Javier Sancho

List of Publications by Year
in descending order

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146
papers

5,772
citations

71102
41
h-index

95266
68
g-index

149
all docs

149
docs citations

149
times ranked

5616
citing authors

#	ARTICLE	IF	CITATIONS
1	Î±-Helix stability in proteins. Journal of Molecular Biology, 1992, 227, 544-559.	4.2	323
2	Histidine-aromatic interactions in barnase. Journal of Molecular Biology, 1992, 224, 759-770.	4.2	207
3	Effect of alanine versus glycine in Î±-helices on protein stability. Nature, 1992, 356, 453-455.	27.8	204
4	Flavodoxins: sequence, folding, binding, function and beyond. Cellular and Molecular Life Sciences, 2006, 63, 855-864.	5.4	175
5	Circular dichroism studies of barnase and its mutants: Characterization of the contribution of aromatic side chains. Biochemistry, 1993, 32, 10303-10313.	2.5	166
6	Small molecule inhibits Î±-synuclein aggregation, disrupts amyloid fibrils, and prevents degeneration of dopaminergic neurons. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 10481-10486.	7.1	166
7	Identification of pharmacological chaperones as potential therapeutic agents to treat phenylketonuria. Journal of Clinical Investigation, 2008, 118, 2858-2867.	8.2	145
8	Fluorescence spectrum of barnase: contributions of three tryptophan residues and a histidine-related pH dependence. Biochemistry, 1991, 30, 6775-6779.	2.5	143
9	Histidine residues at the N- and C-termini of .alpha.-helixes: perturbed pKas and protein stability. Biochemistry, 1992, 31, 2253-2258.	2.5	138
10	Miglustat (NB-DNJ) works as a chaperone for mutated acid Î²-glucosidase in cells transfected with several Gaucher disease mutations. Blood Cells, Molecules, and Diseases, 2005, 35, 268-276.	1.4	115
11	The Tryptophan/Histidine interaction in Î±-helices. Journal of Molecular Biology, 1997, 267, 184-197.	4.2	101
12	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
13	Differential Stabilization of the Three FMN Redox Forms by Tyrosine 94 and Tryptophan 57 in Flavodoxin fromAnabaenaand Its Influence on the Redox Potentialsâ€. Biochemistry, 1997, 36, 14334-14344.	2.5	92
14	Closure of a tyrosine/tryptophan aromatic gate leads to a compact fold in apo flavodoxin. Nature Structural and Molecular Biology, 1996, 3, 329-332.	8.2	87
15	Long-Range Surface Charge-Charge Interactions in Proteins. Journal of Molecular Biology, 1993, 232, 574-583.	4.2	86
16	Dissection of an enzyme by protein engineering. Journal of Molecular Biology, 1992, 224, 741-747.	4.2	84
17	Folding of Barnase in Parts. Biochemistry, 1994, 33, 3778-3786.	2.5	83
18	The active site of pepsin is formed in the intermediate conformation dominant at mildly acidic pH. FEBS Letters, 2003, 538, 89-95.	2.8	82

