

# Faizan Ahmad

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2549/publications.pdf>

Version: 2024-02-01

276  
papers

8,701  
citations

44042

48  
h-index

82499

72  
g-index

279  
all docs

279  
docs citations

279  
times ranked

7849  
citing authors

#	ARTICLE	IF	CITATIONS
1	The SARS Coronavirus 3a Protein Causes Endoplasmic Reticulum Stress and Induces Ligand-Independent Downregulation of the Type 1 Interferon Receptor. <i>PLoS ONE</i> , 2009, 4, e8342.	1.1	219
2	Luminol-Based Chemiluminescent Signals: Clinical and Non-clinical Application and Future Uses. <i>Applied Biochemistry and Biotechnology</i> , 2014, 173, 333-355.	1.4	212
3	Structure, function and applications of carbonic anhydrase isozymes. <i>Bioorganic and Medicinal Chemistry</i> , 2013, 21, 1570-1582.	1.4	203
4	Zinc $\beta$ 2-Glycoprotein: A Multidisciplinary Protein. <i>Molecular Cancer Research</i> , 2008, 6, 892-906.	1.5	200
5	A Review of Methods Available to Estimate Solvent-Accessible Surface Areas of Soluble Proteins in the Folded and Unfolded States. <i>Current Protein and Peptide Science</i> , 2014, 15, 456-476.	0.7	197
6	Protein aggregation and neurodegenerative diseases: From theory to therapy. <i>European Journal of Medicinal Chemistry</i> , 2016, 124, 1105-1120.	2.6	120
7	Naturally occurring organic osmolytes: From cell physiology to disease prevention. <i>IUBMB Life</i> , 2010, 62, 891-895.	1.5	116
8	Identification and evaluation of bioactive natural products as potential inhibitors of human microtubule affinity-regulating kinase 4 (MARK4). <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 1813-1829.	2.0	114
9	Rosmarinic Acid Exhibits Anticancer Effects via MARK4 Inhibition. <i>Scientific Reports</i> , 2020, 10, 10300.	1.6	114
10	The role of key residues in structure, function, and stability of cytochrome-c. <i>Cellular and Molecular Life Sciences</i> , 2014, 71, 229-255.	2.4	113
11	Formation of the molten globule-like state during prolonged glycation of human serum albumin. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2007, 1770, 933-942.	1.1	109
12	Counteracting Osmolyte Trimethylamine N-Oxide Destabilizes Proteins at pH below Its pK. <i>Journal of Biological Chemistry</i> , 2005, 280, 11035-11042.	1.6	104
13	Effect of polyol osmolytes on $\Delta G$ , the Gibbs energy of stabilisation of proteins at different pH values. <i>Biophysical Chemistry</i> , 2005, 117, 1-12.	1.5	101
14	Investigation of molecular mechanism of recognition between citral and MARK4: A newer therapeutic approach to attenuate cancer cell progression. <i>International Journal of Biological Macromolecules</i> , 2018, 107, 2580-2589.	3.6	96
15	Microtubule Affinity-Regulating Kinase 4: Structure, Function, and Regulation. <i>Cell Biochemistry and Biophysics</i> , 2013, 67, 485-499.	0.9	94
16	Compatibility of osmolytes with Gibbs energy of stabilization of proteins. <i>BBA - Proteins and Proteomics</i> , 2000, 1476, 75-84.	2.1	93
17	Functional Annotation of Conserved Hypothetical Proteins from <i>Haemophilus influenzae</i> Rd KW20. <i>PLoS ONE</i> , 2013, 8, e84263.	1.1	93
18	Elucidation of Dietary Polyphenolics as Potential Inhibitor of Microtubule Affinity Regulating Kinase 4: In silico and In vitro Studies. <i>Scientific Reports</i> , 2017, 7, 9470.	1.6	91

#	ARTICLE	IF	CITATIONS
19	Protein and DNA destabilization by osmolytes: The other side of the coin. <i>Life Sciences</i> , 2011, 88, 117-125.	2.0	89
20	Virtual Screening Approach to Identify High-Affinity Inhibitors of Serum and Glucocorticoid-Regulated Kinase 1 among Bioactive Natural Products: Combined Molecular Docking and Simulation Studies. <i>Molecules</i> , 2020, 25, 823.	1.7	89
21	Size-dependent studies of macromolecular crowding on the thermodynamic stability, structure and functional activity of proteins: in vitro and in silico approaches. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 178-197.	1.1	86
22	Enzymatic digestion and antioxidant activity of the native and molten globule states of camel $\beta$ -lactalbumin: Possible significance for use in infant formula. <i>International Dairy Journal</i> , 2009, 19, 518-523.	1.5	83
23	Influence of temperature on the intrinsic viscosities of proteins in random coil conformation. <i>Biochemistry</i> , 1974, 13, 245-249.	1.2	80
24	Investigation of inhibitory potential of quercetin to the pyruvate dehydrogenase kinase 3: Towards implications in anticancer therapy. <i>International Journal of Biological Macromolecules</i> , 2019, 136, 1076-1085.	3.6	80
25	Large scale analysis of the mutational landscape in $\beta$ -glucuronidase: A major player of mucopolysaccharidosis type VII. <i>Gene</i> , 2016, 576, 36-44.	1.0	79
26	A New Method for the Determination of Stability Parameters of Proteins from Their Heat-Induced Denaturation Curves. <i>Analytical Biochemistry</i> , 2000, 283, 207-213.	1.1	78
27	Protein Stability: Urea-Induced versus Guanidine-Induced Unfolding of Metmyoglobin. <i>Biochemistry</i> , 1996, 35, 11925-11930.	1.2	74
28	Effect of monomeric and oligomeric sugar osmolytes on $\Delta G$ , the Gibbs energy of stabilization of the protein at different pH values: Is the sum effect of monosaccharide individually additive in a mixture?. <i>Biophysical Chemistry</i> , 2008, 138, 120-129.	1.5	74
29	Curcumin specifically binds to the human calcium-calmodulin-dependent protein kinase IV: fluorescence and molecular dynamics simulation studies. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 572-584.	2.0	68
30	Binding studies and biological evaluation of $\beta$ -carotene as a potential inhibitor of human calcium/calmodulin-dependent protein kinase IV. <i>International Journal of Biological Macromolecules</i> , 2017, 96, 161-170.	3.6	67
31	Heavy metals assessment in water, soil, vegetables and their associated health risks via consumption of vegetables, District Kasur, Pakistan. <i>SN Applied Sciences</i> , 2021, 3, 1.	1.5	61
32	Glycine betaine may have opposite effects on protein stability at high and low pH values. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 929-935.	1.1	60
33	Role of N-terminal residues on folding and stability of C-phycoerythrin: simulation and urea-induced denaturation studies. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 121-133.	2.0	60
34	High throughput screening, docking, and molecular dynamics studies to identify potential inhibitors of human calcium/calmodulin-dependent protein kinase IV. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 2179-2192.	2.0	60
35	Spectroscopic, calorimetric and molecular docking insight into the interaction of Alzheimer's drug donepezil with human transferrin: implications of Alzheimer's drug. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 1094-1102.	2.0	60
36	Purification and characterization of a trypsin inhibitor from <i>Putranjiva roxburghii</i> seeds. <i>Phytochemistry</i> , 2008, 69, 2120-2126.	1.4	59

