

Jose Luis Neira

List of Publications by Year in descending order

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168
papers

3,794
citations

117625

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168389

53
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169
all docs

169
docs citations

169
times ranked

3487
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. | 3.0 | 12 |
| 2 | Human Enzyme PADI4 Binds to the Nuclear Carrier Importin β 3. Cells, 2022, 11, 2166. | 4.1 | 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. | 3.4 | 5 |
| 4 | Investigation of action pattern of a novel chondroitin sulfate/dermatan sulfate 4-O-sulfatase. Biochemical Journal, 2021, 478, 281-298. | 3.7 | 2 |
| 5 | Intrinsically disordered protein NUPR1 binds to the armadillo-repeat domain of Plakophilin 1. International Journal of Biological Macromolecules, 2021, 170, 549-560. | 7.5 | 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. | 4.1 | 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. | 3.0 | 2 |
| 8 | Crowding Effects on the Structure and Dynamics of the Intrinsically Disordered Nuclear Chromatin Protein NUPR1. Frontiers in Molecular Biosciences, 2021, 8, 684622. | 3.5 | 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. | 2.4 | 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. | 2.3 | 6 |
| 11 | NUPR1 inhibitor ZZW-115 induces ferroptosis in a mitochondria-dependent manner. Cell Death Discovery, 2021, 7, 269. | 4.7 | 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. | 2.4 | 4 |
| 13 | Design of Inhibitors of the Intrinsically Disordered Protein NUPR1: Balance between Drug Affinity and Target Function. Biomolecules, 2021, 11, 1453. | 4.0 | 15 |
| 14 | Discrimination of sulfated isomers of chondroitin sulfate disaccharides by HILIC-MS. Analytical and Bioanalytical Chemistry, 2021, 413, 7107-7117. | 3.7 | 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. | 4.1 | 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. | 2.8 | 2 |
| 17 | Targeting intrinsically disordered proteins involved in cancer. Cellular and Molecular Life Sciences, 2020, 77, 1695-1707. | 5.4 | 74 |
| 18 | A Phosphorylation-Induced Switch in the Nuclear Localization Sequence of the Intrinsically Disordered NUPR1 Hampers Binding to Importin. Biomolecules, 2020, 10, 1313. | 4.0 | 13 |

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|----|---|------|-----------|
| 19 | The Paralogue 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. | 4.1 | 7 |
| 20 | Intrinsically disordered proteins in biology: One for all, all for one. <i>Archives of Biochemistry and Biophysics</i> , 2020, 684, 108328. | 3.0 | 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. | 2.8 | 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. | 3.0 | 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. | 2.4 | 11 |
| 25 | ZZW-115-dependent inhibition of NUPR1 nuclear translocation sensitizes cancer cells to genotoxic agents. <i>JCI Insight</i> , 2020, 5, . | 5.0 | 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. | 2.3 | 8 |
| 27 | Kinetic and thermodynamic effects of phosphorylation on p53 binding to MDM2. <i>Scientific Reports</i> , 2019, 9, 693. | 3.3 | 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. | 3.0 | 10 |
| 29 | Dendrimers as Competitors of Protein-Protein Interactions of the Intrinsically Disordered Nuclear Chromatin Protein NUPR1. <i>Biomacromolecules</i> , 2019, 20, 2567-2576. | 5.4 | 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. | 14.5 | 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. | 0.7 | 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. | 2.4 | 11 |
| 33 | Targeting the Stress-Induced Protein NUPR1 to Treat Pancreatic Adenocarcinoma. <i>Cells</i> , 2019, 8, 1453. | 4.1 | 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. | 7.5 | 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. | 8.2 | 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. | 3.0 | 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. | 2.4 | 22 |
| 38 | Inactivation of NUPR1 promotes cell death by coupling ER-stress responses with necrosis. <i>Scientific Reports</i> , 2018, 8, 16999. | 3.3 | 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. | 4.1 | 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. | 4.1 | 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. | 3.7 | 9 |
| 42 | Identification of a Drug Targeting an Intrinsically Disordered Protein Involved in Pancreatic Adenocarcinoma. <i>Scientific Reports</i> , 2017, 7, 39732. | 3.3 | 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. | 2.8 | 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. | 7.6 | 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. | 3.0 | 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. | 3.3 | 35 |
| 47 | Enhanced vulnerability of human proteins towards disease-associated inactivation through divergent evolution. <i>Human Molecular Genetics</i> , 2017, 26, 3531-3544. | 2.9 | 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. | 7.1 | 39 |
| 49 | An introduction to the special issue on biomolecular NMR. <i>Archives of Biochemistry and Biophysics</i> , 2017, 628, 1-2. | 3.0 | 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. | 2.5 | 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. | 3.0 | 32 |
| 52 | The Monomeric Species of the Regulatory Domain of Tyrosine Hydroxylase Has a Low Conformational Stability. <i>Biochemistry</i> , 2016, 55, 3418-3431. | 2.5 | 29 |
| 53 | Dissecting the Binding between Glutamine Synthetase and Its Two Natively Unfolded Protein Inhibitors. <i>Biochemistry</i> , 2016, 55, 3370-3382. | 2.5 | 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. | 2.6 | 9 |