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19	ProtSA: a web application for calculating sequence specific protein solvent accessibilities in the unfolded ensemble. BMC Bioinformatics, 2009, 10, 104.	2.6	77
20	Conformational stability of apoflavodoxin. Protein Science, 1996, 5, 1376-1388.	7.6	74
21	Energetics of a hydrogen bond (charged and neutral) and of a cation-Ï€ interaction in apoflavodoxin 1 1Edited by A. R. Fersht. Journal of Molecular Biology, 1999, 290, 319-330.	4.2	73
22	Discovering putative prion sequences in complete proteomes using probabilistic representations of Q/N-rich domains. BMC Genomics, 2013, 14, 316.	2.8	73
23	An intragenic suppressor in the cytochrome c oxidase I gene of mouse mitochondrial DNA. Human Molecular Genetics, 2003, 12, 329-339.	2.9	71
24	Purification and properties of ferredoxin-NADP+ oxidoreductase from the nitrogen-fixing cyanobacteria Anabaena variabilis. Archives of Biochemistry and Biophysics, 1988, 260, 200-207.	3.0	69
25	Dissecting the Energetics of the Apoflavodoxin-FMN Complex. Journal of Biological Chemistry, 2000, 275, 9518-9526.	3.4	67
26	High-Throughput Screening Methodology to Identify Alpha-Synuclein Aggregation Inhibitors. International Journal of Molecular Sciences, 2017, 18, 478.	4.1	66
27	Flavodoxin:Quinone Reductase (FqrB): a Redox Partner of Pyruvate:Ferredoxin Oxidoreductase That Reversibly Couples Pyruvate Oxidation to NADPH Production in Helicobacter pylori and Campylobacter jejuni. Journal of Bacteriology, 2007, 189, 4764-4773.	2.2	63
28	Î±-helix stabilization by alanine relative to glycine: Roles of polar and apolar solvent exposures and of backbone entropy. Proteins: Structure, Function and Bioinformatics, 2006, 64, 769-778.	2.6	59
29	Native hydrogen bonds in a molten globule: the apoflavodoxin thermal intermediate. Journal of Molecular Biology, 2001, 306, 877-888.	4.2	56
30	Mapping transition states of protein unfolding by protein engineering of ligand-binding sites. Journal of Molecular Biology, 1991, 221, 1007-1014.	4.2	55
31	Structure of Stable Protein Folding Intermediates by Equilibrium Ï•-Analysis: The Apoflavodoxin Thermal Intermediate. Journal of Molecular Biology, 2004, 344, 239-255.	4.2	55
32	Determination of the excited-state lifetimes of the tryptophan residues in barnase, via multifrequency phase fluorometry of tryptophan mutants. Biochemistry, 1992, 31, 711-716.	2.5	54
33	The stability of 2-state, 3-state and more-state proteins from simple spectroscopic techniques... plus the structure of the equilibrium intermediates at the same time. Archives of Biochemistry and Biophysics, 2013, 531, 4-13.	3.0	51
34	Apoflavodoxin Folding Mechanism:â€‰ An Î±/Î² Protein with an Essentially Off-Pathway Intermediate. Biochemistry, 2001, 40, 15234-15245.	2.5	49
35	The<i>Mycobacterium tuberculosis phoPR</i>Operon Is Positively Autoregulated in the Virulent Strain H37Rv. Journal of Bacteriology, 2008, 190, 7068-7078.	2.2	49
36	Sequence-Specific Solvent Accessibilities of Protein Residues in Unfolded Protein Ensembles. Biophysical Journal, 2006, 91, 4536-4543.	0.5	48