#	ARTICLE	IF	CITATIONS
37	Human $\alpha$ -Glucuronidase: Structure, Function, and Application in Enzyme Replacement Therapy. <i>Rejuvenation Research</i> , 2013, 16, 352-363.	0.9	59
38	Therapeutic progress in amyotrophic lateral sclerosis-beginning to learning. <i>European Journal of Medicinal Chemistry</i> , 2016, 121, 903-917.	2.6	59
39	Protein Stability: A Functional Dependence of Denaturational Gibbs Energy on Urea Concentration. <i>Biochemistry</i> , 1999, 38, 2471-2479.	1.2	56
40	Evidence of vanillin binding to CAMKIV explains the anti-cancer mechanism in human hepatic carcinoma and neuroblastoma cells. <i>Molecular and Cellular Biochemistry</i> , 2018, 438, 35-45.	1.4	56
41	FND5/Irisin: Physiology and Pathophysiology. <i>Molecules</i> , 2022, 27, 1118.	1.7	56
42	Calcium/calmodulin-dependent protein kinase IV: A multifunctional enzyme and potential therapeutic target. <i>Progress in Biophysics and Molecular Biology</i> , 2016, 121, 54-65.	1.4	54
43	Reversible unfolding of the major fraction of ovalbumin by guanidine hydrochloride. <i>Biochemistry</i> , 1976, 15, 5168-5175.	1.2	53
44	Thermodynamics of the denaturation of pepsinogen by urea. <i>Biochemistry</i> , 1978, 17, 241-246.	1.2	53
45	Structural Analysis and Conformational Dynamics of STN1 Gene Mutations Involved in Coat Plus Syndrome. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 41.	1.6	53
46	Comparative analysis of naturally occurring L-amino acid osmolytes and their D-isomers on protection of <i>Escherichia coli</i> against environmental stresses. <i>Journal of Biosciences</i> , 2002, 27, 515-520.	0.5	52
47	Molecular mechanism of Ras-related protein Rab-5A and effect of mutations in the catalytically active phosphate-binding loop. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 105-118.	2.0	52
48	Probing the interaction of Rivastigmine Tartrate, an important Alzheimer's drug, with serum albumin: Attempting treatment of Alzheimer's disease. <i>International Journal of Biological Macromolecules</i> , 2020, 148, 533-542.	3.6	52
49	Functional annotation of putative hypothetical proteins from <i>Candida dubliniensis</i> . <i>Gene</i> , 2014, 543, 93-100.	1.0	51
50	Structural characterization of MG and pre-MG states of proteins by MD simulations, NMR, and other techniques. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 2267-2284.	2.0	51
51	Spectroscopic Studies of the Effects of Glycation of Human Serum Albumin on L-Trp Binding. <i>Protein and Peptide Letters</i> , 2007, 14, 13-18.	0.4	50
52	Design, Synthesis, and Biological Evaluation of a New Palladium(II) Complex: $\beta$ -Lactoglobulin and K562 as Targets. <i>Journal of Physical Chemistry B</i> , 2010, 114, 3639-3647.	1.2	50
53	Structure and function of von Willebrand factor. <i>Blood Coagulation and Fibrinolysis</i> , 2012, 23, 11-22.	0.5	50
54	Designing New Kinase Inhibitor Derivatives as Therapeutics Against Common Complex Diseases: Structural Basis of Microtubule Affinity-Regulating Kinase 4 (MARK4) Inhibition. <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 700-711.	1.0	50

#	ARTICLE	IF	CITATIONS
55	Relationship between functional activity and protein stability in the presence of all classes of stabilizing osmolytes. <i>FEBS Journal</i> , 2009, 276, 6024-6032.	2.2	49
56	Conformational and Thermodynamic Characterization of the Molten Globule State Occurring during Unfolding of Cytochromes-c by Weak Salt Denaturants. <i>Biochemistry</i> , 2003, 42, 1684-1695.	1.2	46
57	Unraveling Binding Mechanism of Alzheimer's Drug Rivastigmine Tartrate with Human Transferrin: Molecular Docking and Multi-Spectroscopic Approach towards Neurodegenerative Diseases. <i>Biomolecules</i> , 2019, 9, 495.	1.8	46
58	Estimation of the stability of globular proteins. <i>Biopolymers</i> , 1986, 25, 1623-1633.	1.2	45
59	Role of non-compatible osmolytes in the stabilization of proteins during heat stress. <i>Biochemical Journal</i> , 1998, 329, 137-143.	1.7	45
60	Effects of mobile phone radiofrequency on the structure and function of the normal human hemoglobin. <i>International Journal of Biological Macromolecules</i> , 2009, 44, 278-285.	3.6	45
61	Exploring molecular insights into the interaction mechanism of cholesterol derivatives with the Mce4A: A combined spectroscopic and molecular dynamic simulation studies. <i>International Journal of Biological Macromolecules</i> , 2018, 111, 548-560.	3.6	45
62	Amphiphilic nature of polyethylene glycols and their role in medical research. <i>Polymer Testing</i> , 2020, 82, 106316.	2.3	45
63	Protein aggregation, misfolding and consequential human neurodegenerative diseases. <i>International Journal of Neuroscience</i> , 2017, 127, 1047-1057.	0.8	44
64	Structure-based investigation of MARK4 inhibitory potential of Naringenin for therapeutic management of cancer and neurodegenerative diseases. <i>Journal of Cellular Biochemistry</i> , 2021, 122, 1445-1459.	1.2	44
65	Stability of proteins in the presence of polyols estimated from their guanidinium chloride-induced transition curves at different pH values and 25 °C. <i>Biophysical Chemistry</i> , 2006, 119, 224-233.	1.5	43
66	Protein-Protein Interactions: Principles, Techniques, and their Potential Role in New Drug Development. <i>Journal of Biomolecular Structure and Dynamics</i> , 2011, 28, 929-938.	2.0	43
67	2/3D-QSAR, molecular docking and MD simulation studies of FtsZ protein targeting benzimidazoles derivatives. <i>Computational Biology and Chemistry</i> , 2019, 78, 398-413.	1.1	43
68	Interaction of DNA Minor Groove Binder Hoechst 33258 with Bovine Serum Albumin. <i>Chemical and Pharmaceutical Bulletin</i> , 2009, 57, 481-486.	0.6	42
69	Structural and functional analysis of human prostatic acid phosphatase. <i>Expert Review of Anticancer Therapy</i> , 2010, 10, 1055-1068.	1.1	42
70	Relationship between protein stability and functional activity in the presence of macromolecular crowding agents alone and in mixture: An insight into stability-activity trade-off. <i>Archives of Biochemistry and Biophysics</i> , 2015, 584, 42-50.	1.4	42
71	Biological Evaluation of a New Synthesized Pt(II) Complex by Cytotoxic and Spectroscopic Studies. <i>Cell Biochemistry and Biophysics</i> , 2015, 71, 1415-1424.	0.9	42
72	Testing the paradigm that the denaturing effect of urea on protein stability is offset by methylamines at the physiological concentration ratio of 2:1 (urea:methylamines). <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2007, 1774, 1555-1562.	1.1	41

