

Adrian Velazquez-Campoy

List of Publications by Year in descending order

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224
papers

6,902
citations

66234

42
h-index

95083

68
g-index

235
all docs

235
docs citations

235
times ranked

8660
citing authors

#	ARTICLE	IF	CITATIONS
1	Isothermal titration calorimetry to determine association constants for high-affinity ligands. <i>Nature Protocols</i> , 2006, 1, 186-191.	5.5	267
2	Identification of Novel Inhibitors of the SARS Coronavirus Main Protease 3CLpro. <i>Biochemistry</i> , 2004, 43, 4906-4912.	1.2	211
3	ITC in the post-genomic era. <i>Biophysical Chemistry</i> , 2005, 115, 115-124.	1.5	192
4	Structural stability of SARS-CoV-2 3CLpro and identification of quercetin as an inhibitor by experimental screening. <i>International Journal of Biological Macromolecules</i> , 2020, 164, 1693-1703.	3.6	184
5	Characterization of Protein-Protein Interactions by Isothermal Titration Calorimetry. <i>Journal of Molecular Biology</i> , 2004, 261, 035-054.		183
6	The Binding Energetics of First- and Second-Generation HIV-1 Protease Inhibitors: Implications for Drug Design. <i>Archives of Biochemistry and Biophysics</i> , 2001, 390, 169-175.	1.4	151
7	Identification of pharmacological chaperones as potential therapeutic agents to treat phenylketonuria. <i>Journal of Clinical Investigation</i> , 2008, 118, 2858-2867.	3.9	145
8	HIV-1 Protease Inhibitors: Enthalpic versus Entropic Optimization of the Binding Affinity. <i>Biochemistry</i> , 2000, 39, 2201-2207.	1.2	144
9	Catalytic efficiency and vitality of HIV-1 proteases from African viral subtypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 6062-6067.	3.3	144
10	Chapter 5 Isothermal Titration Calorimetry. <i>Methods in Enzymology</i> , 2009, 455, 127-155.	0.4	142
11	Repositioning tolcapone as a potent inhibitor of transthyretin amyloidogenesis and associated cellular toxicity. <i>Nature Communications</i> , 2016, 7, 10787.	5.8	139
12	Isothermal Titration Calorimetry. <i>Current Protocols in Cell Biology</i> , 2004, 23, Unit 17.8.	2.3	123
13	Thermodynamic Basis of Resistance to HIV-1 Protease Inhibition: Calorimetric Analysis of the V82F/I84V Active Site Resistant Mutant. <i>Biochemistry</i> , 2000, 39, 11876-11883.	1.2	118
14	Identification of a Drug Targeting an Intrinsically Disordered Protein Involved in Pancreatic Adenocarcinoma. <i>Scientific Reports</i> , 2017, 7, 39732.	1.6	101
15	Overcoming drug resistance in HIV-1 chemotherapy: The binding thermodynamics of Amprenavir and TMC-126 to wild-type and drug-resistant mutants of the HIV-1 protease. <i>Protein Science</i> , 2002, 11, 1908-1916.	3.1	98
16	Evolutionarily conserved proteins MnmE and GidA catalyze the formation of two methyluridine derivatives at tRNA wobble positions. <i>Nucleic Acids Research</i> , 2009, 37, 7177-7193.	6.5	95
17	Thermodynamic dissection of the binding energetics of KNI-272, a potent HIV-1 protease inhibitor. <i>Protein Science</i> , 2000, 9, 1801-1809.	3.1	90
18	Cytochrome c speeds up caspase cascade activation by blocking 14-3-3 μ -dependent Apaf-1 inhibition. <i>Cell Death and Disease</i> , 2018, 9, 365.	2.7	88