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37	Discovery of Specific Flavodoxin Inhibitors as Potential Therapeutic Agents against <i>Helicobacter pylori</i> Infection. ACS Chemical Biology, 2009, 4, 928-938.	3.4	48
38	Interaction of ferredoxin-NADP+ reductase from Anabaena with its substrates. Archives of Biochemistry and Biophysics, 1991, 288, 231-238.	3.0	46
39	Therapeutic Strategies for Gaucher Disease: Miglustat (NB-DNJ) as a Pharmacological Chaperone for Glucocerebrosidase and the Different Thermostability of Velaglucerase Alfa and Imiglucerase. Molecular Pharmaceutics, 2011, 8, 2390-2397.	4.6	45
40	Antimicrobial Susceptibility and Resistance Patterns among Helicobacter pylori Strains from The Gambia, West Africa. Antimicrobial Agents and Chemotherapy, 2013, 57, 1231-1237.	3.2	45
41	Towards a new therapeutic target: Helicobacter pylori flavodoxin. Biophysical Chemistry, 2005, 115, 267-276.	2.8	44
42	Mechanism of Low Density Lipoprotein (LDL) Release in the Endosome. Journal of Biological Chemistry, 2008, 283, 22670-22679.	3.4	43
43	PrionScan: an online database of predicted prion domains in complete proteomes. BMC Genomics, 2014, 15, 102.	2.8	42
44	Structure of <scp>R</scp>dx<scp>A</scp>Ââ€“Âan oxygenâ€insensitive nitroreductase essential for metronidazole activation in <i><scp>H</scp>elicobacterÂpylori</i>. FEBS Journal, 2012, 279, 4306-4317.	4.7	41
45	The FurA regulon in Anabaena sp. PCC 7120: in silico prediction and experimental validation of novel target genes. Nucleic Acids Research, 2014, 42, 4833-4846.	14.5	41
46	How FMN Binds to Anabaena Apoflavodoxin. Journal of Biological Chemistry, 2003, 278, 24053-24061.	3.4	40
47	Do Proteins Always Benefit from a Stability Increase? Relevant and Residual Stabilisation in a Three-state Protein by Charge Optimisation. Journal of Molecular Biology, 2004, 344, 223-237.	4.2	40
48	The Long and Short Flavodoxins. Journal of Biological Chemistry, 2004, 279, 47177-47183.	3.4	39
49	Discovery of Novel Inhibitors of Amyloid Î²-Peptide 1â€“42 Aggregation. Journal of Medicinal Chemistry, 2012, 55, 9521-9530.	6.4	39
50	Four-State Equilibrium Unfolding of an scFv Antibody Fragmentâ€. Biochemistry, 2002, 41, 9873-9884.	2.5	38
51	Benzbromarone, Quercetin, and Folic Acid Inhibit Amylin Aggregation. International Journal of Molecular Sciences, 2016, 17, 964.	4.1	38
52	Theoretical Analysis of the Electron Spin Density Distribution of the Flavin Semiquinone Isoalloxazine Ring within Model Protein Environments. Journal of Physical Chemistry A, 2002, 106, 4729-4735.	2.5	37
53	Identifying potential novel drugs against Helicobacter pylori by targeting the essential response regulator HsrA. Scientific Reports, 2019, 9, 11294.	3.3	35
54	Cooperative Stabilization of a Molten Globule Apoflavodoxin Fragmentâ€. Biochemistry, 1998, 37, 10589-10596.	2.5	34

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55	Stabilization of apoflavodoxin by replacing hydrogen-bonded charged Asp or Glu residues by the neutral isosteric Asn or Gln. Protein Engineering, Design and Selection, 2001, 14, 173-181.	2.1	33
56	Thermal stability of Î²-lactoglobulin in the presence of aqueous solution of alcohols and polyols. International Journal of Biological Macromolecules, 2007, 40, 423-428.	7.5	32
57	The Flavodoxin from <i>Helicobacter pylori</i>:â€‰ Structural Determinants of Thermostability and FMN Cofactor Binding. Biochemistry, 2008, 47, 627-639.	2.5	32
58	Contribution of Disulfide Bonds to Stability, Folding, and Amyloid Fibril Formation: The PI3-SH3 Domain Case. Antioxidants and Redox Signaling, 2012, 16, 1-15.	5.4	32
59	ZPD-2, a Small Compound That Inhibits Î±-Synuclein Amyloid Aggregation and Its Seeded Polymerization. Frontiers in Molecular Neuroscience, 2019, 12, 306.	2.9	32
60	Anabaena sp. PCC 7119 Flavodoxin as Electron Carrier from Photosystem I to Ferredoxin-NADP+Reductase. Journal of Biological Chemistry, 2002, 277, 22338-22344.	3.4	31
61	The Long and Short Flavodoxins. Journal of Biological Chemistry, 2004, 279, 47184-47191.	3.4	30
62	The native-state ensemble of proteins provides clues for folding, misfolding and function. Trends in Biochemical Sciences, 2006, 31, 494-496.	7.5	30
63	<scp>LDL</scp> receptor/lipoprotein recognition: endosomal weakening of ApoB and ApoE binding to the convex face of the <scp>LR</scp>5 repeat. FEBS Journal, 2014, 281, 1534-1546.	4.7	30
64	Molecular dynamics simulations for genetic interpretation in protein coding regions: where we are, where to go and when. Briefings in Bioinformatics, 2021, 22, 3-19.	6.5	30
65	Role of Neighboring FMN Side Chains in the Modulation of Flavin Reduction Potentials and in the Energetics of the FMN:Apoprotein Interaction inAnabaenaFlavodoxinâ€. Biochemistry, 2004, 43, 15111-15121.	2.5	28
66	Allosteric Inhibitors of the NS3 Protease from the Hepatitis C Virus. PLoS ONE, 2013, 8, e69773.	2.5	28
67	Structural Analysis of an Equilibrium Folding Intermediate in the Apoflavodoxin Native Ensemble by Small-Angle X-ray Scattering. Journal of Molecular Biology, 2011, 406, 604-619.	4.2	27
68	Arginyl groups involved in the binding of Anabaena ferredoxin-NADP+ reductase to NADP+ and to ferredoxin. FEBS Journal, 1990, 187, 39-48.	0.2	26
69	Improved Flavodoxin Inhibitors with Potential Therapeutic Effects against <i>Helicobacter pylori</i> Infection. Journal of Medicinal Chemistry, 2013, 56, 6248-6258.	6.4	26
70	Design and Structure of an Equilibrium Protein Folding Intermediate: A Hint into Dynamical Regions of Proteins. Journal of Molecular Biology, 2010, 400, 922-934.	4.2	25
71	Electron-Nuclear Double Resonance and Hyperfine Sublevel Correlation Spectroscopic Studies of Flavodoxin Mutants from Anabaena sp. PCC 7119. Biophysical Journal, 1999, 77, 1712-1720.	0.5	24
72	Anabaenaapoflavodoxin hydrogen exchange: On the stable exchange core of the Î±/Î²(21345) flavodoxin-like family. Proteins: Structure, Function and Bioinformatics, 2001, 43, 476-488.	2.6	24

