

Asimul Islam

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

207
papers

3,551
citations

31
h-index

45
g-index

217
ext. papers

4,647
ext. citations

4.9
avg, IF

5.95
L-index

#	Paper	IF	Citations
207	Application of circular dichroism spectroscopy in studying protein folding, stability, and interaction 2022 , 213-224		0
206	Natural products can be used in therapeutic management of COVID-19: Probable mechanistic insights.. <i>Biomedicine and Pharmacotherapy</i> , 2022 , 147, 112658	7.5	7
205	Effect of pH on the structure and function of cyclin-dependent kinase 6.. <i>PLoS ONE</i> , 2022 , 17, e0263693	3.7	0
204	FNDC5/Irisin: Physiology and Pathophysiology.. <i>Molecules</i> , 2022 , 27,	4.8	3
203	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	3.4	2
202	Targeting pyruvate kinase M2 signaling for development of effective cancer therapy 2022 , 199-222		
201	Interaction of fungal lipase with potential phytotherapeutics. <i>PLoS ONE</i> , 2022 , 17, e0264460	3.7	
200	Unraveling the Binding Mechanism of Alzheimer's Drugs with Irisin: Spectroscopic, Calorimetric, and Computational Approaches. <i>International Journal of Molecular Sciences</i> , 2022 , 23, 5965	6.3	1
199	Investigating single amino acid substitutions in PIM1 kinase: A structural genomics approach. <i>PLoS ONE</i> , 2021 , 16, e0258929	3.7	5
198	PEG mediated destabilization of holo lactalbumin probed by and studies: deviation from excluded volume effect. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 1-13	3.6	0
197	Therapeutic Potential of Ursolic Acid in Cancer and Diabetic Neuropathy Diseases. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	10
196	Myricetin inhibits breast and lung cancer cells proliferation via inhibiting MARK4. <i>Journal of Cellular Biochemistry</i> , 2021 ,	4.7	4
195	Delineating the Aggregation-Prone Hotspot Regions (Peptides) in the Human Cu/Zn Superoxide Dismutase 1.. <i>ACS Omega</i> , 2021 , 6, 33985-33994	3.9	
194	An Insight Into Mitochondrial Dysfunction and its Implications in Neurological Diseases. <i>Current Drug Targets</i> , 2021 , 22, 1585-1595	3	1
193	MAP/Microtubule Affinity Regulating Kinase 4 Inhibitory Potential of Irisin: A New Therapeutic Strategy to Combat Cancer and Alzheimer's Disease. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	7
192	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	3.6	0
191	Multispectroscopic and Molecular Docking Insight into Elucidating the Interaction of Irisin with Rivastigmine Tartrate: A Combinational Therapy Approach to Fight Alzheimer's Disease. <i>ACS Omega</i> , 2021 , 6, 7910-7921	3.9	4

