

Javier Sancho

List of Publications by Year in descending order

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146
papers

5,772
citations

70961

41
h-index

95083

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.	2.0	323
2	Histidine-aromatic interactions in barnase. Journal of Molecular Biology, 1992, 224, 759-770.	2.0	207
3	Effect of alanine versus glycine in Î±-helices on protein stability. Nature, 1992, 356, 453-455.	13.7	204
4	Flavodoxins: sequence, folding, binding, function and beyond. Cellular and Molecular Life Sciences, 2006, 63, 855-864.	2.4	175
5	Circular dichroism studies of barnase and its mutants: Characterization of the contribution of aromatic side chains. Biochemistry, 1993, 32, 10303-10313.	1.2	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.	3.3	166
7	Identification of pharmacological chaperones as potential therapeutic agents to treat phenylketonuria. Journal of Clinical Investigation, 2008, 118, 2858-2867.	3.9	145
8	Fluorescence spectrum of barnase: contributions of three tryptophan residues and a histidine-related pH dependence. Biochemistry, 1991, 30, 6775-6779.	1.2	143
9	Histidine residues at the N- and C-termini of .alpha.-helices: perturbed pKas and protein stability. Biochemistry, 1992, 31, 2253-2258.	1.2	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.	0.6	115
11	The Tryptophan/Histidine interaction in Î±-helices. Journal of Molecular Biology, 1997, 267, 184-197.	2.0	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.	2.0	93
13	Differential Stabilization of the Three FMN Redox Forms by Tyrosine 94 and Tryptophan 57 in Flavodoxin from Anabaena and Its Influence on the Redox Potentials. Biochemistry, 1997, 36, 14334-14344.	1.2	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.	3.6	87
15	Long-Range Surface Charge-Charge Interactions in Proteins. Journal of Molecular Biology, 1993, 232, 574-583.	2.0	86
16	Dissection of an enzyme by protein engineering. Journal of Molecular Biology, 1992, 224, 741-747.	2.0	84
17	Folding of Barnase in Parts. Biochemistry, 1994, 33, 3778-3786.	1.2	83
18	The active site of pepsin is formed in the intermediate conformation dominant at mildly acidic pH. FEBS Letters, 2003, 538, 89-95.	1.3	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.	1.2	77
20	Conformational stability of apoflavodoxin. Protein Science, 1996, 5, 1376-1388.	3.1	74
21	Energetics of a hydrogen bond (charged and neutral) and of a cation- π interaction in apoflavodoxin 1 Edited by A. R. Fersht. Journal of Molecular Biology, 1999, 290, 319-330.	2.0	73
22	Discovering putative prion sequences in complete proteomes using probabilistic representations of Q/N-rich domains. BMC Genomics, 2013, 14, 316.	1.2	73
23	An intragenic suppressor in the cytochrome c oxidase I gene of mouse mitochondrial DNA. Human Molecular Genetics, 2003, 12, 329-339.	1.4	71
24	Purification and properties of ferredoxin-NADP ⁺ oxidoreductase from the nitrogen-fixing cyanobacteria <i>Anabaena variabilis</i> . Archives of Biochemistry and Biophysics, 1988, 260, 200-207.	1.4	69
25	Dissecting the Energetics of the Apoflavodoxin-FMN Complex. Journal of Biological Chemistry, 2000, 275, 9518-9526.	1.6	67
26	High-Throughput Screening Methodology to Identify Alpha-Synuclein Aggregation Inhibitors. International Journal of Molecular Sciences, 2017, 18, 478.	1.8	66
27	Flavodoxin:Quinone Reductase (FqrB): a Redox Partner of Pyruvate:Ferredoxin Oxidoreductase That Reversibly Couples Pyruvate Oxidation to NADPH Production in <i>Helicobacter pylori</i> and <i>Campylobacter jejuni</i> . Journal of Bacteriology, 2007, 189, 4764-4773.	1.0	63
28	$\hat{\alpha}$ -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.	1.5	59
29	Native hydrogen bonds in a molten globule: the apoflavodoxin thermal intermediate. Journal of Molecular Biology, 2001, 306, 877-888.	2.0	56
30	Mapping transition states of protein unfolding by protein engineering of ligand-binding sites. Journal of Molecular Biology, 1991, 221, 1007-1014.	2.0	55
31	Structure of Stable Protein Folding Intermediates by Equilibrium $\hat{\pi}$ -Analysis: The Apoflavodoxin Thermal Intermediate. Journal of Molecular Biology, 2004, 344, 239-255.	2.0	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.	1.2	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.	1.4	51
34	Apoflavodoxin Folding Mechanism: An $\hat{\alpha}$ / $\hat{\beta}$ Protein with an Essentially Off-Pathway Intermediate. Biochemistry, 2001, 40, 15234-15245.	1.2	49
35	The <i>Mycobacterium tuberculosis</i> <i>phoPR</i> Operon Is Positively Autoregulated in the Virulent Strain H37Rv. Journal of Bacteriology, 2008, 190, 7068-7078.	1.0	49
36	Sequence-Specific Solvent Accessibilities of Protein Residues in Unfolded Protein Ensembles. Biophysical Journal, 2006, 91, 4536-4543.	0.2	48

