovine pancreatic ribonuclease A. FEBS Journal, 1989, 183, 623-638.	0.2	69
13	Hydrogen exchange in chymotrypsin inhibitor 2 probed by mutagenesis. Journal of Molecular Biology, 1997, 270, 99-110.	4.2	68
14	Ligand-based design identifies a potent NUPR1 inhibitor exerting anticancer activity via necroptosis. Journal of Clinical Investigation, 2019, 129, 2500-2513.	8.2	68
15	Hydrogen exchange in ribonuclease A and ribonuclease S: evidence for residual structure in the unfolded state under native conditions 1 Edited by P. E. Wright. Journal of Molecular Biology, 1999, 285, 627-643.	4.2	67
16	Conformational Pathway of the Polypeptide Chain of Chymotrypsin Inhibitor-2 Growing from its N Terminus in vitro. Parallels with the Protein Folding Pathway. Journal of Molecular Biology, 1995, 254, 968-979.	4.2	66
17	Folding studies on ribonuclease A, a model protein. Folding & Design, 1997, 2, R1-R11.	4.5	61
18	Unfolding and Refolding in Vitro of a Tetrameric, $\hat{\Delta}$ -Helical Membrane Protein: $\hat{\Delta}$ The Prokaryotic Potassium Channel KcsA. Biochemistry, 2005, 44, 14344-14352.	2.5	60

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19	Thermodynamic Dissection of a Low Affinity Protein-Protein Interface Involved in Human Immunodeficiency Virus Assembly. <i>Journal of Biological Chemistry</i> , 2003, 278, 27923-27929.	3.4	59
20	Biochemical analysis of the recombinant Fur (ferric uptake regulator) protein from <i>Anabaena PCC 7119</i> : factors affecting its oligomerization state. <i>Biochemical Journal</i> , 2002, 366, 315-322.	3.7	51
21	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.	0.5	48
22	Discovery of Specific Flavodoxin Inhibitors as Potential Therapeutic Agents against <i>Helicobacter pylori</i> Infection. <i>ACS Chemical Biology</i> , 2009, 4, 928-938.	3.4	48
23	The Isolated C-Terminal Domain of Ring1B Is a Dimer Made of Stable, Well-Structured Monomers. <i>Biochemistry</i> , 2007, 46, 12764-12776.	2.5	46
24	p8/nupr1 regulates DNA repair activity after double-strand gamma irradiation-induced DNA damage. <i>Journal of Cellular Physiology</i> , 2009, 221, 594-602.	4.1	46
25	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.	7.6	44
26	Inactivation of NUPR1 promotes cell death by coupling ER-stress responses with necrosis. <i>Scientific Reports</i> , 2018, 8, 16999.	3.3	44
27	3D structure of bovine pancreatic ribonuclease A in aqueous solution: An approach to tertiary structure determination from a small basis of 1H NMR NOE correlations. <i>Journal of Biomolecular NMR</i> , 1991, 1, 283-298.	2.8	43
28	Dendrimers as Potential Inhibitors of the Dimerization of the Capsid Protein of HIV-1. <i>Biomacromolecules</i> , 2010, 11, 2069-2078.	5.4	41
29	The inactivating factor of glutamine synthetase, IF7, is a natively unfolded protein. <i>Protein Science</i> , 2003, 12, 1443-1454.	7.6	39
30	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.	7.1	39
31	Towards the complete structural characterization of a protein folding pathway: the structures of the denatured, transition and native states for the association/folding of two complementary fragments of cleaved chymotrypsin inhibitor 2. Direct evidence for a nucleation-condensation mechanism. <i>Folding & Design</i> , 1996, 1, 189-208.	4.5	37
32	The Transcriptional Repressor RYBP Is a Natively Unfolded Protein Which Folds upon Binding to DNA. <i>Biochemistry</i> , 2009, 48, 1348-1360.	2.5	37
33	The Basic Helix-Loop-Helix Region of Human Neurogenin 1 Is a Monomeric Natively Unfolded Protein Which Forms a Fuzzy Complex upon DNA Binding. <i>Biochemistry</i> , 2010, 49, 1577-1589.	2.5	36
34	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.	3.3	35
35	Acquisition of native-like interactions in C-terminal fragments of barnase 1 Edited by J. Karn. <i>Journal of Molecular Biology</i> , 1999, 287, 421-432.	4.2	34
36	Enhanced vulnerability of human proteins towards disease-associated inactivation through divergent evolution. <i>Human Molecular Genetics</i> , 2017, 26, 3531-3544.	2.9	34