190	A computational study on active constituents of and as inhibitors of SARS-CoV-2 main protease. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 1-12	3.6	1
189	Elucidating the Interaction of Human Ferritin with Quercetin and Naringenin: Implication of Natural Products in Neurodegenerative Diseases: Molecular Docking and Dynamics Simulation Insight. <i>ACS Omega</i> , 2021 , 6, 7922-7930	3.9	20
188	Interaction of polyethylene glycol with cytochrome c investigated via in vitro and in silico approaches. <i>Scientific Reports</i> , 2021 , 11, 6475	4.9	6
187	Stability of uniformly labeled (C and N) cytochrome c and its L94G mutant. <i>Scientific Reports</i> , 2021 , 11, 6804	4.9	0
186	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	5.1	3
185	Structural Characterization and Binding Studies of the Ectodomain G Protein of Respiratory Syncytial Virus Reveal the Crucial Role of pH with Possible Implications in Host-Pathogen Interactions. <i>ACS Omega</i> , 2021 , 6, 10403-10414	3.9	0
184	Glossary of phytoconstituents: Can these be repurposed against SARS CoV-2? A quick in silico screening of various phytoconstituents from plant <i>Glycyrrhiza glabra</i> with SARS CoV-2 main protease. <i>Food and Chemical Toxicology</i> , 2021 , 150, 112057	4.7	8
183	Potential drug targets of SARS-CoV-2: From genomics to therapeutics. <i>International Journal of Biological Macromolecules</i> , 2021 , 177, 1-9	7.9	34
182	Targeting the Sphingosine Kinase/Sphingosine-1-Phosphate Signaling Axis in Drug Discovery for Cancer Therapy. <i>Cancers</i> , 2021 , 13,	6.6	11
181	Structural Refolding and Thermal Stability of Myoglobin in the Presence of Mixture of Crowders: Importance of Various Interactions for Protein Stabilization in Crowded Conditions. <i>Molecules</i> , 2021 , 26,	4.8	2
180	Structural genomics approach to investigate deleterious impact of nsSNPs in conserved telomere maintenance component 1. <i>Scientific Reports</i> , 2021 , 11, 10202	4.9	12
179	Aurora B kinase: a potential drug target for cancer therapy. <i>Journal of Cancer Research and Clinical Oncology</i> , 2021 , 147, 2187-2198	4.9	4
178	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	7.9	0
177	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	4.7	10
176	Parkinson's disease: A current perspectives on Parkinson's disease and key bioactive natural compounds as future potential drug candidates. <i>Current Drug Targets</i> , 2021 ,	3	2
175	Phytochemicals targeting NF-B signaling: Potential anti-cancer interventions. <i>Journal of Pharmaceutical Analysis</i> , 2021 ,	14	3
174	Mechanistic insight into the binding of graphene oxide with human serum albumin: Multispectroscopic and molecular docking approach. <i>Spectrochimica Acta - Part A: Molecular and Biomolecular Spectroscopy</i> , 2021 , 256, 119750	4.4	10
173	Targeting metacaspase-3 from towards antimalarial therapy: A combined approach of and investigation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 39, 421-430	3.6	4

172	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	3.6	13
171	Identification of high-affinity inhibitors of pyruvate dehydrogenase kinase-3: towards therapeutic management of cancer. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 39, 586-594	3.6	15
170	Biological Implications of Polyethylene Glycol and PEGylation: Therapeutic Approaches Based on Biophysical Studies and Protein Structure-Based Drug Design Tools 2021 , 273-294		2
169	Heparin Accelerates the Protein Aggregation via the Downhill Polymerization Mechanism: Multi-Spectroscopic Studies to Delineate the Implications on Proteinopathies. <i>ACS Omega</i> , 2021 , 6, 23282-23397		7
168	Effect of Antioxidants on Heavy Metals Induced Conformational Alteration of Cytochrome C and Myoglobin. <i>Protein and Peptide Letters</i> , 2021 , 28, 31-42	1.9	0
167	Investigation of sphingosine kinase 1 inhibitory potential of cinchonine and colcemid targeting anticancer therapy. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 1-13	3.6	4
166	Trehalose Restrains the Fibril Load towards β -Lactalbumin Aggregation and Halts Fibrillation in a Concentration-Dependent Manner. <i>Biomolecules</i> , 2021 , 11,	5.9	2
165	Impact of single amino acid substitution on the structure and function of TANK-binding kinase-1. <i>Journal of Cellular Biochemistry</i> , 2021 , 122, 1475-1490	4.7	5
164	Targeting pyruvate dehydrogenase kinase signaling in the development of effective cancer therapy. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2021 , 1876, 188568	11.2	13
163	Exploring the molecular interactions of Galantamine with human Transferrin: In-silico and in vitro insight. <i>Journal of Molecular Liquids</i> , 2021 , 335, 116227	6	2
162	Probing the interaction of memantine, an important Alzheimer's drug, with human serum albumin: In silico and in vitro approach. <i>Journal of Molecular Liquids</i> , 2021 , 340, 116888	6	8
161	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	6	0
160	Spectroscopic, calorimetric and in silico insight into the molecular interactions of Memantine with human transferrin: Implications of Alzheimer's drugs. <i>International Journal of Biological Macromolecules</i> , 2021 , 190, 660-666	7.9	2
159	The Pathogenesis and Complications Associated with Autism Spectrum Disorder and Alzheimer's Disease: A Comparative Study 2021 , 43-61		
158	Therapeutic Potential of Polyphenols in Alzheimer's Therapy: Broad-Spectrum and Minimal Side Effects as Key Aspects 2021 , 111-133		0
157	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> , 2020 , 1-11	3.6	6
156	Biophysical Elucidation of Fibrillation Inhibition by Sugar Osmolytes in β -Lactalbumin: Multispectroscopic and Molecular Docking Approaches. <i>ACS Omega</i> , 2020 , 5, 26871-26882	3.9	5
155	Ellagic Acid Controls Cell Proliferation and Induces Apoptosis in Breast Cancer Cells via Inhibition of Cyclin-Dependent Kinase 6. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	36