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19	Amplification of the Effects of Drug Resistance Mutations by Background Polymorphisms in HIV-1 Protease from African Subtypes. <i>Biochemistry</i> , 2002, 41, 8613-8619.	1.2	87
20	Exact Analysis of Heterotropic Interactions in Proteins: Characterization of Cooperative Ligand Binding by Isothermal Titration Calorimetry. <i>Biophysical Journal</i> , 2006, 91, 1887-1904.	0.2	80
21	Structural and Functional Analysis of Novel Human Cytochrome c Targets in Apoptosis. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1439-1456.	2.5	74
22	Targeting intrinsically disordered proteins involved in cancer. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 1695-1707.	2.4	74
23	AFFINImeter: A software to analyze molecular recognition processes from experimental data. <i>Analytical Biochemistry</i> , 2019, 577, 117-134.	1.1	71
24	Thermodynamic rules for the design of high affinity HIV-1 protease inhibitors with adaptability to mutations and high selectivity towards unwanted targets. <i>International Journal of Biochemistry and Cell Biology</i> , 2004, 36, 1787-1799.	1.2	70
25	A unified framework based on the binding polynomial for characterizing biological systems by isothermal titration calorimetry. <i>Methods</i> , 2015, 76, 99-115.	1.9	70
26	Ligand-based design identifies a potent NUPR1 inhibitor exerting anticancer activity via necroptosis. <i>Journal of Clinical Investigation</i> , 2019, 129, 2500-2513.	3.9	68
27	Complex coacervates of hyaluronic acid and lysozyme: Effect on protein structure and physical stability. <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , 2014, 88, 325-331.	2.0	63
28	Guanine nucleotide binding to the Bateman domain mediates the allosteric inhibition of eukaryotic IMP dehydrogenases. <i>Nature Communications</i> , 2015, 6, 8923.	5.8	63
29	A look at ligand binding thermodynamics in drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2017, 12, 363-377.	2.5	61
30	On the link between conformational changes, ligand binding and heat capacity. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 868-878.	1.1	60
31	Structural Basis for the Interaction of Unstructured Neuron Specific Substrates Neuromodulin and Neurogranin with Calmodulin. <i>Scientific Reports</i> , 2013, 3, 1392.	1.6	57
32	Rutin Is a Low Micromolar Inhibitor of SARS-CoV-2 Main Protease 3CLpro: Implications for Drug Design of Quercetin Analogs. <i>Biomedicines</i> , 2021, 9, 375.	1.4	57
33	Structural and Thermodynamic Basis of Resistance to HIV-1 Protease Inhibition: Implications for Inhibitor Design. <i>Current Drug Targets Infectious Disorders</i> , 2003, 3, 311-328.	2.1	57
34	A structural and thermodynamic escape mechanism from a drug resistant mutation of the HIV-1 protease. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 594-602.	1.5	56
35	Structural basis of mitochondrial dysfunction in response to cytochrome <i>c</i> phosphorylation at tyrosine 48. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3041-E3050.	3.3	53
36	Characterization of Protein-Protein Interactions by Isothermal Titration Calorimetry. <i>Methods in Molecular Biology</i> , 2015, 1278, 183-204.	0.4	53

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37	Structural basis for inhibition of the histone chaperone activity of SET/TAF- \hat{I}^2 by cytochrome <i>c</i> . Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 9908-9913.	3.3	52
38	Histone chaperone activity of Arabidopsis thaliana NRP1 is blocked by cytochrome c. Nucleic Acids Research, 2017, 45, 2150-2165.	6.5	50
39	MeCP2-E1 isoform is a dynamically expressed, weakly DNA-bound protein with different protein and DNA interactions compared to MeCP2-E2. Epigenetics and Chromatin, 2019, 12, 63.	1.8	50
40	Discovery of Specific Flavodoxin Inhibitors as Potential Therapeutic Agents against <i>Helicobacter pylori</i> Infection. ACS Chemical Biology, 2009, 4, 928-938.	1.6	48
41	The application of thermodynamic methods in drug design. Thermochemica Acta, 2001, 380, 217-227.	1.2	46
42	Structural Characterization of Myotoxic Ecarpholin S From Echis carinatus Venom. Biophysical Journal, 2008, 95, 3366-3380.	0.2	45
43	Structure-Function Analysis of <i>Escherichia coli</i> MnmG (GidA), a Highly Conserved tRNA-Modifying Enzyme. Journal of Bacteriology, 2009, 191, 7614-7619.	1.0	45
44	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.	2.3	45
45	A Mechanism for Histone Chaperoning Activity of Nucleoplasmin: Thermodynamic and Structural Models. Journal of Molecular Biology, 2009, 393, 448-463.	2.0	44
46	Seleno-Functionalization of Quercetin Improves the Non-Covalent Inhibition of Mpro and Its Antiviral Activity in Cells against SARS-CoV-2. International Journal of Molecular Sciences, 2021, 22, 7048.	1.8	44
47	Mechanism of Low Density Lipoprotein (LDL) Release in the Endosome. Journal of Biological Chemistry, 2008, 283, 22670-22679.	1.6	43
48	Structural and functional characterization of phosphomimetic mutants of cytochrome c at threonine 28 and serine 47. Biochimica Et Biophysica Acta - Bioenergetics, 2016, 1857, 387-395.	0.5	42
49	Binding Thermodynamics of Ferredoxin:NADP+ Reductase: Two Different Protein Substrates and One Energetics. Biophysical Journal, 2009, 96, 4966-4975.	0.2	41
50	Dendrimers as Potential Inhibitors of the Dimerization of the Capsid Protein of HIV-1. Biomacromolecules, 2010, 11, 2069-2078.	2.6	41
51	Kinetics and Thermodynamics of Chlorpromazine Interaction with Lipid Bilayers: Effect of Charge and Cholesterol. Journal of the American Chemical Society, 2012, 134, 4184-4195.	6.6	41
52	Mechanism of the allosteric activation of the ClpP protease machinery by substrates and active-site inhibitors. Science Advances, 2019, 5, eaaw3818.	4.7	41
53	Structure of GrlR-GrlA complex that prevents GrlA activation of virulence genes. Nature Communications, 2013, 4, 2546.	5.8	38
54	Plant tumour biocontrol agent employs a tRNA-dependent mechanism to inhibit leucyl-tRNA synthetase. Nature Communications, 2013, 4, 1417.	5.8	37