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37	Deciphering the Binding between Nupr1 and MSL1 and Their DNA-Repairing Activity. PLoS ONE, 2013, 8, e78101.	2.5	33
38	NUPR1 inhibitor ZZW-115 induces ferroptosis in a mitochondria-dependent manner. Cell Death Discovery, 2021, 7, 269.	4.7	33
39	Determinants of the pKa values of ionizable residues in an intrinsically disordered protein. Archives of Biochemistry and Biophysics, 2016, 598, 18-27.	3.0	32
40	Following co-operative formation of secondary and tertiary structure in a single protein module. Journal of Molecular Biology, 1997, 268, 185-197.	4.2	30
41	Equilibrium Unfolding of the C-Terminal SAM Domain of p73. Biochemistry, 2002, 41, 5743-5753.	2.5	29
42	The Monomeric Species of the Regulatory Domain of Tyrosine Hydroxylase Has a Low Conformational Stability. Biochemistry, 2016, 55, 3418-3431.	2.5	29
43	Targeting the Stress-Induced Protein NUPR1 to Treat Pancreatic Adenocarcinoma. Cells, 2019, 8, 1453.	4.1	28
44	Insights into the Functionality of the Putative Residues Involved in Enterocin AS-48 Maturation. Applied and Environmental Microbiology, 2010, 76, 7268-7276.	3.1	27
45	Peptide group chemical shift computation. Magnetic Resonance in Chemistry, 1992, 30, 1012-1018.	1.9	26
46	The capsid protein of human immunodeficiency virus: designing inhibitors of capsid assembly. FEBS Journal, 2009, 276, 6110-6117.	4.7	26
47	Conformational Stability of Hepatitis C Virus NS3 Protease. Biophysical Journal, 2010, 99, 3811-3820.	0.5	26
48	Kinetic and thermodynamic effects of phosphorylation on p53 binding to MDM2. Scientific Reports, 2019, 9, 693.	3.3	25
49	An extensive thermodynamic characterization of the dimerization domain of the HIV-1 capsid protein. Protein Science, 2005, 14, 2387-2404.	7.6	24
50	ZZW-115-dependent inhibition of NUPR1 nuclear translocation sensitizes cancer cells to genotoxic agents. JCI Insight, 2020, 5, .	5.0	24
51	Rationally Designed Interfacial Peptides Are Efficient In Vitro Inhibitors of HIV-1 Capsid Assembly with Antiviral Activity. PLoS ONE, 2011, 6, e23877.	2.5	24
52	Filling Small, Empty Protein Cavities: Structural and Energetic Consequences. Journal of Molecular Biology, 2006, 358, 701-712.	4.2	23
53	Isolation and characterization of a thermostable β -xylosidase in the thermophilic bacterium Geobacillus pallidus. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2007, 1774, 510-518.	2.3	23
54	Structural mobility of the monomeric C-terminal domain of the HIV-1 capsid protein. FEBS Journal, 2008, 275, 3299-3311.	4.7	23

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55	An NMR study on the \hat{I}^2 -hairpin region of barnase. <i>Folding & Design</i> , 1996, 1, 231-241.	4.5	22
56	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.	2.4	22
57	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.	2.5	22
58	Thermodynamics of zinc binding to hepatitis C virus NS3 protease: A folding by binding event. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 624-636.	2.6	21
59	Structure and dynamics of the potato carboxypeptidase inhibitor by 1H and 15N NMR. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 50, 410-422.	2.6	19
60	p8 and Prothymosin Alpha : Unity is Strength. <i>Cell Cycle</i> , 2006, 5, 829-830.	2.6	17
61	The family 52 \hat{I}^2 -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.	2.3	17
62	NMR as a tool to identify and characterize protein folding intermediates. <i>Archives of Biochemistry and Biophysics</i> , 2013, 531, 90-99.	3.0	17
63	Crowding Effects on the Structure and Dynamics of the Intrinsically Disordered Nuclear Chromatin Protein NUPR1. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 684622.	3.5	17
64	The conformational stability of the <i>Streptomyces coelicolor</i> histidine-phosphocarrier protein. <i>FEBS Journal</i> , 2004, 271, 2165-2181.	0.2	16
65	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.	3.1	16
66	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.	4.1	16
67	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.	5.4	16
68	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
69	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.	2.8	15