154	Structure, function and therapeutic implications of OB-fold proteins: A lesson from past to present. <i>Briefings in Functional Genomics</i> , 2020 , 19, 377-389	4.9	2
153	Effects of Ethylene Glycol on the Structure and Stability of Myoglobin Using Spectroscopic, Interaction, and Approaches: Monomer Is Different from Those of Its Polymers. <i>ACS Omega</i> , 2020 , 5, 13840-13850	3.9	11
152	Corona virus versus existence of human on the earth: A computational and biophysical approach. <i>International Journal of Biological Macromolecules</i> , 2020 , 161, 271-281	7.9	20
151	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	7.9	17
150	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,	5.9	11
149	Rosmarinic Acid Exhibits Anticancer Effects via MARK4 Inhibition. <i>Scientific Reports</i> , 2020 , 10, 10300	4.9	51
148	Discovery of 4-(2-(dimethylamino)ethoxy)benzohydrazide derivatives as prospective microtubule affinity regulating kinase 4 inhibitors.. <i>RSC Advances</i> , 2020 , 10, 20129-20137	3.7	9
147	Structural Features of Nucleoprotein CST/Shelterin Complex Involved in the Telomere Maintenance and Its Association with Disease Mutations. <i>Cells</i> , 2020 , 9,	7.9	15
146	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,	4.8	42
145	The anti-oxidant enzyme, Prdx6 might have cis-acting regulatory sequence(s). <i>International Journal of Biological Macromolecules</i> , 2020 , 149, 1139-1150	7.9	1
144	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	7.9	10
143	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	7.9	16
142	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	7.9	30
141	MARK4 Inhibited by AChE Inhibitors, Donepezil and Rivastigmine Tartrate: Insights into Alzheimer's Disease Therapy. <i>Biomolecules</i> , 2020 , 10,	5.9	34
140	Molecular basis of pathogenic parasitic infections: insights from parasite kinome. <i>Frontiers in Bioscience - Landmark</i> , 2020 , 25, 1488-1509	2.8	
139	Management of Insulin Through Co-Solute Engineering: A Therapeutic Approach 2020 , 283-315		1
138	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	7.9	1
137	Glecaprevir and Maraviroc are high-affinity inhibitors of SARS-CoV-2 main protease: possible implication in COVID-19 therapy. <i>Bioscience Reports</i> , 2020 , 40,	4.1	90

136	Backbone and side chain H, N and 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	0.7	1
135	Investigation of guanidinium chloride-induced unfolding pathway of sphingosine kinase 1. <i>International Journal of Biological Macromolecules</i> , 2020 , 147, 177-186	7.9	8
134	Amphiphilic nature of polyethylene glycols and their role in medical research. <i>Polymer Testing</i> , 2020 , 82, 106316	4.5	20
133	Urea Stress: Myo-inositol's efficacy to counteract destabilization of TIM- β -globin complex by urea is as good as that of the methylamine. <i>International Journal of Biological Macromolecules</i> , 2020 , 151, 1108-1115	7.9	2
132	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	7.9	9
131	Inhibiting CDK6 Activity by Quercetin Is an Attractive Strategy for Cancer Therapy. <i>ACS Omega</i> , 2020 , 5, 27480-27491	3.9	22
130	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, 1245875	6.7	10
129	Heme-iron ligand (M80-Fe) in cytochrome is destabilizing: combined and approaches to monitor changes in structure, stability and dynamics of the protein on mutation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020 , 1-18	3.6	9
128	Conformational changes in cytochrome c directed by ethylene glycol accompanying complex formation: Protein-solvent preferential interaction or/and kosmotropic effect. <i>Spectrochimica Acta - Part A: Molecular and Biomolecular Spectroscopy</i> , 2020 , 242, 118788	4.4	5
127	Concentration dependent effect of ethylene glycol on the structure and stability of holo β actalbumin: Characterization of intermediate state amidst soft interactions. <i>International Journal of Biological Macromolecules</i> , 2020 , 164, 2151-2161	7.9	3
126	Identification of high-affinity inhibitors of SARS-CoV-2 main protease: Towards the development of effective COVID-19 therapy. <i>Virus Research</i> , 2020 , 288, 198102	6.4	43
125	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	3.8	2
124	Optimization of parameters for expression and purification of G glycoprotein ectodomain of respiratory syncytial virus. <i>Future Virology</i> , 2020 , 15, 225-235	2.4	0
123	Identification of Potential Inhibitors of Calcium/Calmodulin-Dependent Protein Kinase IV from Bioactive Phytoconstituents. <i>Oxidative Medicine and Cellular Longevity</i> , 2020 , 2020, 2094635	6.7	19
122	Biophysical Insights into Implications of PEG-400 on the β Crystallin Structure: Multispectroscopic and Microscopic Approach. <i>ACS Omega</i> , 2020 , 5, 19210-19216	3.9	6
121	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	3.6	22
120	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	3.6	36
119	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	3.6	13