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73	Salt-induced stabilization of apoflavodoxin at neutral pH is mediated through cation-specific effects. Protein Science, 2002, 11, 1260-1273.	7.6	24
74	An extensive thermodynamic characterization of the dimerization domain of the HIV-1 capsid protein. Protein Science, 2005, 14, 2387-2404.	7.6	24
75	Native-specific stabilization of flavodoxin by the FMN cofactor: Structural and thermodynamical explanation. Proteins: Structure, Function and Bioinformatics, 2006, 63, 581-594.	2.6	24
76	Common conformational changes in flavodoxins induced by FMN and anion binding: The structure of <i>Helicobacter pylori</i> apoflavodoxin. Proteins: Structure, Function and Bioinformatics, 2007, 69, 581-594.	2.6	24
77	A Double-Deletion Method to Quantifying Incremental Binding Energies in Proteins from Experiment: Example of a Destabilizing Hydrogen Bonding Pair. Biophysical Journal, 2005, 88, 1311-1321.	0.5	23
78	Filling Small, Empty Protein Cavities: Structural and Energetic Consequences. Journal of Molecular Biology, 2006, 358, 701-712.	4.2	23
79	Distant and New Mutations in CTX-M-1 Î²-Lactamase Affect Cefotaxime Hydrolysis. Antimicrobial Agents and Chemotherapy, 2011, 55, 4361-4368.	3.2	23
80	Design, Synthesis, and Efficacy Testing of Nitroethylene- and 7-Nitrobenzoxadiazol-Based Flavodoxin Inhibitors against <i>Helicobacter pylori</i> Drug-Resistant Clinical Strains and in <i>Helicobacter pylori</i>-Infected Mice. Journal of Medicinal Chemistry, 2019, 62, 6102-6115.	6.4	23
81	Flavodoxins as Novel Therapeutic Targets against Helicobacter pylori and Other Gastric Pathogens. International Journal of Molecular Sciences, 2020, 21, 1881.	4.1	23
82	Protein haploinsufficiency drivers identify MYBPC3 variants that cause hypertrophic cardiomyopathy. Journal of Biological Chemistry, 2021, 297, 100854.	3.4	23
83	Do Proteins with Similar Folds Have Similar Transition State Structures? A Diffuse Transition State of the 169 Residue Apoflavodoxin. Journal of Molecular Biology, 2006, 359, 813-824.	4.2	22
84	VSDMIP: virtual screening data management on an integrated platform. Journal of Computer-Aided Molecular Design, 2009, 23, 171-184.	2.9	22
85	Scrambled Isomers as Key Intermediates in the Oxidative Folding of Ligand Binding Module 5 of the Low Density Lipoprotein Receptor. Journal of Biological Chemistry, 2008, 283, 13627-13637.	3.4	21
86	Molten Globule and Native State Ensemble of Helicobacter pylori Flavodoxin: Can Crowding, Osmolytes or Cofactors Stabilize the Native Conformation Relative to the Molten Globule?. Biophysical Journal, 2008, 95, 1913-1927.	0.5	20
87	Rational stabilization of complex proteins: a divide and combine approach. Scientific Reports, 2015, 5, 9129.	3.3	20
88	Energetics of aliphatic deletions in protein cores. Protein Science, 2006, 15, 1858-1872.	7.6	19
89	Helix propensities of conformationally restricted amino acids. Non-natural substitutes for helix breaking proline and helix forming alanine. Organic and Biomolecular Chemistry, 2010, 8, 788.	2.8	19
90	Thermodynamics of proteinâ€cation interaction: Ca⁺² and Mg⁺² binding to the fifth binding module of the LDL receptor. Proteins: Structure, Function and Bioinformatics, 2010, 78, 950-961.	2.6	18