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37	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
38	Interaction of ferredoxin-NADP ⁺ reductase from <i>Anabaena</i> with its substrates. <i>Archives of Biochemistry and Biophysics</i> , 1991, 288, 231-238.	1.4	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. <i>Molecular Pharmaceutics</i> , 2011, 8, 2390-2397.	2.3	45
40	Antimicrobial Susceptibility and Resistance Patterns among <i>Helicobacter pylori</i> Strains from The Gambia, West Africa. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 1231-1237.	1.4	45
41	Towards a new therapeutic target: <i>Helicobacter pylori</i> flavodoxin. <i>Biophysical Chemistry</i> , 2005, 115, 267-276.	1.5	44
42	Mechanism of Low Density Lipoprotein (LDL) Release in the Endosome. <i>Journal of Biological Chemistry</i> , 2008, 283, 22670-22679.	1.6	43
43	PrionScan: an online database of predicted prion domains in complete proteomes. <i>BMC Genomics</i> , 2014, 15, 102.	1.2	42
44	Structure of <i>RdxA</i> , an oxygen-insensitive nitroreductase essential for metronidazole activation in <i>Helicobacter pylori</i> . <i>FEBS Journal</i> , 2012, 279, 4306-4317.	2.2	41
45	The FurA regulon in <i>Anabaena</i> sp. PCC 7120: in silico prediction and experimental validation of novel target genes. <i>Nucleic Acids Research</i> , 2014, 42, 4833-4846.	6.5	41
46	How FMN Binds to <i>Anabaena</i> Apoflavodoxin. <i>Journal of Biological Chemistry</i> , 2003, 278, 24053-24061.	1.6	40
47	Do Proteins Always Benefit from a Stability Increase? Relevant and Residual Stabilisation in a Three-state Protein by Charge Optimisation. <i>Journal of Molecular Biology</i> , 2004, 344, 223-237.	2.0	40
48	The Long and Short Flavodoxins. <i>Journal of Biological Chemistry</i> , 2004, 279, 47177-47183.	1.6	39
49	Discovery of Novel Inhibitors of Amyloid β -Peptide 1-42 Aggregation. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 9521-9530.	2.9	39
50	Four-State Equilibrium Unfolding of an scFv Antibody Fragment. <i>Biochemistry</i> , 2002, 41, 9873-9884.	1.2	38
51	Benzbromarone, Quercetin, and Folic Acid Inhibit Amylin Aggregation. <i>International Journal of Molecular Sciences</i> , 2016, 17, 964.	1.8	38
52	Theoretical Analysis of the Electron Spin Density Distribution of the Flavin Semiquinone Isoalloxazine Ring within Model Protein Environments. <i>Journal of Physical Chemistry A</i> , 2002, 106, 4729-4735.	1.1	37
53	Identifying potential novel drugs against <i>Helicobacter pylori</i> by targeting the essential response regulator HsrA. <i>Scientific Reports</i> , 2019, 9, 11294.	1.6	35
54	Cooperative Stabilization of a Molten Globule Apoflavodoxin Fragment. <i>Biochemistry</i> , 1998, 37, 10589-10596.	1.2	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. <i>Protein Engineering, Design and Selection</i> , 2001, 14, 173-181.	1.0	33
56	Thermal stability of β^2 -lactoglobulin in the presence of aqueous solution of alcohols and polyols. <i>International Journal of Biological Macromolecules</i> , 2007, 40, 423-428.	3.6	32
57	The Flavodoxin from <i>Helicobacter pylori</i> : Structural Determinants of Thermostability and FMN Cofactor Binding. <i>Biochemistry</i> , 2008, 47, 627-639.	1.2	32
58	Contribution of Disulfide Bonds to Stability, Folding, and Amyloid Fibril Formation: The PI3-SH3 Domain Case. <i>Antioxidants and Redox Signaling</i> , 2012, 16, 1-15.	2.5	32
59	ZPD-2, a Small Compound That Inhibits β -Synuclein Amyloid Aggregation and Its Seeded Polymerization. <i>Frontiers in Molecular Neuroscience</i> , 2019, 12, 306.	1.4	32
60	Anabaena sp. PCC 7119 Flavodoxin as Electron Carrier from Photosystem I to Ferredoxin-NADP+Reductase. <i>Journal of Biological Chemistry</i> , 2002, 277, 22338-22344.	1.6	31
61	The Long and Short Flavodoxins. <i>Journal of Biological Chemistry</i> , 2004, 279, 47184-47191.	1.6	30
62	The native-state ensemble of proteins provides clues for folding, misfolding and function. <i>Trends in Biochemical Sciences</i> , 2006, 31, 494-496.	3.7	30
63	LDL receptor/lipoprotein recognition: endosomal weakening of ApoB and ApoE binding to the convex face of the LR5 repeat. <i>FEBS Journal</i> , 2014, 281, 1534-1546.	2.2	30
64	Molecular dynamics simulations for genetic interpretation in protein coding regions: where we are, where to go and when. <i>Briefings in Bioinformatics</i> , 2021, 22, 3-19.	3.2	30
65	Role of Neighboring FMN Side Chains in the Modulation of Flavin Reduction Potentials and in the Energetics of the FMN:Apoprotein Interaction in Anabaena Flavodoxin. <i>Biochemistry</i> , 2004, 43, 15111-15121.	1.2	28
66	Allosteric Inhibitors of the NS3 Protease from the Hepatitis C Virus. <i>PLoS ONE</i> , 2013, 8, e69773.	1.1	28
67	Structural Analysis of an Equilibrium Folding Intermediate in the Apoflavodoxin Native Ensemble by Small-Angle X-ray Scattering. <i>Journal of Molecular Biology</i> , 2011, 406, 604-619.	2.0	27
68	Arginyl groups involved in the binding of Anabaena ferredoxin-NADP+ reductase to NADP+ and to ferredoxin. <i>FEBS Journal</i> , 1990, 187, 39-48.	0.2	26
69	Improved Flavodoxin Inhibitors with Potential Therapeutic Effects against <i>Helicobacter pylori</i> Infection. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 6248-6258.	2.9	26
70	Design and Structure of an Equilibrium Protein Folding Intermediate: A Hint into Dynamical Regions of Proteins. <i>Journal of Molecular Biology</i> , 2010, 400, 922-934.	2.0	25
71	Electron-Nuclear Double Resonance and Hyperfine Sublevel Correlation Spectroscopic Studies of Flavodoxin Mutants from Anabaena sp. PCC 7119. <i>Biophysical Journal</i> , 1999, 77, 1712-1720.	0.2	24
72	Anabaena apoflavodoxin hydrogen exchange: On the stable exchange core of the β^2 (21345) flavodoxin-like family. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 43, 476-488.	1.5	24