#	ARTICLE	IF	CITATIONS
73	Progastriscin: Structure, Function, and Its Role in Tumor Progression. <i>Journal of Molecular Cell Biology</i> , 2010, 2, 118-127.	1.5	41
74	The denaturation of ribonuclease A by combinations of urea and salt denaturants. <i>Journal of Molecular Biology</i> , 1979, 131, 607-617.	2.0	39
75	Biophysical Analyses of Human Resistin: Oligomer Formation Suggests Novel Biological Function. <i>Biochemistry</i> , 2008, 47, 12457-12466.	1.2	39
76	Identification of Potential Inhibitors of Calcium/Calmodulin-Dependent Protein Kinase IV from Bioactive Phytoconstituents. <i>Oxidative Medicine and Cellular Longevity</i> , 2020, 2020, 1-14.	1.9	39
77	Testing polyolsâ€™ compatibility with Gibbs energy of stabilization of proteins under conditions in which they behave as compatible osmolytes. <i>FEBS Letters</i> , 2005, 579, 3891-3898.	1.3	38
78	Identification of Functional Candidates amongst Hypothetical Proteins of <i>Treponema pallidum</i> ssp. <i>pallidum</i> . <i>PLoS ONE</i> , 2015, 10, e0124177.	1.1	38
79	Macromolecular crowding induces molten globule state in the native myoglobin at physiological pH. <i>International Journal of Biological Macromolecules</i> , 2018, 106, 130-139.	3.6	38
80	A Unique Molten Globule State Occurs during Unfolding of Cytochrome c by LiClO <sub>4</sub> Near Physiological pH and Temperature: Structural and Thermodynamic Characterization. <i>Biochemistry</i> , 2006, 45, 4695-4702.	1.2	37
81	Evaluation of pyrazolopyrimidine derivatives as microtubule affinity regulating kinase 4 inhibitors: Towards therapeutic management of Alzheimerâ€™s disease. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 3892-3907.	2.0	37
82	Structural and biochemical investigation of MARK4 inhibitory potential of cholic acid: Towards therapeutic implications in neurodegenerative diseases. <i>International Journal of Biological Macromolecules</i> , 2020, 161, 596-604.	3.6	37
83	A single mutation induces molten globule formation and a drastic destabilization of wild-type cytochrome c at pH 6.0. <i>Journal of Biological Inorganic Chemistry</i> , 2009, 14, 751-760.	1.1	36
84	Thermal Stabilization of Proteins by Mono- and Oligosaccharides: Measurement and Analysis in the Context of an Excluded Volume Model. <i>Biochemistry</i> , 2015, 54, 3594-3603.	1.2	35
85	First evidence of formation of pre-molten globule state in myoglobin: A macromolecular crowding approach towards protein folding in vivo. <i>International Journal of Biological Macromolecules</i> , 2019, 126, 1288-1294.	3.6	35
86	Structural diversity of class I MHC-like molecules and its implications in binding specificities. <i>Advances in Protein Chemistry and Structural Biology</i> , 2011, 83, 223-270.	1.0	34
87	Structure guided design of potential inhibitors of human calciumâ€™ calmodulin dependent protein kinase IV containing pyrimidine scaffold. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2016, 26, 782-788.	1.0	34
88	Computing disease-linked SOD1 mutations: deciphering protein stability and patient-phenotype relations. <i>Scientific Reports</i> , 2017, 7, 4678.	1.6	34
89	Equilibrium studies of the effect of difference in sequence homology on the mechanism of denaturation of bovine and horse cytochromes-c. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2003, 1646, 49-56.	1.1	33
90	The pH Dependence of Saccharides' Influence on Thermal Denaturation of Two Model Proteins Supports an Excluded Volume Model for Stabilization Generalized to Allow for Intramolecular Electrostatic Interactions. <i>Journal of Biological Chemistry</i> , 2017, 292, 505-511.	1.6	33

#	ARTICLE	IF	CITATIONS
91	Investigation of deleterious effects of nsSNPs in the <i>POT1</i> gene: a structural genomics-based approach to understand the mechanism of cancer development. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 10281-10294.	1.2	32
92	Virtual high-throughput screening of natural compounds in-search of potential inhibitors for protection of telomeres 1 (POT1). <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 4625-4634.	2.0	32
93	Thermodynamic stability of proteins in salt solutions: A comparison of the effectiveness of protein stabilizers. <i>The Protein Journal</i> , 1986, 5, 355-367.	1.1	31
94	Comparative Studies on the Interaction Between Bovine $\beta$ -lacto-globulin Type A and B and a New Designed Pd(II) Complex with Anti-tumor Activity at Different Temperatures. <i>Journal of Biomolecular Structure and Dynamics</i> , 2009, 26, 587-597.	2.0	31
95	In vitro and in silico studies of urea-induced denaturation of yeast iso-1-cytochrome c and its deletants at pH 6.0 and 25 °C. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 1493-1502.	2.0	31
96	Effect of pH on the structure, function, and stability of human calcium/calmodulin-dependent protein kinase IV: combined spectroscopic and MD simulation studies. <i>Biochemistry and Cell Biology</i> , 2016, 94, 221-228.	0.9	31
97	Mechanistic insights into the urea-induced denaturation of kinase domain of human integrin linked kinase. <i>International Journal of Biological Macromolecules</i> , 2018, 111, 208-218.	3.6	31
98	Carbohydrate-Based Macromolecular Crowding-Induced Stabilization of Proteins: Towards Understanding the Significance of the Size of the Crowder. <i>Biomolecules</i> , 2019, 9, 477.	1.8	31
99	Design and synthesis of a novel class of carbonic anhydrase-IX inhibitor 1-(3-(phenyl/4-fluorophenyl)-7-imino-3H-[1,2,3]triazolo[4,5d]pyrimidin-6(7H)yl)urea. <i>Journal of Molecular Graphics and Modelling</i> , 2016, 64, 101-109.	1.3	30
100	Fragile histidine triad protein: structure, function, and its association with tumorigenesis. <i>Journal of Cancer Research and Clinical Oncology</i> , 2010, 136, 333-350.	1.2	29
101	Effect of pH on structure, function, and stability of mitochondrial carbonic anhydrase VA. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 449-461.	2.0	29
102	Impact of Gln94Glu mutation on the structure and function of protection of telomere 1, a cause of cutaneous familial melanoma. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 1514-1524.	2.0	29
103	Conformational and thermodynamic characterization of the premolten globule state occurring during unfolding of the molten globule state of cytochrome c. <i>Journal of Biological Inorganic Chemistry</i> , 2010, 15, 1319-1329.	1.1	28
104	PKR-inhibitor binds efficiently with human microtubule affinity-regulating kinase 4. <i>Journal of Molecular Graphics and Modelling</i> , 2015, 62, 245-252.	1.3	28
105	Molecular basis of the structural stability of hemochromatosis factor <i>HFE</i> : A combined molecular dynamic simulation and GdmCl <sub>2</sub> -induced denaturation study. <i>Biopolymers</i> , 2016, 105, 133-142.	1.2	28
106	Design, synthesis, and biological evaluation of pyrimidine derivatives as potential inhibitors of human calcium/calmodulin-dependent protein kinase <i>IV</i> . <i>Chemical Biology and Drug Design</i> , 2017, 89, 741-754.	1.5	28
107	Evidence of non-coincidence of normalized sigmoidal curves of two different structural properties for two-state protein folding/unfolding. <i>Journal of Chemical Thermodynamics</i> , 2013, 58, 351-358.	1.0	27
108	Structure-based functional annotation of hypothetical proteins from <i>Candida dubliniensis</i> : a quest for potential drug targets. <i>3 Biotech</i> , 2015, 5, 561-576.	1.1	27