70	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.	1.8	15
71	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.	7.5	15
72	Design of Inhibitors of the Intrinsically Disordered Protein NUPR1: Balance between Drug Affinity and Target Function. <i>Biomolecules</i> , 2021, 11, 1453.	4.0	15

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73	Stability and folding of the protein complexes of barnase. FEBS Journal, 2000, 267, 2859-2870.	0.2	14
74	Biophysical Characterization of the Enzyme I of the Streptomyces coelicolor Phosphoenolpyruvate: Sugar Phosphotransferase System. Biophysical Journal, 2006, 90, 4592-4604.	0.5	14
75	Functional Characterization of Nupr1L, A Novel p53-Regulated Isoform of the High-Mobility Group (HMG)-Related Protumoral Protein Nupr1. Journal of Cellular Physiology, 2015, 230, 2936-2950.	4.1	14
76	Dissecting the Binding between Glutamine Synthetase and Its Two Natively Unfolded Protein Inhibitors. Biochemistry, 2016, 55, 3370-3382.	2.5	14
77	Three-Dimensional Solution Structure and Stability of Thioredoxin m from Spinach. Biochemistry, 2001, 40, 15246-15256.	2.5	13
78	Conformational Stability of Helicobacter pylori Flavodoxin. Journal of Biological Chemistry, 2008, 283, 2883-2895.	3.4	13
79	Metal-triggered changes in the stability and secondary structure of a tetrameric dihydropyrimidinase: A biophysical characterization. Biophysical Chemistry, 2009, 139, 42-52.	2.8	13
80	The Structure of BRMS1 Nuclear Export Signal and SNX6 Interacting Region Reveals a Hexamer Formed by Antiparallel Coiled Coils. Journal of Molecular Biology, 2011, 411, 1114-1127.	4.2	13
81	A Phosphorylation-Induced Switch in the Nuclear Localization Sequence of the Intrinsically Disordered NUPR1 Hampers Binding to Importin. Biomolecules, 2020, 10, 1313.	4.0	13
82	N-type Inactivation of the Potassium Channel KcsA by the Shaker B α -Peptide. Journal of Biological Chemistry, 2008, 283, 18076-18085.	3.4	12
83	The CBS domain protein MJ0729 of <i>Methanocaldococcus jannaschii</i> binds DNA. FEBS Letters, 2010, 584, 4485-4489.	2.8	12
84	Biochemical and biophysical characterization of PADI4 supports its involvement in cancer. Archives of Biochemistry and Biophysics, 2022, 717, 109125.	3.0	12
85	Site-directed mutagenesis indicates an important role of cysteines 76 and 181 in the catalysis of hydantoin racemase from <i>Sinorhizobium meliloti</i> . Protein Science, 2006, 15, 2729-2738.	7.6	11
86	Defining the Epitope Region of a Peptide from the Streptomyces coelicolor Phosphoenolpyruvate: Sugar Phosphotransferase System Able to Bind to the Enzyme I. Biophysical Journal, 2008, 95, 1336-1348.	0.5	11
87	Dendrimers as Competitors of Protein-Protein Interactions of the Intrinsically Disordered Nuclear Chromatin Protein NUPR1. Biomacromolecules, 2019, 20, 2567-2576.	5.4	11
88	The C-terminal SAM domain of p73 binds to the N terminus of MDM2. Biochimica Et Biophysica Acta - General Subjects, 2019, 1863, 760-770.	2.4	11
89	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. Biochimica Et Biophysica Acta - General Subjects, 2020, 1864, 129609.	2.4	11
90	Hydrogen exchange of the tetramerization domain of the human tumour suppressor p53 probed by denaturants and temperature. FEBS Journal, 2001, 268, 4868-4877.	0.2	10

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91	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.	0.5	10
92	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.	3.7	10
93	Envelope Lipids Regulate the In Vitro Assembly of the HIV-1 Capsid. <i>Biophysical Journal</i> , 2008, 94, L08-L10.	0.5	10
94	Structure and conformational stability of a tetrameric thermostable α -succinylamino acid racemase. <i>Biopolymers</i> , 2009, 91, 757-772.	2.4	10
95	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.	2.5	10
96	High-recovery one-step purification of the DNA-binding protein Fur by mild guanidinium chloride treatment. <i>Process Biochemistry</i> , 2010, 45, 292-296.	3.7	10
97	Evidence of non-functional redundancy between two pea h-type thioredoxins by specificity and stability studies. <i>Journal of Plant Physiology</i> , 2010, 167, 423-429.	3.5	10
