

Adrian Velazquez-Campoy

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209
papers

5,250
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38
h-index

62
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235
ext. papers

6,264
ext. citations

5.5
avg, IF

5.81
L-index

#	Paper	IF	Citations
209	Isothermal titration calorimetry to determine association constants for high-affinity ligands. <i>Nature Protocols</i> , 2006 , 1, 186-91	18.8	223
208	Identification of novel inhibitors of the SARS coronavirus main protease 3CLpro. <i>Biochemistry</i> , 2004 , 43, 4906-12	3.2	180
207	ITC in the post-genomic era...? Priceless. <i>Biophysical Chemistry</i> , 2005 , 115, 115-24	3.5	172
206	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, 169-75	4.1	135
205	Characterization of protein-protein interactions by isothermal titration calorimetry. <i>Methods in Molecular Biology</i> , 2004 , 261, 35-54	1.4	134
204	HIV-1 protease inhibitors: enthalpic versus entropic optimization of the binding affinity. <i>Biochemistry</i> , 2000 , 39, 2201-7	3.2	131
203	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, 6062-7	11.5	123
202	Identification of pharmacological chaperones as potential therapeutic agents to treat phenylketonuria. <i>Journal of Clinical Investigation</i> , 2008 , 118, 2858-67	15.9	119
201	Isothermal titration calorimetry: general formalism using binding polynomials. <i>Methods in Enzymology</i> , 2009 , 455, 127-55	1.7	111
200	Thermodynamic basis of resistance to HIV-1 protease inhibition: calorimetric analysis of the V82F/I84V active site resistant mutant. <i>Biochemistry</i> , 2000 , 39, 11876-83	3.2	111
199	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	7.9	102
198	Repositioning tolcapone as a potent inhibitor of transthyretin amyloidogenesis and associated cellular toxicity. <i>Nature Communications</i> , 2016 , 7, 10787	17.4	102
197	Isothermal titration calorimetry. <i>Current Protocols in Cell Biology</i> , 2004 , Chapter 17, Unit 17.8	2.3	97
196	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, 1908-16	6.3	85
195	Thermodynamic dissection of the binding energetics of KNI-272, a potent HIV-1 protease inhibitor. <i>Protein Science</i> , 2000 , 9, 1801-9	6.3	85
194	Amplification of the effects of drug resistance mutations by background polymorphisms in HIV-1 protease from African subtypes. <i>Biochemistry</i> , 2002 , 41, 8613-9	3.2	84
193	Identification of a Drug Targeting an Intrinsically Disordered Protein Involved in Pancreatic Adenocarcinoma. <i>Scientific Reports</i> , 2017 , 7, 39732	4.9	81

192	Evolutionarily conserved proteins MnmE and GidA catalyze the formation of two methyluridine derivatives at tRNA wobble positions. <i>Nucleic Acids Research</i> , 2009 , 37, 7177-93	20.1	81
191	Experimental validation of in silico target predictions on synergistic protein targets. <i>Journal of Cheminformatics</i> , 2013 , 5,	8.6	78
190	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, 1787-99	5.6	63
189	A unified framework based on the binding polynomial for characterizing biological systems by isothermal titration calorimetry. <i>Methods</i> , 2015 , 76, 99-115	4.6	56
188	Exact analysis of heterotropic interactions in proteins: Characterization of cooperative ligand binding by isothermal titration calorimetry. <i>Biophysical Journal</i> , 2006 , 91, 1887-904	2.9	54
187	Structural and functional analysis of novel human cytochrome C targets in apoptosis. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 1439-56	7.6	52
186	Complex coacervates of hyaluronic acid and lysozyme: effect on protein structure and physical stability. <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , 2014 , 88, 325-31	5.7	50
185	Cytochrome c speeds up caspase cascade activation by blocking 14-3-3-dependent Apaf-1 inhibition. <i>Cell Death and Disease</i> , 2018 , 9, 365	9.8	49
184	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	4.2	49
183	Structural and thermodynamic basis of resistance to HIV-1 protease inhibition: implications for inhibitor design. <i>Current Drug Targets Infectious Disorders</i> , 2003 , 3, 311-28		48
182	Ligand-based design identifies a potent NUPR1 inhibitor exerting anticancer activity via necroptosis. <i>Journal of Clinical Investigation</i> , 2019 , 129, 2500-2513	15.9	47
181	Structural basis of mitochondrial dysfunction in response to cytochrome phosphorylation at tyrosine 48. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E3041-E3050	11.5	46
180	AFFINImeter: A software to analyze molecular recognition processes from experimental data. <i>Analytical Biochemistry</i> , 2019 , 577, 117-134	3.1	44
179	On the link between conformational changes, ligand binding and heat capacity. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016 , 1860, 868-878	4	44
178	Structural basis for the interaction of unstructured neuron specific substrates neuromodulin and neurogranin with Calmodulin. <i>Scientific Reports</i> , 2013 , 3, 1392	4.9	44
177	Guanine nucleotide binding to the Bateman domain mediates the allosteric inhibition of eukaryotic IMP dehydrogenases. <i>Nature Communications</i> , 2015 , 6, 8923	17.4	42
176	The application of thermodynamic methods in drug design. <i>Thermochimica Acta</i> , 2001 , 380, 217-227	2.9	42
175	Characterization of protein-protein interactions by isothermal titration calorimetry. <i>Methods in Molecular Biology</i> , 2015 , 1278, 183-204	1.4	41