#	ARTICLE	IF	CITATIONS
109	Characterization of intermediate state of myoglobin in the presence of PEG 10 under physiological conditions. <i>International Journal of Biological Macromolecules</i> , 2017, 99, 241-248.	3.6	27
110	Effect of sequential deletion of extra N-terminal residues on the structure and stability of yeast iso-1-cytochrome-c. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 2005-2016.	2.0	26
111	In silico approaches for the identification of virulence candidates amongst hypothetical proteins of <i>Mycoplasma pneumoniae</i> 309. <i>Computational Biology and Chemistry</i> , 2015, 59, 67-80.	1.1	26
112	Evaluation of Binding of Rosmarinic Acid with Human Transferrin and Its Impact on the Protein Structure: Targeting Polyphenolic Acid-Induced Protection of Neurodegenerative Disorders. <i>Oxidative Medicine and Cellular Longevity</i> , 2020, 2020, 1-14.	1.9	26
113	Interactions Under Crowding Milieu: Chemical-Induced Denaturation of Myoglobin is Determined by the Extent of Heme Dissociation on Interaction with Crowders. <i>Biomolecules</i> , 2020, 10, 490.	1.8	26
114	Interaction of polyethylene glycol with cytochrome c investigated via in vitro and in silico approaches. <i>Scientific Reports</i> , 2021, 11, 6475.	1.6	26
115	Cloning, Expression, Purification and Refolding of Microtubule Affinity-Regulating Kinase 4 Expressed in <i>Escherichia coli</i> . <i>Applied Biochemistry and Biotechnology</i> , 2014, 172, 2838-2848.	1.4	25
116	Structural insight into C9orf72 hexanucleotide repeat expansions: Towards new therapeutic targets in FTD-ALS. <i>Neurochemistry International</i> , 2016, 100, 11-20.	1.9	25
117	Urea-induced denaturation of human calcium/calmodulin-dependent protein kinase IV: a combined spectroscopic and MD simulation studies. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 463-475.	2.0	25
118	Characterization of folding intermediates during urea-induced denaturation of human carbonic anhydrase II. <i>International Journal of Biological Macromolecules</i> , 2017, 95, 881-887.	3.6	25
119	Sequence, structure and evolutionary analysis of cold shock domain proteins, a member of OB fold family. <i>Journal of Evolutionary Biology</i> , 2018, 31, 1903-1917.	0.8	25
120	Mixture of Macromolecular Crowding Agents Has a Non-additive Effect on the Stability of Proteins. <i>Applied Biochemistry and Biotechnology</i> , 2019, 188, 927-941.	1.4	25
121	Formation of molten globule state in horse heart cytochrome c under physiological conditions: Importance of soft interactions and spectroscopic approach in crowded milieu. <i>International Journal of Biological Macromolecules</i> , 2020, 148, 192-200.	3.6	25
122	Characterization of pre-molten globule state of yeast iso-1-cytochrome c and its deletants at pH 6.0 and 25 Å°C. <i>International Journal of Biological Macromolecules</i> , 2015, 72, 1406-1418.	3.6	24
123	Ubiquitin-associated domain of MARK4 provides stability at physiological pH. <i>International Journal of Biological Macromolecules</i> , 2016, 93, 1147-1154.	3.6	24
124	Structural Features of Nucleoprotein CST/Shelterin Complex Involved in the Telomere Maintenance and Its Association with Disease Mutations. <i>Cells</i> , 2020, 9, 359.	1.8	24
125	Cooperative Unfolding of Residual Structure in Heat Denatured Proteins by Urea and Guanidinium Chloride. <i>PLoS ONE</i> , 2015, 10, e0128740.	1.1	24
126	Acidic pH enhances structure and structural stability of the capsid protein of hepatitis E virus. <i>Biochemical and Biophysical Research Communications</i> , 2004, 313, 67-73.	1.0	23



#	ARTICLE	IF	CITATIONS
127	THE DENATURATION OF COVALENTLY INHIBITED SWINE PEPSIN. International Journal of Peptide and Protein Research, 1978, 12, 155-163.	0.1	23
128	Atypical PKC phosphorylates microtubule affinity-regulating kinase 4 in vitro. Molecular and Cellular Biochemistry, 2015, 410, 223-228.	1.4	23
129	Spectroscopic and MD simulation studies on unfolding processes of mitochondrial carbonic anhydrase VA induced by urea. Journal of Biomolecular Structure and Dynamics, 2016, 34, 1987-1997.	2.0	23
130	Comparison of the thermal stabilization of proteins by oligosaccharides and monosaccharide mixtures: Measurement and analysis in the context of excluded volume theory. Biophysical Chemistry, 2018, 237, 31-37.	1.5	23
131	Biophysical Elucidation of Fibrillation Inhibition by Sugar Osmolytes in $\hat{\pm}$ -Lactalbumin: Multispectroscopic and Molecular Docking Approaches. ACS Omega, 2020, 5, 26871-26882.	1.6	23
132	Testing the Ability of Non-Methylamine Osmolytes Present in Kidney Cells to Counteract the Deleterious Effects of Urea on Structure, Stability and Function of Proteins. PLoS ONE, 2013, 8, e72533.	1.1	22
133	Delineating the relationship between amyotrophic lateral sclerosis and frontotemporal dementia: Sequence and structure-based predictions. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2016, 1862, 1742-1754.	1.8	22
134	GdmCl-induced unfolding studies of human carbonic anhydrase IX: a combined spectroscopic and MD simulation approach. Journal of Biomolecular Structure and Dynamics, 2017, 35, 1295-1306.	2.0	22
135	Sugar osmolytes-induced stabilization of RNase A in macromolecular crowded cellular environment. International Journal of Biological Macromolecules, 2018, 115, 349-357.	3.6	22
136	Immobilized angiotensin II type I receptor: A powerful method of high throughput screening for antihypertensive compound identification through binding interaction analysis. Journal of Chromatography A, 2020, 1620, 461003.	1.8	22
137	A New Method for Testing the Functional Dependence of Unfolding Free Energy Changes on Denaturant Concentration. Journal of Biochemistry, 1994, 115, 322-327.	0.9	21
138	Structural basis of urea-induced unfolding: Unraveling the folding pathway of hemochromatosis factor E. International Journal of Biological Macromolecules, 2016, 91, 1051-1061.	3.6	21
139	Characterisation of molten globule-like state of sheep serum albumin at physiological pH. International Journal of Biological Macromolecules, 2016, 89, 605-613.	3.6	21
140	Effects of Ethylene Glycol on the Structure and Stability of Myoglobin Using Spectroscopic, Interaction, and <i>In Silico</i> Approaches: Monomer Is Different from Those of Its Polymers. ACS Omega, 2020, 5, 13840-13850.	1.6	21
141	A possible origin of differences between calorimetric and equilibrium estimates of stability parameters of proteins. Biochemical Journal, 2000, 345, 711.	1.7	20
142	Guanidinium chloride and urea denaturations of $\hat{I}^2$ -Lactoglobulin A at pH 2.0 and 25 $\hat{\hat{A}}^\circ\text{C}$ : The equilibrium intermediate contains non-native structures (helix, tryptophan and hydrophobic patches). Biophysical Chemistry, 2007, 127, 140-148.	1.5	20
143	Heparin Accelerates the Protein Aggregation via the Downhill Polymerization Mechanism: Multi-Spectroscopic Studies to Delineate the Implications on Proteinopathies. ACS Omega, 2021, 6, 2328-2339.	1.6	20
144	The intrinsic viscosity of glycoproteins. International Journal of Biochemistry & Cell Biology, 1980, 11, 91-96.	0.8	19