118	Evaluation of pyrazolopyrimidine derivatives as microtubule affinity regulating kinase 4 inhibitors: Towards therapeutic management of Alzheimer's disease. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020 , 38, 3892-3907	3.6	17
117	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,	5.9	24
116	Carbohydrate-Based Macromolecular Crowding-Induced Stabilization of Proteins: Towards Understanding the Significance of the Size of the Crowder. <i>Biomolecules</i> , 2019 , 9,	5.9	15
115	Structural Analysis and Conformational Dynamics of Gene Mutations Involved in Coat Plus Syndrome. <i>Frontiers in Molecular Biosciences</i> , 2019 , 6, 41	5.6	31
114	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, 1076-1083	7.9	49
113	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	7.9	11
112	Unfoldness of the denatured state of proteins determines urea: Methylamine counteraction in terms of Gibbs free energy of stabilization. <i>International Journal of Biological Macromolecules</i> , 2019 , 132, 666-676	7.9	6
111	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	3.2	15
110	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	3.6	46
109	Exploration of Fungal Lipase as Direct Target of Eugenol through Spectroscopic Techniques. <i>Protein and Peptide Letters</i> , 2019 , 26, 919-929	1.9	1
108	Ionic Liquid Green Assembly-Mediated Migration of Piperine from Calf-Thymus DNA: A New Possibility of the Tunable Drug Delivery System. <i>ACS Omega</i> , 2019 , 4, 21005-21017	3.9	6
107	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	7.9	3
106	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	7.9	26
105	Investigation of deleterious effects of nsSNPs in the POT1 gene: a structural genomics-based approach to understand the mechanism of cancer development. <i>Journal of Cellular Biochemistry</i> , 2019 , 120, 10281-10294	4.7	25
104	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	3.6	21
103	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	7.9	3
102	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	7.9	10
101	Circulation of single serotype of Dengue Virus (DENV-3) in New Delhi, India during 2016: A change in the epidemiological trend. <i>Journal of Infection and Public Health</i> , 2019 , 12, 49-56	7.4	10

100	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	3.6	77
99	Estimation of pH effect on the structure and stability of kinase domain of human integrin-linked kinase. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019 , 37, 156-165	3.6	10
98	Comparison of the thermal stabilization of proteins by oligosaccharides and monosaccharide mixtures: Measurement and analysis in the context of excluded volume theory. <i>Biophysical Chemistry</i> , 2018 , 237, 31-37	3.5	22
97	Sugar osmolytes-induced stabilization of RNase A in macromolecular crowded cellular environment. <i>International Journal of Biological Macromolecules</i> , 2018 , 115, 349-357	7.9	11
96	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	7.9	29
95	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	7.9	23
94	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	4.2	36
93	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	7.9	6
92	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	7.9	64
91	Unravelling the unfolding mechanism of human integrin linked kinase by GdmCl-induced denaturation. <i>International Journal of Biological Macromolecules</i> , 2018 , 117, 1252-1263	7.9	13
90	Macromolecular crowding induces molten globule state in the native myoglobin at physiological pH. <i>International Journal of Biological Macromolecules</i> , 2018 , 106, 130-139	7.9	27
89	Identification of potential inhibitors of sortase A: Binding studies, in-silico docking and protein-protein interaction studies of sortase A from <i>Enterococcus faecalis</i> . <i>International Journal of Biological Macromolecules</i> , 2018 , 120, 1906-1916	7.9	2
88	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	2.3	16
87	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	3.6	21
86	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	3.6	24
85	Denatured states of yeast cytochrome c induced by heat and guanidinium chloride are structurally and thermodynamically different. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017 , 35, 1420-1435	3.6	10
84	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	3.6	16
83	GdmCl-induced unfolding studies of human carbonic anhydrase IX: a combined spectroscopic and MD simulation approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017 , 35, 1295-1306	3.6	20