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|----|--|-----|-----------|
| 55 | Human COA3 Is an Oligomeric Highly Flexible Protein in Solution. <i>Biochemistry</i> , 2016, 55, 6209-6220. | 2.5 | 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. | 5.4 | 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. | 4.1 | 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. | 0.5 | 3 |
| 59 | The Carboxy-Terminal Domain of Erb1 Is a Seven-Bladed Å-Propeller that Binds RNA. <i>PLoS ONE</i> , 2015, 10, e0123463. | 2.5 | 10 |
| 60 | Biochemical and mutational studies of allantoinase from <i>Bacillus licheniformis</i> CECT 20T. <i>Biochimie</i> , 2014, 99, 178-188. | 2.6 | 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. | 2.1 | 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. | 3.0 | 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. | 1.8 | 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. | 2.5 | 22 |
| 65 | Falling Down: Landscape and Kinetics of One-Dimensional Protein Folding. <i>Structure</i> , 2013, 21, 1905-1907. | 3.3 | 2 |
| 66 | Protein folding and stability: A Prague cemetery. <i>Archives of Biochemistry and Biophysics</i> , 2013, 531, 1-3. | 3.0 | 3 |
| 67 | 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 |
| 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. | 4.2 | 5 |
| 69 | Nuclear Magnetic Resonance Spectroscopy to Study Virus Structure. <i>Sub-Cellular Biochemistry</i> , 2013, 68, 145-176. | 2.4 | 1 |
| 70 | Fluorescence, Circular Dichroism and Mass Spectrometry as Tools to Study Virus Structure. <i>Sub-Cellular Biochemistry</i> , 2013, 68, 177-202. | 2.4 | 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. | 2.5 | 8 |
| 72 | Deciphering the Binding between Nupr1 and MSL1 and Their DNA-Repairing Activity. <i>PLoS ONE</i> , 2013, 8, e78101. | 2.5 | 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. | 4.1 | 16 |
| 74 | An N-terminally Truncated Mutant of Human Chemokine CXCL14 has Biological Activity. <i>Protein and Peptide Letters</i> , 2013, 20, 955-967. | 0.9 | 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. | 1.4 | 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. | 2.8 | 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. | 2.5 | 7 |
| 78 | Mutation of Ser-50 and Cys-66 in Snapin Modulates Protein Structure and Stability. <i>Biochemistry</i> , 2012, 51, 3470-3484. | 2.5 | 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. | 3.0 | 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. | 1.9 | 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. | 2.3 | 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. | 2.8 | 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. | 3.1 | 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. | 2.5 | 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. | 5.4 | 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. | 4.2 | 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. | 2.3 | 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. | 2.1 | 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. | 2.5 | 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. | 2.5 | 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. | 2.8 | 8 |
| 92 | The CBS domain protein MJ0729 of <i>Methanocaldococcus jannaschii</i> binds DNA. FEBS Letters, 2010, 584, 4485-4489. | 2.8 | 12 |
| 93 | High-recovery one-step purification of the DNA-binding protein Fur by mild guanidinium chloride treatment. Process Biochemistry, 2010, 45, 292-296. | 3.7 | 10 |
| 94 | The Bronze Age of science in Spain. EMBO Reports, 2010, 11, 12-13. | 4.5 | 2 |