#	ARTICLE	IF	CITATIONS
145	Conformation and thermodynamic stability of pre-molten and molten globule states of mammalian cytochromes-c. <i>Metallomics</i> , 2011, 3, 327.	1.0	19
146	Testing the dependence of stabilizing effect of osmolytes on the fractional increase in the accessible surface area on thermal and chemical denaturations of proteins. <i>Archives of Biochemistry and Biophysics</i> , 2016, 591, 7-17.	1.4	19
147	Effect of pH on the stability of hemochromatosis factor E: a combined spectroscopic and molecular dynamics simulation-based study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 1582-1598.	2.0	19
148	Estimation of thermodynamic stability of human carbonic anhydrase IX from urea-induced denaturation and MD simulation studies. <i>International Journal of Biological Macromolecules</i> , 2017, 105, 183-189.	3.6	19
149	Insight into the binding of PEG-400 with eye protein alpha-crystallin: Multi spectroscopic and computational approach: possible therapeutics targeting eye diseases. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 4496-4506.	2.0	19
150	Living with urea stress. <i>Journal of Biosciences</i> , 2009, 34, 321-331.	0.5	18
151	The SARS Coronavirus 3a protein binds calcium in its cytoplasmic domain. <i>Virus Research</i> , 2014, 191, 180-183.	1.1	18
152	Towards New Drug Targets? Function Prediction of Putative Proteins of <i>Neisseria meningitidis</i> MC58 and Their Virulence Characterization. <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 416-434.	1.0	18
153	Protein folding: Molecular dynamics simulations and in vitro studies for probing mechanism of urea- and guanidinium chloride-induced unfolding of horse cytochrome-c. <i>International Journal of Biological Macromolecules</i> , 2019, 122, 695-704.	3.6	18
154	Molecular and macromolecular crowding-induced stabilization of proteins: Effect of dextran and its building block alone and their mixtures on stability and structure of lysozyme. <i>International Journal of Biological Macromolecules</i> , 2020, 150, 1238-1248.	3.6	18
155	Investigation of conformational dynamics of Tyr89Cys mutation in protection of telomeres 1 gene associated with familial melanoma. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 35-44.	2.0	18
156	Sequence and stability of the goat cytochrome c. <i>Biophysical Chemistry</i> , 2008, 138, 23-28.	1.5	17
157	Effect of a Synthesized Amyl-Glycine1, 10-Phenanthroline Platinum Nitrate on Structure and Stability of Human Blood Carrier Protein, Albumin: Spectroscopic and Modeling Approaches. <i>Journal of Fluorescence</i> , 2017, 27, 1829-1838.	1.3	17
158	Investigating architecture and structure-function relationships in cold shock DNA-binding domain family using structural genomics-based approach. <i>International Journal of Biological Macromolecules</i> , 2019, 133, 484-494.	3.6	17
159	Structural and functional impact of non-synonymous SNPs in the CST complex subunit TEN1: structural genomics approach. <i>Bioscience Reports</i> , 2019, 39, .	1.1	17
160	Two-state irreversible thermal denaturation of <i>Euphorbia characias</i> latex amine oxidase. <i>Biophysical Chemistry</i> , 2007, 125, 254-259.	1.5	16
161	Heterogeneity of Equilibrium Molten Globule State of Cytochrome c Induced by Weak Salt Denaturants under Physiological Condition. <i>PLoS ONE</i> , 2015, 10, e0120465.	1.1	16
162	Identification of functional candidates amongst hypothetical proteins of <i>Mycobacterium leprae</i> Br4923, a causative agent of leprosy. <i>Genome</i> , 2015, 58, 25-42.	0.9	16

#	ARTICLE	IF	CITATIONS
163	GdnHCl-induced unfolding intermediate in the mitochondrial carbonic anhydrase VA. <i>International Journal of Biological Macromolecules</i> , 2016, 91, 1151-1160.	3.6	16
164	Human microtubule affinity-regulating kinase 4 is stable at extremes of pH. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 1241-1251.	2.0	16
165	Evaluation of human microtubule affinity-regulating kinase 4 inhibitors: fluorescence binding studies, enzyme, and cell assays. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 3194-3203.	2.0	16
166	Effect of pH on the structure and function of pyruvate dehydrogenase kinase 3: Combined spectroscopic and MD simulation studies. <i>International Journal of Biological Macromolecules</i> , 2020, 147, 768-777.	3.6	16
167	Functional Role of Glutamine 28 and Arginine 39 in Double Stranded RNA Cleavage by Human Pancreatic Ribonuclease. <i>PLoS ONE</i> , 2011, 6, e17159.	1.1	16
168	Thermodynamics of solvation of proteins in guanidine hydrochloride. <i>Biopolymers</i> , 1990, 29, 1593-1598.	1.2	15
169	A new method for determining the constant-pressure heat capacity change associated with the protein denaturation induced by guanidinium chloride (or urea). <i>Biophysical Chemistry</i> , 2008, 133, 81-89.	1.5	15
170	Structure-based functional annotation of putative conserved proteins having lyase activity from <i>Haemophilus influenzae</i> . <i>3 Biotech</i> , 2015, 5, 317-336.	1.1	15
171	Structural and thermodynamic characterisation of L94F mutant of horse cytochrome c. <i>International Journal of Biological Macromolecules</i> , 2016, 92, 202-212.	3.6	15
172	Fabrication of a p <sup>n</sup> Heterojunction Using Topological Insulator Bi <sub>2</sub> Te <sub>3</sub> Si and Its Annealing Response. <i>Journal of Electronic Materials</i> , 2018, 47, 6972-6983.	1.0	15
173	Unravelling the unfolding mechanism of human integrin linked kinase by GdmCl-induced denaturation. <i>International Journal of Biological Macromolecules</i> , 2018, 117, 1252-1263.	3.6	15
174	Structural Characterization, Homology Modeling and Docking Studies of ARG674 Mutation in MyH8 Gene Associated with Trismus-Pseudocamptodactyly Syndrome. <i>Letters in Drug Design and Discovery</i> , 2014, 11, 1177-1187.	0.4	15
175	A C-terminal Hydrophobic Region is Required for Homo-Oligomerization of the Hepatitis E Virus Capsid (ORF2) Protein. <i>Journal of Biomedicine and Biotechnology</i> , 2001, 1, 122-128.	3.0	14
176	Structure-function studies of <i>Murraya koenigii</i> trypsin inhibitor revealed a stable core beta sheet structure surrounded by $\alpha$ -helices with a possible role for $\alpha$ -helix in inhibitory function. <i>International Journal of Biological Macromolecules</i> , 2007, 41, 410-414.	3.6	14
177	Inhibitory Effects of $\beta$ -Cyclodextrin and Trehalose on Nanofibril and AGE Formation During Glycation of Human Serum Albumin. <i>Protein and Peptide Letters</i> , 2009, 16, 653-659.	0.4	14
178	Structure-based function analysis of putative conserved proteins with isomerase activity from <i>Haemophilus influenzae</i> . <i>3 Biotech</i> , 2015, 5, 741-763.	1.1	14
179	Domain unfolding and the stability of thermolysin in guanidine hydrochloride. <i>Biochemistry and Cell Biology</i> , 1986, 64, 953-961.	0.9	13
180	Effect of salts and sodium dodecyl sulfate on chaperone activity of camel $\alpha$ S1-CN: Insulin as the target protein. <i>Colloids and Surfaces B: Biointerfaces</i> , 2009, 71, 300-305.	2.5	13