174	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, 2390-7	5.6	39
173	Discovery of specific flavodoxin inhibitors as potential therapeutic agents against Helicobacter pylori infection. <i>ACS Chemical Biology</i> , 2009 , 4, 928-38	4.9	39
172	Mechanism of low density lipoprotein (LDL) release in the endosome: implications of the stability and Ca ²⁺ affinity of the fifth binding module of the LDL receptor. <i>Journal of Biological Chemistry</i> , 2008 , 283, 22670-9	5.4	39
171	A look at ligand binding thermodynamics in drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2017 , 12, 363-377	6.2	38
170	Dendrimers as potential inhibitors of the dimerization of the capsid protein of HIV-1. <i>Biomacromolecules</i> , 2010 , 11, 2069-78	6.9	38
169	Binding thermodynamics of ferredoxin:NADP ⁺ reductase: two different protein substrates and one energetics. <i>Biophysical Journal</i> , 2009 , 96, 4966-75	2.9	38
168	Structure-function analysis of Escherichia coli MnmG (GidA), a highly conserved tRNA-modifying enzyme. <i>Journal of Bacteriology</i> , 2009 , 191, 7614-9	3.5	37
167	A mechanism for histone chaperoning activity of nucleoplasmin: thermodynamic and structural models. <i>Journal of Molecular Biology</i> , 2009 , 393, 448-63	6.5	36
166	Structural characterization of myotoxic ecarpholin S from Echis carinatus venom. <i>Biophysical Journal</i> , 2008 , 95, 3366-80	2.9	36
165	Structural basis for inhibition of the histone chaperone activity of SET/TAF-III by cytochrome c. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 9908-13	11.5	35
164	Histone chaperone activity of Arabidopsis thaliana NRP1 is blocked by cytochrome c. <i>Nucleic Acids Research</i> , 2017 , 45, 2150-2165	20.1	34
163	Plant tumour biocontrol agent employs a tRNA-dependent mechanism to inhibit leucyl-tRNA synthetase. <i>Nature Communications</i> , 2013 , 4, 1417	17.4	33
162	Kinetics and thermodynamics of chlorpromazine interaction with lipid bilayers: effect of charge and cholesterol. <i>Journal of the American Chemical Society</i> , 2012 , 134, 4184-95	16.4	32
161	Structural and functional characterization of phosphomimetic mutants of cytochrome c at threonine 28 and serine 47. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2016 , 1857, 387-95	4.6	32
160	Protease inhibition in African subtypes of HIV-1. <i>AIDS Reviews</i> , 2003 , 5, 165-71	1.5	32
159	Deciphering the binding between Nupr1 and MSL1 and their DNA-repairing activity. <i>PLoS ONE</i> , 2013 , 8, e78101	3.7	31
158	Structure of GrlR-GrlA complex that prevents GrlA activation of virulence genes. <i>Nature Communications</i> , 2013 , 4, 2546	17.4	28
157	The mechanism of allosteric coupling in choline kinase β revealed by the action of a rationally designed inhibitor. <i>Angewandte Chemie - International Edition</i> , 2013 , 52, 4582-6	16.4	28