| 95 | Folded and Unfolded Conformations of Proteins Involved in Pancreatic Cancer: a Layman's Guide. Scientific World Journal, The, 2010, 10, 1612-1633. | 2.1 | 4 |
| 96 | Pancreatic Cancer: Molecular, Biochemical, Chemopreventive, and Therapeutic Aspects. Scientific World Journal, The, 2010, 10, 1967-1970. | 2.1 | 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. | 2.1 | 7 |
| 98 | Structural characterisation of the natively unfolded enterocin EJ97. Protein Engineering, Design and Selection, 2010, 23, 507-518. | 2.1 | 7 |
| 99 | Conformational Stability of Hepatitis C Virus NS3 Protease. Biophysical Journal, 2010, 99, 3811-3820. | 0.5 | 26 |
| 100 | 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 |
| 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. | 2.5 | 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. | 3.5 | 10 |
| 103 | Dendrimers as Potential Inhibitors of the Dimerization of the Capsid Protein of HIV-1. Biomacromolecules, 2010, 11, 2069-2078. | 5.4 | 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. | 2.1 | 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. | 2.1 | 1 |
| 106 | p8/nupr1 regulates DNA repair activity after double-strand gamma irradiation-induced DNA damage. Journal of Cellular Physiology, 2009, 221, 594-602. | 4.1 | 46 |
| 107 | Structure and conformational stability of a tetrameric thermostable <i>N</i> -succinylamino acid racemase. Biopolymers, 2009, 91, 757-772. | 2.4 | 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. | 2.6 | 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. | 4.7 | 2 |
| 110 | The capsid protein of human immunodeficiency virus: designing inhibitors of capsid assembly. <i>FEBS Journal</i> , 2009, 276, 6110-6117. | 4.7 | 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. | 2.8 | 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. | 2.5 | 10 |
| 113 | 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 |
| 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. | 3.4 | 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. | 2.3 | 17 |
| 116 | Structural mobility of the monomeric C-terminal domain of the HIV-1 capsid protein. <i>FEBS Journal</i> , 2008, 275, 3299-3311. | 4.7 | 23 |
| 117 | Spain should implement a model that's known to work. <i>Nature</i> , 2008, 453, 26-27. | 27.8 | 5 |
| 118 | Envelope Lipids Regulate the In Vitro Assembly of the HIV-1 Capsid. <i>Biophysical Journal</i> , 2008, 94, L08-L10. | 0.5 | 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. | 0.5 | 11 |
| 120 | Conformational Stability of <i>Helicobacter pylori</i> Flavodoxin. <i>Journal of Biological Chemistry</i> , 2008, 283, 2883-2895. | 3.4 | 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. | 3.4 | 12 |
| 122 | Into the Lipid Realm: Stability and Thermodynamics of Membrane Proteins. <i>Current Protein and Peptide Science</i> , 2008, 9, 626-637. | 1.4 | 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. | 0.9 | 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. | 2.5 | 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. | 2.5 | 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. | 0.5 | 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. | 2.3 | 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. | 0.5 | 14 |
| 129 | Filling Small, Empty Protein Cavities: Structural and Energetic Consequences. <i>Journal of Molecular Biology</i> , 2006, 358, 701-712. | 4.2 | 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. | 3.7 | 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. | 7.6 | 11 |
| 132 | p8 and Prothymosin Alpha : Unity is Strength. <i>Cell Cycle</i> , 2006, 5, 829-830. | 2.6 | 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. | 7.1 | 109 |
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