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91	Protein-Cation Interactions: Structural and Thermodynamic Aspects. Current Protein and Peptide Science, 2011, 12, 325-338.	1.4	18
92	Identification of Specific Pluripotent Stem Cell Deathâ€”Inducing Small Molecules by Chemical Screening. Stem Cell Reviews and Reports, 2012, 8, 116-127.	5.6	18
93	Preparation and properties of a cross-linked complex between ferredoxin-NADP+ reductase and flavodoxin. FEBS Journal, 1989, 183, 539-544.	0.2	17
94	Apoflavodoxin: Structure, stability, and FMN binding. Biochimie, 1998, 80, 813-820.	2.6	17
95	Equilibrium Î¦-Analysis of a Molten Globule: The 1-149 Apoflavodoxin Fragment. Journal of Molecular Biology, 2006, 356, 354-366.	4.2	16
96	Repurposing Dihydropyridines for Treatment of Helicobacter pylori Infection. Pharmaceutics, 2019, 11, 681.	4.5	16
97	Biophysical Screening for Identifying Pharmacological Chaperones and Inhibitors Against Conformational and Infectious Diseases. Current Drug Targets, 2016, 17, 1492-1505.	2.1	16
98	Thermodynamic study of the influence of polyols and glucose on the thermal stability of holo-bovine Î±-lactalbumin. Journal of Thermal Analysis and Calorimetry, 2009, 98, 165-171.	3.6	15
99	The â€˜Relevantâ€™ Stability of Proteins with Equilibrium Intermediates. Scientific World Journal, The, 2002, 2, 1209-1215.	2.1	14
100	Defining the Nature of Thermal Intermediate in 3 State Folding Proteins: Apoflavodoxin, a Study Case. PLoS Computational Biology, 2012, 8, e1002647.	3.2	14
101	Structural and Mechanistic Basis of the Interaction between a Pharmacological Chaperone and Human Phenylalanine Hydroxylase. ChemBioChem, 2012, 13, 1266-1269.	2.6	14
102	Accurate Calculation of Barnase and SNase Folding Energetics Using Short Molecular Dynamics Simulations and an Atomistic Model of the Unfolded Ensemble: Evaluation of Force Fields and Water Models. Journal of Chemical Information and Modeling, 2019, 59, 4350-4360.	5.4	14
103	Insights into immune evasion of human metapneumovirus: novel 180- and 111-nucleotide duplications within viral G gene throughout 2014-2017 seasons in Barcelona, Spain. Journal of Clinical Virology, 2020, 132, 104590.	3.1	14
104	Small Molecule Inhibitors of the Response Regulator ArsR Exhibit Bactericidal Activity against Helicobacter pylori. Microorganisms, 2020, 8, 503.	3.6	14
105	Pathway of protein folding. Faraday Discussions, 1992, 93, 183.	3.2	13
106	Intrahelical side chain interactions in Î±-helices: poor correlation between energetics and frequency. FEBS Letters, 1998, 429, 99-103.	2.8	13
107	Conformational Stability of Helicobacter pylori Flavodoxin. Journal of Biological Chemistry, 2008, 283, 2883-2895.	3.4	13
108	Underexposed polar residues and protein stabilization. Protein Engineering, Design and Selection, 2011, 24, 171-177.	2.1	13