98	Structural dissection of the C-terminal sterile alpha motif (SAM) of human p73. <i>Archives of Biochemistry and Biophysics</i> , 2014, 558, 133-142.	3.0	10
99	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.	3.0	10
100	A group II intron-encoded protein interacts with the cellular replicative machinery through the β -sliding clamp. <i>Nucleic Acids Research</i> , 2019, 47, 7605-7617.	14.5	10
101	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.	0.7	10
102	The Carboxy-Terminal Domain of Erb1 Is a Seven-Bladed β -Propeller that Binds RNA. <i>PLoS ONE</i> , 2015, 10, e0123463.	2.5	10
103	Equilibrium unfolding studies of the rat liver methionine adenosyltransferase III, a dimeric enzyme with intersubunit active sites. <i>Biochemical Journal</i> , 2002, 361, 307.	3.7	9
104	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.	2.8	9
105	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.	2.6	9
106	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.	3.7	9
107	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.	2.5	8
108	Biophysical and Structural Studies on the Capsid Protein of the Human Immunodeficiency Virus Type 1: A New Drug Target?. <i>Scientific World Journal</i> , The, 2009, 9, 404-419.	2.1	8

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109	The regulatory factor SipA is a highly stable β class protein with a SH3 fold. FEBS Letters, 2010, 584, 989-994.	2.8	8
110	The Inactivating Factor of Glutamine Synthetase IF17 Is an Intrinsically Disordered Protein, Which Folds upon Binding to Its Target. Biochemistry, 2011, 50, 9767-9778.	2.5	8
111	The Histidine-Phosphocarrier Protein of the Phosphoenolpyruvate: Sugar Phosphotransferase System of <i>Bacillus sphaericus</i> Self-Associates. PLoS ONE, 2013, 8, e69307.	2.5	8
112	Biochemical and mutational studies of allantoinase from <i>Bacillus licheniformis</i> CECT 20T. Biochimie, 2014, 99, 178-188.	2.6	8
113	Dynamics of the intrinsically disordered protein NUPR1 in isolation and in its fuzzy complexes with DNA and prothymosin β . Biochimica Et Biophysica Acta - Proteins and Proteomics, 2019, 1867, 140252.	2.3	8
114	The PipX Protein, When Not Bound to Its Targets, Has Its Signaling C-Terminal Helix in a Flexed Conformation. Biochemistry, 2017, 56, 3211-3224.	2.5	8
115	The Helical Structure Propensity in the First Helix of the Histidine Phosphocarrier Protein of <i>Streptomyces coelicolor</i> . Protein and Peptide Letters, 2007, 14, 281-290.	0.9	7
116	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.	2.1	7
117	Structural characterisation of the natively unfolded enterocin EJ97. Protein Engineering, Design and Selection, 2010, 23, 507-518.	2.1	7
118	Peptides as Inhibitors of the First Phosphorylation Step of the <i>Streptomyces coelicolor</i> Phosphoenolpyruvate: Sugar Phosphotransferase System. Biochemistry, 2012, 51, 7393-7402.	2.5	7
119	Fluorescence, Circular Dichroism and Mass Spectrometry as Tools to Study Virus Structure. Sub-Cellular Biochemistry, 2013, 68, 177-202.	2.4	7
120	The histidine phosphocarrier protein, HPr, binds to the highly thermostable regulator of sigma D protein, Rsd, and its isolated helical fragments. Archives of Biochemistry and Biophysics, 2018, 639, 26-37.	3.0	7
121	The Parologue of the Intrinsically Disordered Nuclear Protein 1 Has a Nuclear Localization Sequence that Binds to Human Importin β 3. International Journal of Molecular Sciences, 2020, 21, 7428.	4.1	7
122	The isolated armadillo-repeat domain of Plakophilin 1 is a monomer in solution with a low conformational stability. Journal of Structural Biology, 2020, 211, 107569.	2.8	7
123	Human Enzyme PADI4 Binds to the Nuclear Carrier Importin β 3. Cells, 2022, 11, 2166.	4.1	7
124	Mutation of Ser-50 and Cys-66 in Snapin Modulates Protein Structure and Stability. Biochemistry, 2012, 51, 3470-3484.	2.5	6
125	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. Archives of Biochemistry and Biophysics, 2012, 526, 44-53.	3.0	6
126	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. Protein Science, 2017, 26, 1105-1115.	7.6	6