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55	Tolcapone, a potent aggregation inhibitor for the treatment of familial leptomeningeal amyloidosis. <i>FEBS Journal</i> , 2021, 288, 310-324.	2.2	37
56	The Mechanism of Allosteric Coupling in Choline Kinase ϵ 1 Revealed by the Action of a Rationally Designed Inhibitor. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 4582-4586.	7.2	36
57	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
58	Incorporating target heterogeneity in drug design. <i>Journal of Cellular Biochemistry</i> , 2001, 84, 82-88.	1.2	34
59	Protease inhibition in African subtypes of HIV-1. <i>AIDS Reviews</i> , 2003, 5, 165-71.	0.5	34
60	Deciphering the Binding between Nupr1 and MSL1 and Their DNA-Repairing Activity. <i>PLoS ONE</i> , 2013, 8, e78101.	1.1	33
61	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
62	On the Temperature Dependence of Complex Formation between Chitosan and Proteins. <i>Biomacromolecules</i> , 2011, 12, 2534-2543.	2.6	32
63	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
64	Partition of amphiphilic molecules to lipid bilayers by isothermal titration calorimetry. <i>Analytical Biochemistry</i> , 2010, 399, 44-47.	1.1	30
65	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
66	Deconvolution Analysis for Classifying Gastric Adenocarcinoma Patients Based on Differential Scanning Calorimetry Serum Thermograms. <i>Scientific Reports</i> , 2015, 5, 7988.	1.6	30
67	Interaction of Bile Salts with Model Membranes Mimicking the Gastrointestinal Epithelium: A Study by Isothermal Titration Calorimetry. <i>Langmuir</i> , 2015, 31, 9097-9104.	1.6	30
68	Role of Key Residues at the Flavin Mononucleotide (FMN):Adenylyltransferase Catalytic Site of the Bifunctional Riboflavin Kinase/Flavin Adenine Dinucleotide (FAD) Synthetase from <i>Corynebacterium ammoniagenes</i> . <i>International Journal of Molecular Sciences</i> , 2012, 13, 14492-14517.	1.8	29
69	Ligand binding to one-dimensional lattice-like macromolecules: Analysis of the McChesney-von Hippel theory implemented in isothermal titration calorimetry. <i>Analytical Biochemistry</i> , 2006, 348, 94-104.	1.1	28
70	Structure and Functional Characterization of Human Aspartate Transcarbamoylase, the Target of the Anti-tumoral Drug PALA. <i>Structure</i> , 2016, 24, 1081-1094.	1.6	28
71	Differential NtcA Responsiveness to 2-Oxoglutarate Underlies the Diversity of C/N Balance Regulation in <i>Prochlorococcus</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2641.	1.5	28
72	Targeting the Stress-Induced Protein NUPR1 to Treat Pancreatic Adenocarcinoma. <i>Cells</i> , 2019, 8, 1453.	1.8	28