156	The flavodoxin from <i>Helicobacter pylori</i> : structural determinants of thermostability and FMN cofactor binding. <i>Biochemistry</i> , 2008 , 47, 627-39	3.2	28
155	Targeting intrinsically disordered proteins involved in cancer. <i>Cellular and Molecular Life Sciences</i> , 2020 , 77, 1695-1707	10.3	28
154	On the temperature dependence of complex formation between chitosan and proteins. <i>Biomacromolecules</i> , 2011 , 12, 2534-43	6.9	27
153	Incorporating target heterogeneity in drug design. <i>Journal of Cellular Biochemistry</i> , 2001 , Suppl 37, 82-8	4.7	27
152	The puzzle of ligand binding to <i>Corynebacterium ammoniagenes</i> FAD synthetase. <i>Journal of Biological Chemistry</i> , 2009 , 284, 6610-9	5.4	26
151	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	8.4	25
150	Molecular recognition in the interaction of chloroplast 2-Cys peroxiredoxin with NADPH-thioredoxin reductase C (NTRC) and thioredoxin x. <i>FEBS Letters</i> , 2014 , 588, 4342-7	3.8	24
149	Deconvolution analysis for classifying gastric adenocarcinoma patients based on differential scanning calorimetry serum thermograms. <i>Scientific Reports</i> , 2015 , 5, 7988	4.9	24
148	Conformational stability of hepatitis C virus NS3 protease. <i>Biophysical Journal</i> , 2010 , 99, 3811-20	2.9	24
147	Role of key residues at the flavin mononucleotide (FMN):adenyltransferase 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, 14492-517	6.3	24
146	Thermodynamic analysis of ferrous ion binding to <i>Escherichia coli</i> ferritin EcFtnA. <i>Biochemistry</i> , 2005 , 44, 13837-46	3.2	24
145	Ligand binding to one-dimensional lattice-like macromolecules: analysis of the McGhee-von Hippel theory implemented in isothermal titration calorimetry. <i>Analytical Biochemistry</i> , 2006 , 348, 94-104	3.1	24
144	Nanostructures based on ammonium-terminated amphiphilic Janus dendrimers as camptothecin carriers with antiviral activity. <i>European Polymer Journal</i> , 2017 , 90, 136-149	5.2	23
143	MeCP2-E1 isoform is a dynamically expressed, weakly DNA-bound protein with different protein and DNA interactions compared to MeCP2-E2. <i>Epigenetics and Chromatin</i> , 2019 , 12, 63	5.8	23
142	Cytochrome c1 exhibits two binding sites for cytochrome c in plants. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014 , 1837, 1717-29	4.6	23
141	Allosteric inhibitors of the NS3 protease from the hepatitis C virus. <i>PLoS ONE</i> , 2013 , 8, e69773	3.7	23
140	Respiratory complexes III and IV can each bind two molecules of cytochrome c at low ionic strength. <i>FEBS Letters</i> , 2015 , 589, 476-83	3.8	22
139	Structural analysis of the regulation of the DYNLL/LC8 binding to Nek9 by phosphorylation. <i>Journal of Biological Chemistry</i> , 2013 , 288, 12283-94	5.4	22

138	Energetics of nucleotide-induced DnaK conformational states. <i>Biochemistry</i> , 2010 , 49, 1338-45	3.2	22
137	Partition of amphiphilic molecules to lipid bilayers by isothermal titration calorimetry. <i>Analytical Biochemistry</i> , 2010 , 399, 44-7	3.1	22
136	Mechanism of the allosteric activation of the ClpP protease machinery by substrates and active-site inhibitors. <i>Science Advances</i> , 2019 , 5, eaaw3818	14.3	21
135	Rationally designed interfacial peptides are efficient in vitro inhibitors of HIV-1 capsid assembly with antiviral activity. <i>PLoS ONE</i> , 2011 , 6, e23877	3.7	21
134	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,	4.8	21
133	Structural and functional evidence for membrane docking and disruption sites on phospholipase A2-like proteins revealed by complexation with the inhibitor suramin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 2066-78		20
132	Identifying potential novel drugs against Helicobacter pylori by targeting the essential response regulator HsrA. <i>Scientific Reports</i> , 2019 , 9, 11294	4.9	20
131	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, 1534-46	5.7	20
130	Improved flavodoxin inhibitors with potential therapeutic effects against Helicobacter pylori infection. <i>Journal of Medicinal Chemistry</i> , 2013 , 56, 6248-58	8.3	20
129	Tolcapone, a potent aggregation inhibitor for the treatment of familial leptomeningeal amyloidosis. <i>FEBS Journal</i> , 2021 , 288, 310-324	5.7	20
128	Shell Cross-Linked Polymeric Micelles as Camptothecin Nanocarriers for Anti-HCV Therapy. <i>Macromolecular Bioscience</i> , 2015 , 15, 1381-91	5.5	19
127	Cyanobacterial electron carrier proteins as electron donors to CYP106A2 from Bacillus megaterium ATCC 13368. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009 , 1794, 1635-42	4	19
126	Interaction of Bile Salts with Model Membranes Mimicking the Gastrointestinal Epithelium: A Study by Isothermal Titration Calorimetry. <i>Langmuir</i> , 2015 , 31, 9097-104	4	18
125	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	4.1	18
124	Energetic effects of magnesium in the recognition of adenosine nucleotides by the F(1)-ATPase beta subunit. <i>Biochemistry</i> , 2010 , 49, 5258-68	3.2	18
123	Thermodynamics of zinc binding to hepatitis C virus NS3 protease: a folding by binding event. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 77, 624-36	4.2	18
122	Identification and characterization of the lipid-binding property of GrlR, a locus of enterocyte effacement regulator. <i>Biochemical Journal</i> , 2009 , 420, 191-9	3.8	18
121	Structure and Functional Characterization of Human Aspartate Transcarbamoylase, the Target of the Anti-tumoral Drug PALA. <i>Structure</i> , 2016 , 24, 1081-94	5.2	17