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127	The nuclear localization sequence of the epigenetic factor RYBP binds to human importin β 3. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2021, 1869, 140670.	2.3	6
128	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.	2.5	6
129	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.	1.4	6
130	Spain should implement a model that's known to work. <i>Nature</i> , 2008, 453, 26-27.	27.8	5
131	Into the Lipid Realm: Stability and Thermodynamics of Membrane Proteins. <i>Current Protein and Peptide Science</i> , 2008, 9, 626-637.	1.4	5
132	Biophysical characterization of the isolated C-terminal region of the transient receptor potential vanilloid 1. <i>FEBS Letters</i> , 2012, 586, 1154-1159.	2.8	5
133	BRMS151 α 98 and BRMS151 α 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.	4.2	5
134	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.	4.1	5
135	The muscle-relaxing C-terminal peptide from troponin I populates a nascent helix, facilitating binding to tropomyosin with a potent therapeutic effect. <i>Journal of Biological Chemistry</i> , 2021, 296, 100228.	3.4	5
136	Folded and Unfolded Conformations of Proteins Involved in Pancreatic Cancer: a Layman's Guide. <i>Scientific World Journal</i> , The, 2010, 10, 1612-1633.	2.1	4
137	Pancreatic Cancer: Molecular, Biochemical, Chemopreventive, and Therapeutic Aspects. <i>Scientific World Journal</i> , The, 2010, 10, 1967-1970.	2.1	4
138	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.	5.4	4
139	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.	1.9	4
140	Human COA3 Is an Oligomeric Highly Flexible Protein in Solution. <i>Biochemistry</i> , 2016, 55, 6209-6220.	2.5	4
141	Intrinsically disordered proteins in biology: One for all, all for one. <i>Archives of Biochemistry and Biophysics</i> , 2020, 684, 108328.	3.0	4
142	Intrinsically disordered protein NUPR1 binds to the armadillo-repeat domain of Plakophilin 1. <i>International Journal of Biological Macromolecules</i> , 2021, 170, 549-560.	7.5	4
143	The Histidine Phosphocarrier Kinase/Phosphorylase from <i>Bacillus Subtilis</i> Is an Oligomer in Solution with a High Thermal Stability. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3231.	4.1	4
144	An N-terminal half fragment of the histidine phosphocarrier protein, HPr, is disordered but binds to HPr partners and shows antibacterial properties. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2021, 1865, 130015.	2.4	4

#	ARTICLE	IF	CITATIONS
145	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.	2.3	3
146	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.	2.1	3
147	Protein folding and stability: A Prague cemetery. <i>Archives of Biochemistry and Biophysics</i> , 2013, 531, 1-3.	3.0	3
148	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.	0.5	3
149	The armadillo-repeat domain of plakophilin 1 binds the C-terminal sterile alpha motif (SAM) of p73. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2021, 1865, 129914.	2.4	3
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152	Falling Down: Landscape and Kinetics of One-Dimensional Protein Folding. <i>Structure</i> , 2013, 21, 1905-1907.	3.3	2
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157	Investigation of action pattern of a novel chondroitin sulfate/dermatan sulfate 4-O-sulfatase. <i>Biochemical Journal</i> , 2021, 478, 281-298.	3.7	2
158	The isolated GTPase-activating-protein-related domain of neurofibromin-1 has a low conformational stability in solution. <i>Archives of Biochemistry and Biophysics</i> , 2021, 700, 108767.	3.0	2
159	An N-terminally Truncated Mutant of Human Chemokine CXCL14 has Biological Activity. <i>Protein and Peptide Letters</i> , 2013, 20, 955-967.	0.9	2
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164	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.	2.3	1
165	Nuclear Magnetic Resonance Spectroscopy to Study Virus Structure. <i>Sub-Cellular Biochemistry</i> , 2013, 68, 145-176.	2.4	1
166	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.	2.8	1
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