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73	Salt-induced stabilization of apoflavodoxin at neutral pH is mediated through cation-specific effects. <i>Protein Science</i> , 2002, 11, 1260-1273.	3.1	24
74	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
75	Native-specific stabilization of flavodoxin by the FMN cofactor: Structural and thermodynamical explanation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 581-594.	1.5	24
76	Common conformational changes in flavodoxins induced by FMN and anion binding: The structure of <i>Helicobacter pylori</i> apoflavodoxin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 581-594.	1.5	24
77	A Double-Deletion Method to Quantifying Incremental Binding Energies in Proteins from Experiment: Example of a Destabilizing Hydrogen Bonding Pair. <i>Biophysical Journal</i> , 2005, 88, 1311-1321.	0.2	23
78	Filling Small, Empty Protein Cavities: Structural and Energetic Consequences. <i>Journal of Molecular Biology</i> , 2006, 358, 701-712.	2.0	23
79	Distant and New Mutations in CTX-M-1 β -Lactamase Affect Cefotaxime Hydrolysis. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 4361-4368.	1.4	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. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 6102-6115.	2.9	23
81	Flavodoxins as Novel Therapeutic Targets against <i>Helicobacter pylori</i> and Other Gastric Pathogens. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1881.	1.8	23
82	Protein haploinsufficiency drivers identify MYBPC3 variants that cause hypertrophic cardiomyopathy. <i>Journal of Biological Chemistry</i> , 2021, 297, 100854.	1.6	23
83	Do Proteins with Similar Folds Have Similar Transition State Structures? A Diffuse Transition State of the 169 Residue Apoflavodoxin. <i>Journal of Molecular Biology</i> , 2006, 359, 813-824.	2.0	22
84	VSDMIP: virtual screening data management on an integrated platform. <i>Journal of Computer-Aided Molecular Design</i> , 2009, 23, 171-184.	1.3	22
85	Scrambled Isomers as Key Intermediates in the Oxidative Folding of Ligand Binding Module 5 of the Low Density Lipoprotein Receptor. <i>Journal of Biological Chemistry</i> , 2008, 283, 13627-13637.	1.6	21
86	Molten Globule and Native State Ensemble of <i>Helicobacter pylori</i> Flavodoxin: Can Crowding, Osmolytes or Cofactors Stabilize the Native Conformation Relative to the Molten Globule?. <i>Biophysical Journal</i> , 2008, 95, 1913-1927.	0.2	20
87	Rational stabilization of complex proteins: a divide and combine approach. <i>Scientific Reports</i> , 2015, 5, 9129.	1.6	20
88	Energetics of aliphatic deletions in protein cores. <i>Protein Science</i> , 2006, 15, 1858-1872.	3.1	19
89	Helix propensities of conformationally restricted amino acids. Non-natural substitutes for helix breaking proline and helix forming alanine. <i>Organic and Biomolecular Chemistry</i> , 2010, 8, 788.	1.5	19
90	Thermodynamics of protein-cation interaction: Ca ⁺² and Mg ⁺² binding to the fifth binding module of the LDL receptor. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 950-961.	1.5	18