82	Effect of mammalian kidney osmolytes on the folding pathway of sheep serum albumin. <i>International Journal of Biological Macromolecules</i> , 2017 , 97, 625-634	7.9	5
81	Data on the role of accessible surface area on osmolytes-induced protein stabilization. <i>Data in Brief</i> , 2017 , 10, 47-56	1.2	6
80	Protein aggregation, misfolding and consequential human neurodegenerative diseases. <i>International Journal of Neuroscience</i> , 2017 , 127, 1047-1057	2	29
79	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	7.9	22
78	Non-enzymatic glycation enhances human serum albumin binding capacity to sodium fluorescein at room temperature: A spectroscopic analysis. <i>Clinica Chimica Acta</i> , 2017 , 469, 180-186	6.2	7
77	Binding studies and biological evaluation of β -carotene as a potential inhibitor of human calcium/calmodulin-dependent protein kinase IV. <i>International Journal of Biological Macromolecules</i> , 2017 , 96, 161-170	7.9	52
76	Purification, preliminary X-ray crystallography and biophysical studies of triose phosphate isomerase- β -globin subunit complex. <i>International Journal of Biological Macromolecules</i> , 2017 , 94, 746-753	7.9	3
75	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	5.4	21
74	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	4.9	78
73	New insights into the antioxidant and apoptotic potential of Glycyrrhiza glabra L. during hydrogen peroxide mediated oxidative stress: An in vitro and in silico evaluation. <i>Biomedicine and Pharmacotherapy</i> , 2017 , 94, 265-279	7.5	18
72	Effect of conservative mutations (L94V and L94I) on the structure and stability of horse cytochrome c. <i>Archives of Biochemistry and Biophysics</i> , 2017 , 633, 40-49	4.1	6
71	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	7.9	13
70	Fas-activated serine/threonine kinase: Structure and function. <i>Gene Reports</i> , 2017 , 8, 117-127	1.4	5
69	Computing disease-linked SOD1 mutations: deciphering protein stability and patient-phenotype relations. <i>Scientific Reports</i> , 2017 , 7, 4678	4.9	24
68	Exploring Missense Mutations in Tyrosine Kinases Implicated with Neurodegeneration. <i>Molecular Neurobiology</i> , 2017 , 54, 5085-5106	6.2	4
67	Characterization of folding intermediates during urea-induced denaturation of human carbonic anhydrase II. <i>International Journal of Biological Macromolecules</i> , 2017 , 95, 881-887	7.9	19
66	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	3.6	11
65	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	4	63