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73	Allosteric Inhibitors of the NS3 Protease from the Hepatitis C Virus. <i>PLoS ONE</i> , 2013, 8, e69773.	1.1	28
74	Respiratory complexes III and IV can each bind two molecules of cytochrome <i>c</i> at low ionic strength. <i>FEBS Letters</i> , 2015, 589, 476-483.	1.3	27
75	Thermodynamic Analysis of Ferrous Ion Binding to <i>Escherichia coli</i> Ferritin EcFtn. <i>Biochemistry</i> , 2005, 44, 13837-13846.	1.2	26
76	The Puzzle of Ligand Binding to <i>Corynebacterium ammoniagenes</i> FAD Synthetase. <i>Journal of Biological Chemistry</i> , 2009, 284, 6610-6619.	1.6	26
77	Conformational Stability of Hepatitis C Virus NS3 Protease. <i>Biophysical Journal</i> , 2010, 99, 3811-3820.	0.2	26
78	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
79	Cytochrome <i>c1</i> exhibits two binding sites for cytochrome <i>c</i> in plants. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, 1717-1729.	0.5	26
80	Nanostructures based on ammonium-terminated amphiphilic Janus dendrimers as camptothecin carriers with antiviral activity. <i>European Polymer Journal</i> , 2017, 90, 136-149.	2.6	26
81	Thermodynamics of cooperative binding of FAD to human NQO1: Implications to understanding cofactor-dependent function and stability of the flavoproteome. <i>Archives of Biochemistry and Biophysics</i> , 2017, 636, 17-27.	1.4	26
82	Molecular recognition in the interaction of chloroplast 2-Cys peroxiredoxin with NADPH-thioredoxin reductase C (NTRC) and thioredoxin. <i>FEBS Letters</i> , 2014, 588, 4342-4347.	1.3	25
83	Structural and functional evidence for membrane docking and disruption sites on phospholipase A ₂ -like proteins revealed by complexation with the inhibitor suramin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2066-2078.	2.5	25
84	Structural Analysis of the Regulation of the DYNLL/LC8 Binding to Nek9 by Phosphorylation. <i>Journal of Biological Chemistry</i> , 2013, 288, 12283-12294.	1.6	24
85	Microcystin-LR Binds Iron, and Iron Promotes Self-Assembly. <i>Environmental Science & Technology</i> , 2017, 51, 4841-4850.	4.6	24
86	ZZW-115-dependent inhibition of NUPR1 nuclear translocation sensitizes cancer cells to genotoxic agents. <i>JCI Insight</i> , 2020, 5, .	2.3	24
87	Rationally Designed Interfacial Peptides Are Efficient In Vitro Inhibitors of HIV-1 Capsid Assembly with Antiviral Activity. <i>PLoS ONE</i> , 2011, 6, e23877.	1.1	24
88	Energetics of Nucleotide-Induced DnaK Conformational States. <i>Biochemistry</i> , 2010, 49, 1338-1345.	1.2	23
89	Shell Cross-Linked Polymeric Micelles as Camptothecin Nanocarriers for Anti-HCV Therapy. <i>Macromolecular Bioscience</i> , 2015, 15, 1381-1391.	2.1	23
90	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