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91	Protein-Cation Interactions: Structural and Thermodynamic Aspects. <i>Current Protein and Peptide Science</i> , 2011, 12, 325-338.	0.7	18
92	Identification of Specific Pluripotent Stem Cell Death-Inducing Small Molecules by Chemical Screening. <i>Stem Cell Reviews and Reports</i> , 2012, 8, 116-127.	5.6	18
93	Preparation and properties of a cross-linked complex between ferredoxin-NADP+ reductase and flavodoxin. <i>FEBS Journal</i> , 1989, 183, 539-544.	0.2	17
94	Apoflavodoxin: Structure, stability, and FMN binding. <i>Biochimie</i> , 1998, 80, 813-820.	1.3	17
95	Equilibrium \hat{I} -Analysis of a Molten Globule: The 1-149 Apoflavodoxin Fragment. <i>Journal of Molecular Biology</i> , 2006, 356, 354-366.	2.0	16
96	Repurposing Dihydropyridines for Treatment of <i>Helicobacter pylori</i> Infection. <i>Pharmaceutics</i> , 2019, 11, 681.	2.0	16
97	Biophysical Screening for Identifying Pharmacological Chaperones and Inhibitors Against Conformational and Infectious Diseases. <i>Current Drug Targets</i> , 2016, 17, 1492-1505.	1.0	16
98	Thermodynamic study of the influence of polyols and glucose on the thermal stability of holo-bovine \hat{I} -lactalbumin. <i>Journal of Thermal Analysis and Calorimetry</i> , 2009, 98, 165-171.	2.0	15
99	The "Relevant" Stability of Proteins with Equilibrium Intermediates. <i>Scientific World Journal</i> , The, 2002, 2, 1209-1215.	0.8	14
100	Defining the Nature of Thermal Intermediate in 3 State Folding Proteins: Apoflavodoxin, a Study Case. <i>PLoS Computational Biology</i> , 2012, 8, e1002647.	1.5	14
101	Structural and Mechanistic Basis of the Interaction between a Pharmacological Chaperone and Human Phenylalanine Hydroxylase. <i>ChemBioChem</i> , 2012, 13, 1266-1269.	1.3	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. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 4350-4360.	2.5	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. <i>Journal of Clinical Virology</i> , 2020, 132, 104590.	1.6	14
104	Small Molecule Inhibitors of the Response Regulator ArsR Exhibit Bactericidal Activity against <i>Helicobacter pylori</i> . <i>Microorganisms</i> , 2020, 8, 503.	1.6	14
105	Pathway of protein folding. <i>Faraday Discussions</i> , 1992, 93, 183.	1.6	13
106	Intrahelical side chain interactions in \hat{I} -helices: poor correlation between energetics and frequency. <i>FEBS Letters</i> , 1998, 429, 99-103.	1.3	13
107	Conformational Stability of <i>Helicobacter pylori</i> Flavodoxin. <i>Journal of Biological Chemistry</i> , 2008, 283, 2883-2895.	1.6	13
108	Underexposed polar residues and protein stabilization. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 171-177.	1.0	13