64	Design, synthesis, and biological evaluation of pyrimidine derivatives as potential inhibitors of human calcium/calmodulin-dependent protein kinase IV. <i>Chemical Biology and Drug Design</i> , 2017 , 89, 741-754	2.9	23
63	Effect of dextran on the thermodynamic stability and structure of ribonuclease A. <i>Journal of the Iranian Chemical Society</i> , 2016 , 13, 181-189	2	10
62	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, 483-8	2.4	3
61	Human microtubule affinity-regulating kinase 4 is stable at extremes of pH. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016 , 34, 1241-51	3.6	14
60	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	0.4	1
59	Effect of 1,4-bis(3-dodecylimidazolium-1-yl) butane bromide on channel form of gramicidin vesicles. <i>Colloids and Surfaces A: Physicochemical and Engineering Aspects</i> , 2016 , 508, 150-158	5.1	24
58	Structural insight into C9orf72 hexanucleotide repeat expansions: Towards new therapeutic targets in FTD-ALS. <i>Neurochemistry International</i> , 2016 , 100, 11-20	4.4	17
57	GdnHCl-induced unfolding intermediate in the mitochondrial carbonic anhydrase VA. <i>International Journal of Biological Macromolecules</i> , 2016 , 91, 1151-60	7.9	16
56	Structural basis of urea-induced unfolding: Unraveling the folding pathway of hemochromatosis factor E. <i>International Journal of Biological Macromolecules</i> , 2016 , 91, 1051-61	7.9	20
55	Purification and structural characterization of Mce4A from <i>Mycobacterium tuberculosis</i> . <i>International Journal of Biological Macromolecules</i> , 2016 , 93, 235-241	7.9	9
54	Delineating the relationship between amyotrophic lateral sclerosis and frontotemporal dementia: Sequence and structure-based predictions. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2016 , 1862, 1742-54	6.9	19
53	Purification and characterization of RGA2, a Rho2 GTPase-activating protein from <i>Tinospora cordifolia</i> . <i>3 Biotech</i> , 2016 , 6, 85	2.8	2
52	Characterisation of molten globule-like state of sheep serum albumin at physiological pH. <i>International Journal of Biological Macromolecules</i> , 2016 , 89, 605-13	7.9	18
51	Human Disease Insight: An integrated knowledge-based platform for disease-gene-drug information. <i>Journal of Infection and Public Health</i> , 2016 , 9, 331-8	7.4	2
50	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, 221-8	3.6	28
49	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	4.7	42
48	Cloning, expression, purification and characterization of human mitochondrial carbonic anhydrase VA. <i>3 Biotech</i> , 2016 , 6, 16	2.8	11
47	Probing pH sensitivity of α -phycoerythrin and its natural truncant: A comparative study. <i>International Journal of Biological Macromolecules</i> , 2016 , 86, 18-27	7.9	10

46	Chikungunya virus: recent advances in epidemiology, host pathogen interaction and vaccine strategies. <i>Pathogens and Disease</i> , 2016 , 74,	4.2	26
45	Purification and characterization of oligonucleotide binding (OB)-fold protein from medicinal plant <i>Tinospora cordifolia</i> . <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2016 , 1008, 38-44	3.2	5
44	Structure guided design of potential inhibitors of human calcium-calmodulin dependent protein kinase IV containing pyrimidine scaffold. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2016 , 26, 782-788	2.9	32
43	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	4.1	19
42	Spectroscopic and MD simulation studies on unfolding processes of mitochondrial carbonic anhydrase VA induced by urea. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016 , 34, 1987-97	3.6	19
41	Purification and characterization of Ras related protein, Rab5a from <i>Tinospora cordifolia</i> . <i>International Journal of Biological Macromolecules</i> , 2016 , 82, 471-9	7.9	8
40	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	0.8	4
39	Sequence Analysis of Hypothetical Proteins from 26695 to Identify Potential Virulence Factors. <i>Genomics and Informatics</i> , 2016 , 14, 125-135	1.9	12
38	Therapeutic progress in amyotrophic lateral sclerosis-beginning to learning. <i>European Journal of Medicinal Chemistry</i> , 2016 , 121, 903-917	6.8	43
37	Molecular basis of the structural stability of hemochromatosis factor E: A combined molecular dynamic simulation and GdmCl-induced denaturation study. <i>Biopolymers</i> , 2016 , 105, 133-42	2.2	23
36	Structural and thermodynamic characterisation of L94F mutant of horse cytochrome c. <i>International Journal of Biological Macromolecules</i> , 2016 , 92, 202-212	7.9	12
35	Refolding of urea denatured cytochrome c: Role of hydrophobic tail of the cationic gemini surfactants. <i>Journal of Colloid and Interface Science</i> , 2016 , 484, 205-212	9.3	20
34	Ubiquitin-associated domain of MARK4 provides stability at physiological pH. <i>International Journal of Biological Macromolecules</i> , 2016 , 93, 1147-1154	7.9	19
33	Protein aggregation and neurodegenerative diseases: From theory to therapy. <i>European Journal of Medicinal Chemistry</i> , 2016 , 124, 1105-1120	6.8	88
32	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	2.8	19
31	Atypical PKC phosphorylates microtubule affinity-regulating kinase 4 in vitro. <i>Molecular and Cellular Biochemistry</i> , 2015 , 410, 223-8	4.2	18
30	PKR-inhibitor binds efficiently with human microtubule affinity-regulating kinase 4. <i>Journal of Molecular Graphics and Modelling</i> , 2015 , 62, 245-252	2.8	25
29	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	4.1	32