#	ARTICLE	IF	CITATIONS
181	Boron stabilizes peroxide mediated changes in the structure of heme proteins. International Journal of Biological Macromolecules, 2010, 47, 109-115.	3.6	13
182	Cloning, expression, purification and characterization of human mitochondrial carbonic anhydrase VA. 3 Biotech, 2016, 6, 16.	1.1	13
183	Effect of dextran on the thermodynamic stability and structure of ribonuclease A. Journal of the Iranian Chemical Society, 2016, 13, 181-189.	1.2	13
184	Estimation of pH effect on the structure and stability of kinase domain of human integrin-linked kinase. Journal of Biomolecular Structure and Dynamics, 2019, 37, 156-165.	2.0	13
185	Effect of Doping and Annealing on Thermoelectric Properties of Bismuth Telluride Thin Films. Journal of Electronic Materials, 2020, 49, 4195-4202.	1.0	13
186	Multispectroscopic and Molecular Docking Insight into Elucidating the Interaction of Irisin with Rivastigmine Tartrate: A Combinational Therapy Approach to Fight Alzheimer's Disease. ACS Omega, 2021, 6, 7910-7921.	1.6	13
187	Identification of Interfacial Residues Involved in Hecpidin-Ferroportin Interaction. Letters in Drug Design and Discovery, 2014, 11, 363-374.	0.4	13
188	Effect of Oligosaccharides and their Monosaccharide Mixtures on the Stability of Proteins: A Scaled Particle Study. Journal of Biomolecular Structure and Dynamics, 2010, 28, 331-341.	2.0	12
189	Folding and stability studies on C-PE and its natural N-terminal truncant. Archives of Biochemistry and Biophysics, 2014, 545, 9-21.	1.4	12
190	Purification and structural characterization of Mce4A from Mycobacterium tuberculosis. International Journal of Biological Macromolecules, 2016, 93, 235-241.	3.6	12
191	Probing pH sensitivity of $\hat{\pm}$ C-phycoerythrin and its natural truncant: A comparative study. International Journal of Biological Macromolecules, 2016, 86, 18-27.	3.6	12
192	Denatured states of yeast cytochrome <i>c</i> induced by heat and guanidinium chloride are structurally and thermodynamically different. Journal of Biomolecular Structure and Dynamics, 2017, 35, 1420-1435.	2.0	12
193	Structural insights into Rab21 GTPase activation mechanism by molecular dynamics simulations. Molecular Simulation, 2018, 44, 179-189.	0.9	12
194	Investigation of guanidinium chloride-induced unfolding pathway of sphingosine kinase 1. International Journal of Biological Macromolecules, 2020, 147, 177-186.	3.6	12
195	Structural Refolding and Thermal Stability of Myoglobin in the Presence of Mixture of Crowders: Importance of Various Interactions for Protein Stabilization in Crowded Conditions. Molecules, 2021, 26, 2807.	1.7	12
196	Biochemical Characterization of Hemoglobins from Caspian Sea Sturgeons ( <i>Acipenser persicus</i> and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.9	11
197	Heme-iron ligand (M80-Fe) in cytochrome c is destabilizing: combined <i>in vitro</i> and <i>in silico</i> approaches to monitor changes in structure, stability and dynamics of the protein on mutation. Journal of Biomolecular Structure and Dynamics, 2020, , 1-18.	2.0	11
198	Conformational changes in cytochrome c directed by ethylene glycol accompanying complex formation: Protein-solvent preferential interaction or/and kosmotropic effect. Spectrochimica Acta - Part A: Molecular and Biomolecular Spectroscopy, 2020, 242, 118788.	2.0	11

#	ARTICLE	IF	CITATIONS
199	Trehalose Restrains the Fibril Load towards $\alpha$ -Lactalbumin Aggregation and Halts Fibrillation in a Concentration-Dependent Manner. <i>Biomolecules</i> , 2021, 11, 414.	1.8	11
200	Dual-quadrant photodetection in topological insulator and silicon-based heterojunction (n-Bi <sub>2</sub> Te <sub>2</sub> Se/p-Si). <i>Applied Surface Science</i> , 2021, 565, 150497.	3.1	11
201	Effect of pH on the structure and stability of irisin, a multifunctional protein: Multispectroscopic and molecular dynamics simulation approach. <i>Journal of Molecular Structure</i> , 2022, 1252, 132141.	1.8	11
202	Charge transfer induced symmetry breaking in GaN/Bi <sub>2</sub> Se <sub>3</sub> topological heterostructure device. <i>Npj 2D Materials and Applications</i> , 2022, 6, .	3.9	11
203	Inorganic salt denaturants stabilize ribonuclease against denaturation by urea. <i>Canadian Journal of Biochemistry</i> , 1978, 56, 1003-1005.	1.4	10
204	Effects of temperature and chromium (III) ion on the structure of bovine b-Lactoglobulin-A. <i>Journal of the Brazilian Chemical Society</i> , 2009, 20, .	0.6	10
205	Characterization of a Neutral and Thermostable Glucoamylase from the Thermophilic Mold <i>Thermomucor indicae-seudaticae</i> : Activity, Stability, and Structural Correlation. <i>Applied Biochemistry and Biotechnology</i> , 2010, 160, 879-890.	1.4	10
206	Purification and characterization of Ras related protein, Rab5a from <i>Tinospora cordifolia</i> . <i>International Journal of Biological Macromolecules</i> , 2016, 82, 471-479.	3.6	10
207	Counteraction of the deleterious effects of urea on structure and stability of mammalian kidney proteins by osmolytes. <i>International Journal of Biological Macromolecules</i> , 2018, 107, 1659-1667.	3.6	10
208	Reversible and site-specific immobilization of $\beta$ 2-adrenergic receptor by aptamer-directed method for receptor-drug interaction analysis. <i>Journal of Chromatography A</i> , 2020, 1622, 461091.	1.8	10
209	Physico-chemical characterization of products of unfolding of cytochrome c by calcium chloride. <i>BBA - Proteins and Proteomics</i> , 1994, 1207, 223-230.	2.1	9
210	Effects of salts of alkali earth metals and calcium chloride on the stability of cytochrome c and myoglobin. <i>BBA - Proteins and Proteomics</i> , 1996, 1294, 63-71.	2.1	9
211	INTRINSIC VISCOSITY OF OVOMUCOID IN RANDOM COIL CONFORMATION. <i>International Journal of Peptide and Protein Research</i> , 2009, 7, 417-421.	0.1	9
212	Enhancement of thermal reversibility and stability of human carbonic anhydrase II by mesoporous nanoparticles. <i>International Journal of Biological Macromolecules</i> , 2015, 75, 67-72.	3.6	9
213	Rationalizing the Role of Monosodium Glutamate in the Protein Aggregation Through Biophysical Approaches: Potential Impact on Neurodegeneration. <i>Frontiers in Neuroscience</i> , 2021, 15, 636454.	1.4	9
214	Characterization of different intermediate states in myoglobin induced by polyethylene glycol: A process of spontaneous molecular self-organization foresees the energy landscape theory via in vitro and in silico approaches. <i>Journal of Molecular Liquids</i> , 2021, 342, 117502.	2.3	9
215	Effect of Different Metallic Contacts on the Device Performance of a p-n Heterostructure of a Topological Insulator and Silicon (p-Bi <sub>2</sub> Te <sub>3</sub> /n-Si). <i>IEEE Transactions on Electron Devices</i> , 2020, 67, 5388-5395.	1.6	9
216	Role of unique basic residues of human pancreatic ribonuclease in its catalysis and structural stability. <i>Biochemical and Biophysical Research Communications</i> , 2007, 360, 809-814.	1.0	8