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109	Inhibition of α -Synuclein Aggregation and Mature Fibril Disassembling With a Minimalistic Compound, ZPDM. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 588947.	2.0	13
110	<i>Streptococcus pneumoniae</i> TIGR4 Flavodoxin: Structural and Biophysical Characterization of a Novel Drug Target. <i>PLoS ONE</i> , 2016, 11, e0161020.	1.1	13
111	A comparative study of the thermal stability of plastocyanin, cytochrome c(6) and Photosystem I in thermophilic and mesophilic cyanobacteria. <i>Photosynthesis Research</i> , 2001, 70, 281-289.	1.6	12
112	Predicting the structure of protein cavities created by mutation. <i>Protein Engineering, Design and Selection</i> , 2002, 15, 669-675.	1.0	12
113	Computational diagnosis of protein conformational diseases: Short molecular dynamics simulations reveal a fast unfolding of r-LDL mutants that cause familial hypercholesterolemia. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 66, 87-95.	1.5	12
114	SIMPLE estimate of the free energy change due to aliphatic mutations: Superior predictions based on first principles. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 850-862.	1.5	12
115	Redox- and Ligand Binding-Dependent Conformational Ensembles in the Human Apoptosis-Inducing Factor Regulate Its Pro-Life and Cell Death Functions. <i>Antioxidants and Redox Signaling</i> , 2019, 30, 2013-2029.	2.5	12
116	Comparison of DNA binding across protein superfamilies. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 52-62.	1.5	11
117	FtsH cleavage of non-native conformations of proteins. <i>Journal of Structural Biology</i> , 2010, 171, 117-124.	1.3	11
118	Protein Dynamics Governed by Interfaces of High Polarity and Low Packing Density. <i>PLoS ONE</i> , 2012, 7, e48212.	1.1	11
119	Inhibition of Pig Phosphoenolpyruvate Carboxykinase Isoenzymes by 3-Mercaptopicolinic Acid and Novel Inhibitors. <i>PLoS ONE</i> , 2016, 11, e0159002.	1.1	11
120	Design, synthesis and structure-activity evaluation of novel 2-pyridone-based inhibitors of α -synuclein aggregation with potentially improved BBB permeability. <i>Bioorganic Chemistry</i> , 2021, 117, 105472.	2.0	11
121	Rescue of Misfolded Proteins and Stabilization by Small Molecules. <i>Methods in Molecular Biology</i> , 2010, 648, 313-324.	0.4	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. <i>European Journal of Medicinal Chemistry</i> , 2019, 171, 401-419.	2.6	10
123	Low-density lipoprotein receptor is a calcium/magnesium sensor—Role of Ca^{2+} and Mg^{2+} ion interaction kinetics in low-density lipoprotein release in the endosome. <i>FEBS Journal</i> , 2014, 281, 2638-2658.	2.2	9
124	Thermal denaturation of α -chymotrypsinogen A in presence of polyols at pH 2.0 and pH 3.0. <i>Journal of Thermal Analysis and Calorimetry</i> , 2015, 120, 489-499.	2.0	9
125	Exploring the complete mutational space of the LDL receptor LA5 domain using molecular dynamics: linking SNPs with disease phenotypes in familial hypercholesterolemia. <i>Human Molecular Genetics</i> , 2016, 25, 1233-1246.	1.4	9
126	DMSO affects α -synuclein's conformation and interactions with aggregation inhibitors as revealed by NMR. <i>RSC Advances</i> , 2015, 5, 69761-69764.	1.7	7