120	Targeting the Stress-Induced Protein NUPR1 to Treat Pancreatic Adenocarcinoma. <i>Cells</i> , 2019 , 8,	7.9	17
119	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	4.295	16
118	Polymeric micelles from block copolymers containing 2,6-diacylaminopyridine units for encapsulation of hydrophobic drugs. <i>RSC Advances</i> , 2016 , 6, 24066-24075	3.7	16
117	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	3.2	16
116	Extending in silico mechanism-of-action analysis by annotating targets with pathways: application to cellular cytotoxicity readouts. <i>Future Medicinal Chemistry</i> , 2014 , 6, 2029-56	4.1	16
115	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, 950-61	4.2	16
114	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	4	15
113	Geometric features of the Wiseman isotherm in isothermal titration calorimetry. <i>Journal of Thermal Analysis and Calorimetry</i> , 2015 , 122, 1477-1483	4.1	15
112	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	4.9	15
111	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, 1054-64	6.5	15
110	Design, Synthesis, and Efficacy Testing of Nitroethylene- and 7-Nitrobenzoxadiazol-Based Flavodoxin Inhibitors against Drug-Resistant Clinical Strains and in -Infected Mice. <i>Journal of Medicinal Chemistry</i> , 2019 , 62, 6102-6115	8.3	14
109	Rational stabilization of complex proteins: a divide and combine approach. <i>Scientific Reports</i> , 2015 , 5, 9129	4.9	14
108	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	3.7	14
107	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	8.4	13
106	Microcystin-LR Binds Iron, and Iron Promotes Self-Assembly. <i>Environmental Science & Technology</i> , 2017 , 51, 4841-4850	10.3	13
105	A Quantitative Characterization of Nucleoplasmin/Histone Complexes Reveals Chaperone Versatility. <i>Scientific Reports</i> , 2016 , 6, 32114	4.9	13
104	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, 2120-31	6.5	13
103	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	4.9	12

102	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	4	12
101	Differential NtcA Responsiveness to 2-Oxoglutarate Underlies the Diversity of C/N Balance Regulation in. <i>Frontiers in Microbiology</i> , 2017 , 8, 2641	5.7	12
100	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	4.9	12
99	A New Member of the Thioredoxin Reductase Family from Early Oxygenic Photosynthetic Organisms. <i>Molecular Plant</i> , 2017 , 10, 212-215	14.4	12
98	Structural Basis for a Unique ATP Synthase Core Complex from <i>Nanoarchaeum equitans</i> . <i>Journal of Biological Chemistry</i> , 2015 , 290, 27280-27296	5.4	12
97	Conformational stability of <i>Helicobacter pylori</i> flavodoxin: fit to function at pH 5. <i>Journal of Biological Chemistry</i> , 2008 , 283, 2883-95	5.4	12
96	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	4.9	11
95	Determination of potential scaffolds for human choline kinase β by chemical deconvolution studies. <i>ChemBioChem</i> , 2013 , 14, 1291-5	3.8	11
94	Determination of the Rigorous Transfer Function of An Isothermal Titration Microcalorimeter with Peltier Compensation. <i>Magyar Árvad Kélemlék</i> , 1999 , 57, 343-359	0	11
93	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	11.5	10
92	Zinc induced folding is essential for TIM15 activity as an mtHsp70 chaperone. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2013 , 1830, 2139-49	4	10
91	Novel histone H3 binding protein ORF158L from the Singapore grouper iridovirus. <i>Journal of Virology</i> , 2011 , 85, 9159-66	6.6	10
90	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, 1336-48	2.9	10
89	Structural basis for dual-inhibition mechanism of a non-classical Kazal-type serine protease inhibitor from horseshoe crab in complex with subtilisin. <i>PLoS ONE</i> , 2011 , 6, e18838	3.7	10
88	Biophysical Screening for Identifying Pharmacological Chaperones and Inhibitors Against Conformational and Infectious Diseases. <i>Current Drug Targets</i> , 2016 , 17, 1492-505	3	10
87	Low-density lipoprotein receptor is a calcium/magnesium sensor - role of LR4 and LR5 ion interaction kinetics in low-density lipoprotein release in the endosome. <i>FEBS Journal</i> , 2014 , 281, 2638-58	5.7	9
86	Dimerization of VirD2 binding protein is essential for <i>Agrobacterium</i> induced tumor formation in plants. <i>PLoS Pathogens</i> , 2014 , 10, e1003948	7.6	9
85	NS3 protease from hepatitis C virus: biophysical studies on an intrinsically disordered protein domain. <i>International Journal of Molecular Sciences</i> , 2013 , 14, 13282-306	6.3	9