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109	Inhibition of Î±-Synuclein Aggregation and Mature Fibril Disassembling With a Minimalistic Compound, ZPDm. Frontiers in Bioengineering and Biotechnology, 2020, 8, 588947.	4.1	13
110	Streptococcus pneumoniae TIGR4 Flavodoxin: Structural and Biophysical Characterization of a Novel Drug Target. PLoS ONE, 2016, 11, e0161020.	2.5	13
111	A comparative study of the thermal stability of plastocyanin, cytochrome c(6) and Photosystem I in thermophilic and mesophilic cyanobacteria. Photosynthesis Research, 2001, 70, 281-289.	2.9	12
112	Predicting the structure of protein cavities created by mutation. Protein Engineering, Design and Selection, 2002, 15, 669-675.	2.1	12
113	Computational diagnosis of protein conformational diseases: Short molecular dynamics simulations reveal a fast unfolding of r-LDL mutants that cause familial hypercholesterolemia. Proteins: Structure, Function and Bioinformatics, 2006, 66, 87-95.	2.6	12
114	SIMPLE estimate of the free energy change due to aliphatic mutations: Superior predictions based on first principles. Proteins: Structure, Function and Bioinformatics, 2007, 68, 850-862.	2.6	12
115	Redox- and Ligand Binding-Dependent Conformational Ensembles in the Human Apoptosis-Inducing Factor Regulate Its Pro-Life and Cell Death Functions. Antioxidants and Redox Signaling, 2019, 30, 2013-2029.	5.4	12
116	Comparison of DNA binding across protein superfamilies. Proteins: Structure, Function and Bioinformatics, 2010, 78, 52-62.	2.6	11
117	FtsH cleavage of non-native conformations of proteins. Journal of Structural Biology, 2010, 171, 117-124.	2.8	11
118	Protein Dynamics Governed by Interfaces of High Polarity and Low Packing Density. PLoS ONE, 2012, 7, e48212.	2.5	11
119	Inhibition of Pig Phosphoenolpyruvate Carboxykinase Isoenzymes by 3-Mercaptopicolinic Acid and Novel Inhibitors. PLoS ONE, 2016, 11, e0159002.	2.5	11
120	Design, synthesis and structure-activity evaluation of novel 2-pyridone-based inhibitors of Î±-synuclein aggregation with potentially improved BBB permeability. Bioorganic Chemistry, 2021, 117, 105472.	4.1	11
121	Rescue of Misfolded Proteins and Stabilization by Small Molecules. Methods in Molecular Biology, 2010, 648, 313-324.	0.9	10
122	Stereoselective synthesis and biological evaluation as inhibitors of hepatitis C virus RNA polymerase of GSK3082 analogues with structural diversity at the 5-position. European Journal of Medicinal Chemistry, 2019, 171, 401-419.	5.5	10
123	Lowâ€density lipoprotein receptor is a calcium/magnesium sensorÂâ€“Ârole of <scp>LR</scp>4 and <scp>LR</scp>5 ion interaction kinetics in lowâ€density lipoprotein release in the endosome. FEBS Journal, 2014, 281, 2638-2658.	4.7	9
124	Thermal denaturation of Î±-chymotrypsinogen A in presence of polyols at pH 2.0 and pH 3.0. Journal of Thermal Analysis and Calorimetry, 2015, 120, 489-499.	3.6	9
125	Exploring the complete mutational space of the LDL receptor LA5 domain using molecular dynamics: linking SNPs with disease phenotypes in familial hypercholesterolemia. Human Molecular Genetics, 2016, 25, 1233-1246.	2.9	9
126	DMSO affects AÎ²_{1â€“40}'s conformation and interactions with aggregation inhibitors as revealed by NMR. RSC Advances, 2015, 5, 69761-69764.	3.6	7