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127	Mechanism of FMN Binding to the Apoflavodoxin from <i>Helicobacter pylori</i> . <i>Biochemistry</i> , 2011, 50, 8703-8711.	1.2	6
128	Identification of Inhibitors Targeting Ferredoxin-NADP+ Reductase from the <i>Xanthomonas citri</i> subsp. <i>citri</i> Phytopathogenic Bacteria. <i>Molecules</i> , 2018, 23, 29.	1.7	6
129	New variant (Val597Ile) in transmembrane region of the TSH receptor with human chorionic gonadotropin hypersensitivity in familial gestational hyperthyroidism. <i>Clinical Endocrinology</i> , 2020, 93, 339-345.	1.2	6
130	Purification of colored photosynthetic proteins for understanding protein isolation principles. <i>Biochemistry and Molecular Biology Education</i> , 2003, 31, 119-122.	0.5	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. <i>FEBS Letters</i> , 2015, 589, 3534-3540.	1.3	5
132	The mechanism of water/ion exchange at a protein surface: a weakly bound chloride in <i>Helicobacter pylori</i> apoflavodoxin. <i>Physical Chemistry Chemical Physics</i> , 2015, 17, 28635-28646.	1.3	4
133	Direct examination of the relevance for folding, binding and electron transfer of a conserved protein folding intermediate. <i>Physical Chemistry Chemical Physics</i> , 2017, 19, 19021-19031.	1.3	4
134	Selective Targeting of Human and Animal Pathogens of the <i>Helicobacter</i> Genus by Flavodoxin Inhibitors: Efficacy, Synergy, Resistance and Mechanistic Studies. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10137.	1.8	4
135	Intradomain Confinement of Disulfides in the Folding of Two Consecutive Modules of the LDL Receptor. <i>PLoS ONE</i> , 2015, 10, e0132141.	1.1	3
136	Protposer: The web server that readily proposes protein stabilizing mutations with high PPV. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2415-2433.	1.9	3
137	Predicting stabilizing mutations in proteins using Poisson-Boltzmann based models: study of unfolded state ensemble models and development of a successful binary classifier based on residue interaction energies. <i>Physical Chemistry Chemical Physics</i> , 2015, 17, 31044-31054.	1.3	2
138	A pyrene-inhibitor fluorescent probe with large Stokes shift for the staining of A β 42, α -synuclein, and amylin amyloid fibrils as well as amyloid-containing <i>Staphylococcus aureus</i> biofilms. <i>Analytical and Bioanalytical Chemistry</i> , 2019, 411, 251-265.	1.9	2
139	Unravelling the Complex Denaturant and Thermal-Induced Unfolding Equilibria of Human Phenylalanine Hydroxylase. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6539.	1.8	2
140	Design of Ligand Binding to an Engineered Protein Cavity Using Virtual Screening and Thermal Up-shift Evaluation. <i>Journal of Computer-Aided Molecular Design</i> , 2005, 19, 421-443.	1.3	1
141	Influence of calcium on the thermal stabilization of bovine α -lactalbumin by selected polyols. <i>Journal of Thermal Analysis and Calorimetry</i> , 2011, 104, 37-44.	2.0	1
142	PirePred. <i>Journal of Molecular Diagnostics</i> , 2022, 24, 406-425.	1.2	1
143	Alchemical Design of Pharmacological Chaperones with Higher Affinity for Phenylalanine Hydroxylase. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4502.	1.8	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

#	ARTICLE	IF	CITATIONS
145	In vivo reconstitution of a homodimeric cytochrome b559 like structure: The role of the N-terminus $\hat{\pm}$ -subunit from <i>Synechocystis</i> sp. PCC 6803. <i>Journal of Photochemistry and Photobiology B: Biology</i> , 2015, 152, 308-317.	1.7	0
146	Protein Engineering: The Present and the Future. <i>Biophysica</i> , 2022, 2, 111-112.	0.6	0