#	ARTICLE	IF	CITATIONS
217	Why is Glycine not a Part of the Osmoticum in the Urea-rich Cells?. Protein and Peptide Letters, 2013, 20, 61-70.	0.4	8
218	Effect of mammalian kidney osmolytes on the folding pathway of sheep serum albumin. International Journal of Biological Macromolecules, 2017, 97, 625-634.	3.6	8
219	Effect of conservative mutations (L94V and L94I) on the structure and stability of horse cytochrome c. Archives of Biochemistry and Biophysics, 2017, 633, 40-49.	1.4	8
220	Exploring Missense Mutations in Tyrosine Kinases Implicated with Neurodegeneration. Molecular Neurobiology, 2017, 54, 5085-5106.	1.9	8
221	Counteraction of the deleterious effects of reactive oxygen species on hemoglobin structure and function by ellagic acid. Journal of Luminescence, 2017, 182, 1-7.	1.5	8
222	Functional Insight into Putative Conserved Proteins of Rickettsia rickettsii and their Virulence Characterization. Current Proteomics, 2015, 12, 101-116.	0.1	8
223	Structural Studies on DNA Triple Helix Formed by Intronic GAA Triplet Repeat Expansion in Friedreich's Ataxia. Nucleosides, Nucleotides and Nucleic Acids, 2003, 22, 1517-1519.	0.4	7
224	Data on the role of accessible surface area on osmolytes-induced protein stabilization. Data in Brief, 2017, 10, 47-56.	0.5	7
225	Biophysical Insights into Implications of PEG-400 on the $\hat{\text{I}}_{\pm}$ -Crystallin Structure: Multispectroscopic and Microscopic Approach. ACS Omega, 2020, 5, 19210-19216.	1.6	7
226	Stability of acetylcholinesterase in guanidine hydrochloride solution. Canadian Journal of Biochemistry, 1981, 59, 551-555.	1.4	6
227	Salt Potentiates Methylamine Counteraction System to Offset the Deleterious Effects of Urea on Protein Stability and Function. PLoS ONE, 2015, 10, e0119597.	1.1	6
228	Purification and characterization of oligonucleotide binding (OB)-fold protein from medicinal plant Tinospora cordifolia. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2016, 1008, 38-44.	1.2	6
229	Fas-activated serine/threonine kinase: Structure and function. Gene Reports, 2017, 8, 117-127.	0.4	6
230	Unfoldness of the denatured state of proteins determines urea: Methylamine counteraction in terms of Gibbs free energy of stabilization. International Journal of Biological Macromolecules, 2019, 132, 666-676.	3.6	6
231	Concentration dependent effect of ethylene glycol on the structure and stability of holo $\hat{\text{I}}_{\pm}$ -lactalbumin: Characterization of intermediate state amidst soft interactions. International Journal of Biological Macromolecules, 2020, 164, 2151-2161.	3.6	6
232	Structure, function and therapeutic implications of OB-fold proteins: A lesson from past to present. Briefings in Functional Genomics, 2020, 19, 377-389.	1.3	6
233	Anomalous magnetic properties in $\text{LaFe}_{11.5}\text{Al}_{1.5}$ . Physical Chemistry Chemical Physics, 2020, 22, 3425-3433.	1.3	6
234	Targeting metacaspase-3 from <i>Plasmodium falciparum</i> towards antimalarial therapy: A combined approach of <i>in-silico</i> and <i>in-vitro</i> investigation. Journal of Biomolecular Structure and Dynamics, 2021, 39, 421-430.	2.0	6