28	Characterization of pre-molten globule state of yeast iso-1-cytochrome c and its deletants at pH 6.0 and 25 °C. <i>International Journal of Biological Macromolecules</i> , 2015 , 72, 1406-18	7.9	19
27	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, 1493-502	3.6	29
26	Heterogeneity of equilibrium molten globule state of cytochrome c induced by weak salt denaturants under physiological condition. <i>PLoS ONE</i> , 2015 , 10, e0120465	3.7	15
25	Thermal Stabilization of Proteins by Mono- and Oligosaccharides: Measurement and Analysis in the Context of an Excluded Volume Model. <i>Biochemistry</i> , 2015 , 54, 3594-603	3.2	27
24	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, 700-11	3.8	39
23	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, 2267-84	3.6	43
22	Cooperative Unfolding of Residual Structure in Heat Denatured Proteins by Urea and Guanidinium Chloride. <i>PLoS ONE</i> , 2015 , 10, e0128740	3.7	18
21	Functional annotation of putative hypothetical proteins from <i>Candida dubliniensis</i> . <i>Gene</i> , 2014 , 543, 93-100	3.8	37
20	Folding and stability studies on C-PE and its natural N-terminal truncant. <i>Archives of Biochemistry and Biophysics</i> , 2014 , 545, 9-21	4.1	11
19	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, 2838-48	3.2	20
18	Purification and characterization of calreticulin: a Ca ²⁺ -binding chaperone from sheep kidney. <i>Applied Biochemistry and Biotechnology</i> , 2014 , 174, 1771-83	3.2	4
17	The role of key residues in structure, function, and stability of cytochrome-c. <i>Cellular and Molecular Life Sciences</i> , 2014 , 71, 229-55	10.3	88
16	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, 2005-16	3.6	25
15	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, 456-76	2.8	98
14	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	0.8	8
13	Microtubule affinity-regulating kinase 4: structure, function, and regulation. <i>Cell Biochemistry and Biophysics</i> , 2013 , 67, 485-99	3.2	67
12	Human β -glucuronidase: structure, function, and application in enzyme replacement therapy. <i>Rejuvenation Research</i> , 2013 , 16, 352-63	2.6	43
11	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	2.9	24

10	Why is Glycine not a Part of the Osmoticum in the Urea-rich Cells?. <i>Protein and Peptide Letters</i> , 2013 , 20, 61-70	1.9	7
9	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. <i>PLoS ONE</i> , 2013 , 8, e72533	3.7	18
8	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, 879-90	3.2	10
7	Biophysical analyses of human resistin: oligomer formation suggests novel biological function. <i>Biochemistry</i> , 2008 , 47, 12457-66	3.2	24
6	Purification and characterization of a trypsin inhibitor from <i>Putranjiva roxburghii</i> seeds. <i>Phytochemistry</i> , 2008 , 69, 2120-6	4	53
5	Guanidinium chloride and urea denaturations of beta-lactoglobulin A at pH 2.0 and 25 degrees C: the equilibrium intermediate contains non-native structures (helix, tryptophan and hydrophobic patches). <i>Biophysical Chemistry</i> , 2007 , 127, 140-8	3.5	20
4	Role of unique basic residues of human pancreatic ribonuclease in its catalysis and structural stability. <i>Biochemical and Biophysical Research Communications</i> , 2007 , 360, 809-14	3.4	6
3	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, 410-4	7.9	12
2	Stability of proteins in the presence of polyols estimated from their guanidinium chloride-induced transition curves at different pH values and 25 degrees C. <i>Biophysical Chemistry</i> , 2006 , 119, 224-33	3.5	38
1	A unique molten globule state occurs during unfolding of cytochrome c by LiClO ₄ near physiological pH and temperature: structural and thermodynamic characterization. <i>Biochemistry</i> , 2006 , 45, 4695-702	3.2	33