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91	Uncertainty in protein–ligand binding constants: asymmetric confidence intervals versus standard errors. <i>European Biophysics Journal</i> , 2021, 50, 661-670.	1.2	23
92	Energetic Effects of Magnesium in the Recognition of Adenosine Nucleotides by the F ₁ -ATPase I ² Subunit. <i>Biochemistry</i> , 2010, 49, 5258-5268.	1.2	22
93	Amphipathic helical peptides hamper protein-protein interactions of the intrinsically disordered chromatin nuclear protein 1 (NUPR1). <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 1283-1295.	1.1	22
94	Enzyme/Nanocopper Hybrid Nanozymes: Modulating Enzyme-like Activity by the Protein Structure for Biosensing and Tumor Catalytic Therapy. <i>ACS Applied Materials & Interfaces</i> , 2021, 13, 5111-5124.	4.0	22
95	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.	1.5	21
96	Cyanobacterial electron carrier proteins as electron donors to CYP106A2 from <i>Bacillus megaterium</i> ATCC 13368. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 1635-1642.	1.1	20
97	Key Residues at the Riboflavin Kinase Catalytic Site of the Bifunctional Riboflavin Kinase/FMN Adenylyltransferase From <i>Corynebacterium ammoniagenes</i> . <i>Cell Biochemistry and Biophysics</i> , 2013, 65, 57-68.	0.9	20
98	Rational stabilization of complex proteins: a divide and combine approach. <i>Scientific Reports</i> , 2015, 5, 9129.	1.6	20
99	Geometric features of the Wiseman isotherm in isothermal titration calorimetry. <i>Journal of Thermal Analysis and Calorimetry</i> , 2015, 122, 1477-1483.	2.0	20
100	GrpE N-terminal Domain Contributes to the Interaction with DnaK and Modulates the Dynamics of the Chaperone Substrate Binding Domain. <i>Journal of Molecular Biology</i> , 2007, 374, 1054-1064.	2.0	19
101	Identification and characterization of the lipid-binding property of GrLR, a locus of enterocyte effacement regulator. <i>Biochemical Journal</i> , 2009, 420, 191-201.	1.7	19
102	Extending <i>in silico</i> mechanism-of-action analysis by annotating targets with pathways: application to cellular cytotoxicity readouts. <i>Future Medicinal Chemistry</i> , 2014, 6, 2029-2056.	1.1	19
103	The intervening domain from MeCP2 enhances the DNA affinity of the methyl binding domain and provides an independent DNA interaction site. <i>Scientific Reports</i> , 2017, 7, 41635.	1.6	19
104	The FAD synthetase from the human pathogen <i>Streptococcus pneumoniae</i> : a bifunctional enzyme exhibiting activity-dependent redox requirements. <i>Scientific Reports</i> , 2017, 7, 7609.	1.6	19
105	Thermal liquid biopsy for monitoring melanoma patients under surveillance during treatment: A pilot study. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 1701-1710.	1.1	19
106	Proposed mechanism for regulation of H ₂ O ₂ -induced programmed cell death in plants by binding of cytochrome <i>c</i> to 14 β proteins. <i>Plant Journal</i> , 2021, 106, 74-85.	2.8	19
107	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
108	Quaternary organization in a bifunctional prokaryotic FAD synthetase: Involvement of an arginine at its adenylyltransferase module on the riboflavin kinase activity. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 897-906.	1.1	18

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109	DNA mismatch repair proteins MLH1 and PMS2 can be imported to the nucleus by a classical nuclear import pathway. <i>Biochimie</i> , 2018, 146, 87-96.	1.3	18
110	NADP ⁺ Binding to the Regulatory Subunit of Methionine Adenosyltransferase II Increases Intersubunit Binding Affinity in the Hetero-Trimer. <i>PLoS ONE</i> , 2012, 7, e50329.	1.1	17
111	A Quantitative Characterization of Nucleoplasmin/Histone Complexes Reveals Chaperone Versatility. <i>Scientific Reports</i> , 2016, 6, 32114.	1.6	17
112	Mechanisms of feedback inhibition and sequential firing of active sites in plant aspartate transcarbamoylase. <i>Nature Communications</i> , 2021, 12, 947.	5.8	17
113	Inhibition of the PP2A activity by the histone chaperone ANP32B is long-range allosterically regulated by respiratory cytochrome c. <i>Redox Biology</i> , 2021, 43, 101967.	3.9	17
114	NS3 Protease from Hepatitis C Virus: Biophysical Studies on an Intrinsically Disordered Protein Domain. <i>International Journal of Molecular Sciences</i> , 2013, 14, 13282-13306.	1.8	16
115	Polymeric micelles from block copolymers containing 2,6-diacylaminopyridine units for encapsulation of hydrophobic drugs. <i>RSC Advances</i> , 2016, 6, 24066-24075.	1.7	16
116	Cysteine Mutational Studies Provide Insight into a Thiol-Based Redox Switch Mechanism of Metal and DNA Binding in FurA from <i>Anabaena</i> sp. PCC 7120. <i>Antioxidants and Redox Signaling</i> , 2016, 24, 173-185.	2.5	16
117	The trimer interface in the quaternary structure of the bifunctional prokaryotic FAD synthetase from <i>Corynebacterium ammoniagenes</i> . <i>Scientific Reports</i> , 2017, 7, 404.	1.6	16
118	Repurposing Dihydropyridines for Treatment of <i>Helicobacter pylori</i> Infection. <i>Pharmaceutics</i> , 2019, 11, 681.	2.0	16
119	Sub-Micromolar Inhibition of SARS-CoV-2 3CLpro by Natural Compounds. <i>Pharmaceutics</i> , 2021, 14, 892.	1.7	16
120	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
121	Determination of Potential Scaffolds for Human Choline Kinase $\hat{\pm}1$ by Chemical Deconvolution Studies. <i>ChemBioChem</i> , 2013, 14, 1291-1295.	1.3	15
122	Structural and Calorimetric Studies Demonstrate that Xeroderma Pigmentosum Type G (XPG) Can Be Imported to the Nucleus by a Classical Nuclear Import Pathway via a Monopartite NLS Sequence. <i>Journal of Molecular Biology</i> , 2016, 428, 2120-2131.	2.0	15
123	A New Member of the Thioredoxin Reductase Family from Early Oxygenic Photosynthetic Organisms. <i>Molecular Plant</i> , 2017, 10, 212-215.	3.9	15
124	Design of Inhibitors of the Intrinsically Disordered Protein NUPR1: Balance between Drug Affinity and Target Function. <i>Biomolecules</i> , 2021, 11, 1453.	1.8	15
125	Structural Basis for a Unique ATP Synthase Core Complex from <i>Nanoarchaeum equitans</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 27280-27296.	1.6	14
126	Kinetics and thermodynamics of the protein-ligand interactions in the riboflavin kinase activity of the FAD synthetase from <i>Corynebacterium ammoniagenes</i> . <i>Scientific Reports</i> , 2017, 7, 7281.	1.6	14