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127	Mechanism of FMN Binding to the Apoflavodoxin from <i>Helicobacter pylori</i>. Biochemistry, 2011, 50, 8703-8711.	2.5	6
128	Identification of Inhibitors Targeting Ferredoxin-NADP+ Reductase from the Xanthomonas citri subsp. citri Phytopathogenic Bacteria. Molecules, 2018, 23, 29.	3.8	6
129	New variant (Val597Ile) in transmembrane region of the TSH receptor with human chorionic gonadotropin hypersensitivity in familial gestational hyperthyroidism. Clinical Endocrinology, 2020, 93, 339-345.	2.4	6
130	Purification of colored photosynthetic proteins for understanding protein isolation principles. Biochemistry and Molecular Biology Education, 2003, 31, 119-122.	1.2	5
131	The closed conformation of the LDL receptor is destabilized by the low Ca⁺⁺ concentration but favored by the high Mg⁺⁺ concentration in the endosome. FEBS Letters, 2015, 589, 3534-3540.	2.8	5
132	The mechanism of water/ion exchange at a protein surface: a weakly bound chloride in Helicobacter pylori apoflavodoxin. Physical Chemistry Chemical Physics, 2015, 17, 28635-28646.	2.8	4
133	Direct examination of the relevance for folding, binding and electron transfer of a conserved protein folding intermediate. Physical Chemistry Chemical Physics, 2017, 19, 19021-19031.	2.8	4
134	Selective Targeting of Human and Animal Pathogens of the Helicobacter Genus by Flavodoxin Inhibitors: Efficacy, Synergy, Resistance and Mechanistic Studies. International Journal of Molecular Sciences, 2021, 22, 10137.	4.1	4
135	Intradomain Confinement of Disulfides in the Folding of Two Consecutive Modules of the LDL Receptor. PLoS ONE, 2015, 10, e0132141.	2.5	3
136	Protposer: The web server that readily proposes protein stabilizing mutations with high PPV. Computational and Structural Biotechnology Journal, 2022, 20, 2415-2433.	4.1	3
137	Predicting stabilizing mutations in proteins using Poissonâ€“Boltzmann based models: study of unfolded state ensemble models and development of a successful binary classifier based on residue interaction energies. Physical Chemistry Chemical Physics, 2015, 17, 31044-31054.	2.8	2
138	A pyrene-inhibitor fluorescent probe with large Stokes shift for the staining of AÎ²1â€“42, Î±-synuclein, and amylin amyloid fibrils as well as amyloid-containing Staphylococcus aureus biofilms. Analytical and Bioanalytical Chemistry, 2019, 411, 251-265.	3.7	2
139	Unravelling the Complex Denaturant and Thermal-Induced Unfolding Equilibria of Human Phenylalanine Hydroxylase. International Journal of Molecular Sciences, 2021, 22, 6539.	4.1	2
140	Design of Ligand Binding to an Engineered Protein Cavity Using Virtual Screening and Thermal Up-shift Evaluation. Journal of Computer-Aided Molecular Design, 2005, 19, 421-443.	2.9	1
141	Influence of calcium on the thermal stabilization of bovine Î±-lactalbumin by selected polyols. Journal of Thermal Analysis and Calorimetry, 2011, 104, 37-44.	3.6	1
142	PirePred. Journal of Molecular Diagnostics, 2022, 24, 406-425.	2.8	1
143	Alchemical Design of Pharmacological Chaperones with Higher Affinity for Phenylalanine Hydroxylase. International Journal of Molecular Sciences, 2022, 23, 4502.	4.1	1
144	<title>Energy transfer and specific fluorescence quenching effects in barnase, studied via multifrequency phase-fluorometry of tryptophan mutants</title>. , 1992, 1640, 729.		0

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145	In vivo reconstitution of a homodimeric cytochrome b559 like structure: The role of the N-terminus Î± -subunit from Synechocystis sp. PCC 6803. Journal of Photochemistry and Photobiology B: Biology, 2015, 152, 308-317.	3.8	0
146	Protein Engineering: The Present and the Future. Biophysica, 2022, 2, 111-112.	1.4	0