#	ARTICLE	IF	CITATIONS
235	Crowding Milleu stabilizes apo-myoglobin against chemical-induced denaturation: Dominance of hardcore repulsions in the heme devoid protein. <i>International Journal of Biological Macromolecules</i> , 2021, 181, 552-560.	3.6	6
236	Characterization of a stable intermediate in the unfolding of diazoacetylglycine ethyl ester?pepsin by urea. <i>Canadian Journal of Biochemistry</i> , 1979, 57, 1090-1092.	1.4	5
237	Purification and Characterization of Calreticulin: a Ca <sup>2+</sup> -Binding Chaperone from Sheep Kidney. <i>Applied Biochemistry and Biotechnology</i> , 2014, 174, 1771-1783.	1.4	5
238	Biophysical characterization of G protein ectodomain of group B human respiratory syncytial virus from <i>E. coli</i> . <i>Preparative Biochemistry and Biotechnology</i> , 2016, 46, 483-488.	1.0	5
239	Material Study of Co <sub>2</sub> CrAl Heusler Alloy Magnetic Thin Film and Co <sub>2</sub> CrAl/n-Si Schottky Junction Device. <i>Journal of Electronic Materials</i> , 2020, 49, 3652-3658.	1.0	5
240	Alanine Counteracts the Destabilizing Effect that Urea has on RNase-A. <i>Protein and Peptide Letters</i> , 2016, 23, 795-799.	0.4	5
241	Spectrophotometric titration of phenolic groups of pepsin. <i>Biochimica Et Biophysica Acta (BBA) - Protein Structure</i> , 1978, 537, 247-254.	1.7	4
242	Intrinsic viscosities of randomly coiled glycoproteins. <i>International Journal of Biochemistry &amp; Cell Biology</i> , 1978, 9, 647-651.	0.8	4
243	Functional annotation of putative conserved proteins from <i>Borrelia burgdorferi</i> to find potential drug targets. <i>International Journal of Computational Biology and Drug Design</i> , 2016, 9, 295.	0.3	4
244	A comparative study of structure, stability and function of sc-tenecteplase in the presence of stabilizing osmolytes. <i>Journal of Biotechnology</i> , 2018, 280, 1-10.	1.9	4
245	Stabilizing osmolytes' effects on the structure, stability and function of tc-tenecteplase: A one peptide bond digested form of tenecteplase. <i>International Journal of Biological Macromolecules</i> , 2019, 130, 863-877.	3.6	4
246	Protein stability: Determination of structure and stability of the transmembrane protein Mce4A from <i>M. tuberculosis</i> in membrane-like environment. <i>International Journal of Biological Macromolecules</i> , 2019, 126, 488-495.	3.6	4
247	Purification, modeling and structural insights of calmodulin-binding receptor like cytoplasmic kinase 2 from <i>Oroxylum Indicum</i> . <i>International Journal of Biological Macromolecules</i> , 2019, 123, 704-712.	3.6	4
248	Characterization of heterogeneous intermediate ensembles on the guanidinium chloride-induced unfolding pathway of Î <sup>2</sup> -lactoglobulin. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 1042-1053.	2.0	4
249	Effects of natural mutations (L94I and L94V) on the stability and mechanism of folding of horse cytochrome c: A combined in vitro and molecular dynamics simulations approach. <i>International Journal of Biological Macromolecules</i> , 2020, 159, 976-985.	3.6	4
250	Despite an Extensive Sequence Analysis Identification of Functional Candidates Amongst Hypothetical Proteins of <i>Neisseria gonorrhoeae</i> . <i>Letters in Drug Design and Discovery</i> , 2016, 13, 451-464.	0.4	4
251	Thermal Dissection of Lentil Seedling Amine Oxidase Domains by Differential Scanning Calorimetry. <i>Bioscience, Biotechnology and Biochemistry</i> , 2007, 71, 1644-1649.	0.6	3
252	Purification and characterization of RGA2, a Rho2 GTPase-activating protein from <i>Tinospora cordifolia</i> . <i>3 Biotech</i> , 2016, 6, 85.	1.1	3

#	ARTICLE	IF	CITATIONS
253	Human Disease Insight: An integrated knowledge-based platform for disease-gene-drug information. <i>Journal of Infection and Public Health</i> , 2016, 9, 331-338.	1.9	3
254	Classification and Functional Analyses of Putative Conserved Proteins from <i>Chlamydomonas reinhardtii</i> CWL029. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2017, 9, 96-106.	2.2	3
255	Purification, preliminary X-ray crystallography and biophysical studies of triose phosphate isomerase- $\beta$ -globin subunit complex. <i>International Journal of Biological Macromolecules</i> , 2017, 94, 746-753.	3.6	3
256	$\beta$ -Cyclodextrin-Modified Magnetic Nanoparticles Immobilized on Sepharose Surface Provide an Effective Matrix for Protein Refolding. <i>Journal of Physical Chemistry B</i> , 2018, 122, 9907-9919.	1.2	3
257	Urea Stress: Myo-inositol's efficacy to counteract destabilization of TIM- $\beta$ -globin complex by urea is as good as that of the methylamine. <i>International Journal of Biological Macromolecules</i> , 2020, 151, 1108-1115.	3.6	3
258	Behavioral profiling: a generationwide study of players' experiences during brain games play. <i>Interactive Learning Environments</i> , 2023, 31, 1265-1278.	4.4	3
259	Stability of uniformly labeled ( $^{13}\text{C}$ and $^{15}\text{N}$ ) cytochrome c and its L94G mutant. <i>Scientific Reports</i> , 2021, 11, 6804.	1.6	3
260	Human seminal proteinase and prostate-specific antigen are the same protein. <i>Journal of Biosciences</i> , 2008, 33, 195-207.	0.5	2
261	Boron increases the transition temperature and enhances thermal stability of heme proteins. <i>Journal of Thermal Analysis and Calorimetry</i> , 2011, 104, 339-342.	2.0	2
262	A Systems View of the Genome Guardians: Mapping the Signaling Circuitry Underlying Oligonucleotide/Oligosaccharide-Binding Fold Proteins. <i>OMICS A Journal of Integrative Biology</i> , 2020, 24, 518-530.	1.0	2
263	Electrical properties of a metal-germanium-topological insulator ( $n\text{-Ge}/p\text{-Bi}_2\text{Te}_3$ ) heterostructure devices. <i>Journal of Materials Science: Materials in Electronics</i> , 2021, 32, 8106-8121.	1.1	2
264	Nanosilver-DNA Hybrid Modified Electrode for Electrochemical Sensing of Buspirone in Biological Samples and Pharmaceutical Preparation. <i>Sensor Letters</i> , 2012, 10, 814-820.	0.4	2
265	PEG mediated destabilization of holo $\alpha$ -lactalbumin probed by <i>in silico</i> and <i>in vitro</i> studies: deviation from excluded volume effect. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 13265-13277.	2.0	2
266	The pH dependence of the reversible unfolding of ovalbumin A1 by guanidine hydrochloride. <i>Biochimica Et Biophysica Acta (BBA) - Protein Structure</i> , 1979, 576, 333-338.	1.7	1
267	The Correlation of Cold Denaturation Temperature with Surface Stability Factor of Proteins. <i>Protein Journal</i> , 2007, 26, 395-402.	0.7	1
268	Fluorescent Dye Conjugates of Rabbit Arylsulfatase A as a Biological Tracer for Protein Endocytosis. <i>Applied Biochemistry and Biotechnology</i> , 2013, 170, 972-979.	1.4	1
269	97. <i>Cytokine</i> , 2014, 70, 51.	1.4	1
270	Backbone and side chain $^1\text{H}$ , $^{15}\text{N}$ and $^{13}\text{C}$ chemical shift assignments of the molten globule state of L94G mutant of horse cytochrome-c. <i>Biomolecular NMR Assignments</i> , 2020, 14, 37-44.	0.4	1



#	ARTICLE	IF	CITATIONS
271	Unravelling the unfolding pathway of human Fas-activated serine/threonine kinase induced by urea. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 5516-5525.	2.0	1
272	Dodecamer d-AGATCTAGATCT and a Homologous Hairpin form Triplex in the Presence of Peptide REWER. <i>PLoS ONE</i> , 2013, 8, e65010.	1.1	1
273	Anomalous Magnetoresistance In Topological Insulator Bi <sub>2</sub> Te <sub>3</sub> . <i>Advanced Materials Proceedings</i> , 2016, 1, 21-24.	0.2	1
274	Transient reflection spectra in topological nanocrystals of Bi <sub>2</sub> Se <sub>3</sub> , Bi <sub>2</sub> Te <sub>3</sub> , Bi <sub>2</sub> Te <sub>2</sub> Se. <i>Advanced Materials Letters</i> , 2017, 8, 423-427.	0.3	1
275	Delineating the Aggregation-Prone Hotspot Regions (Peptides) in the Human Cu/Zn Superoxide Dismutase 1. <i>ACS Omega</i> , 2021, 6, 33985-33994.	1.6	1
276	Molecular basis of pathogenic parasitic infections insights from parasite kinome. <i>Frontiers in Bioscience - Landmark</i> , 2020, 25, 1488-1509.	3.0	0