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127	Biophysical studies and NMR structure of YAP2 WW domain - LATS1 PPxY motif complexes reveal the basis of their interaction. <i>Oncotarget</i> , 2018, 9, 8068-8080.	0.8	14
128	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
129	Isothermal titration calorimetry (ITC): a standard operating procedure (SOP). <i>European Biophysics Journal</i> , 2021, 50, 363-371.	1.2	14
130	Discovery of Diverse Natural Products as Inhibitors of SARS-CoV-2 M ^{pro} Protease through Virtual Screening. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 6094-6106.	2.5	14
131	Conformational Stability of <i>Helicobacter pylori</i> Flavodoxin. <i>Journal of Biological Chemistry</i> , 2008, 283, 2883-2895.	1.6	13
132	A Phosphorylation-Induced Switch in the Nuclear Localization Sequence of the Intrinsically Disordered NUPR1 Hampers Binding to Importin. <i>Biomolecules</i> , 2020, 10, 1313.	1.8	13
133	<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
134	Title is missing!. <i>Magyar Árvad Kézlönyek</i> , 1999, 57, 343-359.	1.4	12
135	Unprecedented pathway of reducing equivalents in a diflavin-linked disulfide oxidoreductase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12725-12730.	3.3	12
136	<i>Arabidopsis</i> FNRL protein is an NADPH-dependent chloroplast oxidoreductase resembling bacterial ferredoxin-NADP ⁺ reductases. <i>Physiologia Plantarum</i> , 2018, 162, 177-190.	2.6	12
137	Thermal Liquid Biopsy (TLB): A Predictive Score Derived from Serum Thermograms as a Clinical Tool for Screening Lung Cancer Patients. <i>Cancers</i> , 2019, 11, 1012.	1.7	12
138	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
139	A multi-laboratory benchmark study of isothermal titration calorimetry (ITC) using Ca ²⁺ and Mg ²⁺ binding to EDTA. <i>European Biophysics Journal</i> , 2021, 50, 429-451.	1.2	12
140	Biochemical and biophysical characterization of PADI4 supports its involvement in cancer. <i>Archives of Biochemistry and Biophysics</i> , 2022, 717, 109125.	1.4	12
141	Defining the Epitope Region of a Peptide from the <i>Streptomyces coelicolor</i> Phosphoenolpyruvate: Sugar Phosphotransferase System Able to Bind to the Enzyme I. <i>Biophysical Journal</i> , 2008, 95, 1336-1348.	0.2	11
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