84	ZZW-115-dependent inhibition of NUPR1 nuclear translocation sensitizes cancer cells to genotoxic agents. <i>JCI Insight</i> , 2020 , 5,	9.9	9
83	Streptococcus pneumoniae TIGR4 Flavodoxin: Structural and Biophysical Characterization of a Novel Drug Target. <i>PLoS ONE</i> , 2016 , 11, e0161020	3.7	9
82	Seleno-Functionalization of Quercetin Improves the Non-Covalent Inhibition of M and Its Antiviral Activity in Cells against SARS-CoV-2. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	9
81	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	8.4	9
80	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	4.6	9
79	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	3.3	9
78	Dendrimers as Competitors of Protein-Protein Interactions of the Intrinsically Disordered Nuclear Chromatin Protein NUPR1. <i>Biomacromolecules</i> , 2019 , 20, 2567-2576	6.9	8
77	Thermal denaturation of Erythromycin 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	4.1	8
76	The histidine-phosphocarrier protein of the phosphoenolpyruvate: sugar phosphotransferase system of Bacillus sphaericus self-associates. <i>PLoS ONE</i> , 2013 , 8, e69307	3.7	8
75	Repurposing Dihydropyridines for Treatment of Infection. <i>Pharmaceutics</i> , 2019 , 11,	6.4	8
74	Proposed mechanism for regulation of H ₂ O ₂ -induced programmed cell death in plants by binding of cytochrome c to 14-3-3 proteins. <i>Plant Journal</i> , 2021 , 106, 74-85	6.9	8
73	Small Molecule Inhibitors of the Response Regulator ArsR Exhibit Bactericidal Activity against. <i>Microorganisms</i> , 2020 , 8,	4.9	7
72	Emissive Enhancement of the Singlet Oxygen Chemiluminescence Probe after Binding to Bovine Serum Albumin. <i>Molecules</i> , 2019 , 24,	4.8	7
71	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,	6.6	7
70	Isolated noncatalytic and catalytic subunits of F1-ATPase exhibit similar, albeit not identical, energetic strategies for recognizing adenosine nucleotides. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014 , 1837, 44-50	4.6	7
69	Experimental validation of in silico target predictions on synergistic protein targets. <i>MedChemComm</i> , 2013 , 4, 278-288	5	7
68	Antimalarial activity of cupredoxins: the interaction of Plasmodium merozoite surface protein 119 (MSP119) and rusticyanin. <i>Journal of Biological Chemistry</i> , 2013 , 288, 20896-20907	5.4	7
67	Inhibition of Pig Phosphoenolpyruvate Carboxykinase Isoenzymes by 3-Mercaptopicolinic Acid and Novel Inhibitors. <i>PLoS ONE</i> , 2016 , 11, e0159002	3.7	7

66	Studying the allosteric energy cycle by isothermal titration calorimetry. <i>Methods in Molecular Biology</i> , 2012 , 796, 53-70	1.4	7
65	Human riboflavin kinase: Species-specific traits in the biosynthesis of the FMN cofactor. <i>FASEB Journal</i> , 2020 , 34, 10871-10886	0.9	7
64	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	11.3	7
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