Asimul Islam

List of Publications by Year
in descending order

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215 papers	5,778 citations	81743 39 h-index	143772 57 g-index
217 all docs	217 docs citations	217 times ranked	4376 citing authors

#	Article	IF	Citations
1	A Review of Methods Available to Estimate Solvent-Accessible Surface Areas of Soluble Proteins in the Folded and Unfolded States. Current Protein and Peptide Science, 2014, 15, 456-476.	0.7	197
2	Glecaprevir and Maraviroc are high-affinity inhibitors of SARS-CoV-2 main protease: possible implication in COVID-19 therapy. Bioscience Reports, 2020, 40, .	1.1	129
3	Protein aggregation and neurodegenerative diseases: From theory to therapy. European Journal of Medicinal Chemistry, 2016, 124, 1105-1120.	2.6	120
4	Identification and evaluation of bioactive natural products as potential inhibitors of human microtubule affinity-regulating kinase 4 (MARK4). Journal of Biomolecular Structure and Dynamics, 2019, 37, 1813-1829.	2.0	114
5	Rosmarinic Acid Exhibits Anticancer Effects via MARK4 Inhibition. Scientific Reports, 2020, 10, 10300.	1.6	114
6	The role of key residues in structure, function, and stability of cytochrome-c. Cellular and Molecular Life Sciences, 2014, 71, 229-255.	2.4	113
7	Investigation of molecular mechanism of recognition between citral and MARK4: A newer therapeutic approach to attenuate cancer cell progression. International Journal of Biological Macromolecules, 2018, 107, 2580-2589.	3.6	96
8	Microtubule Affinity-Regulating Kinase 4: Structure, Function, and Regulation. Cell Biochemistry and Biophysics, 2013, 67, 485-499.	0.9	94
9	Elucidation of Dietary Polyphenolics as Potential Inhibitor of Microtubule Affinity Regulating Kinase 4: In silico and In vitro Studies. Scientific Reports, 2017, 7, 9470.	1.6	91
10	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. Molecules, 2020, 25, 823.	1.7	89
11	Size-dependent studies of macromolecular crowding on the thermodynamic stability, structure and functional activity of proteins: in vitro and in silico approaches. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 178-197.	1.1	86
12	Investigation of inhibitory potential of quercetin to the pyruvate dehydrogenase kinase 3: Towards implications in anticancer therapy. International Journal of Biological Macromolecules, 2019, 136, 1076-1085.	3.6	80
13	Identification of high-affinity inhibitors of SARS-CoV-2 main protease: Towards the development of effective COVID-19 therapy. Virus Research, 2020, 288, 198102.	1.1	79
14	Potential drug targets of SARS-CoV-2: From genomics to therapeutics. International Journal of Biological Macromolecules, 2021, 177, 1-9.	3.6	77
15	MARK4 Inhibited by AChE Inhibitors, Donepezil and Rivastigmine Tartrate: Insights into Alzheimerâ€™s Disease Therapy. Biomolecules, 2020, 10, 789.	1.8	76
16	Targeting pyruvate dehydrogenase kinase signaling in the development of effective cancer therapy. Biochimica Et Biophysica Acta: Reviews on Cancer, 2021, 1876, 188568.	3.3	75
17	Ellagic Acid Controls Cell Proliferation and Induces Apoptosis in Breast Cancer Cells via Inhibition of Cyclin-Dependent Kinase 6. International Journal of Molecular Sciences, 2020, 21, 3526.	1.8	74
18	Binding studies and biological evaluation of Î²-carotene as a potential inhibitor of human calcium/calmodulin-dependent protein kinase IV. International Journal of Biological Macromolecules, 2017, 96, 161-170.	3.6	67

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19	High throughput screening, docking, and molecular dynamics studies to identify potential inhibitors of human calcium/calmodulin-dependent protein kinase IV. Journal of Biomolecular Structure and Dynamics, 2019, 37, 2179-2192.	2.0	60
20	Spectroscopic, calorimetric and molecular docking insight into the interaction of Alzheimerâ€™s drug donepezil with human transferrin: implications of Alzheimerâ€™s drug. Journal of Biomolecular Structure and Dynamics, 2020, 38, 1094-1102.	2.0	60
21	Purification and characterization of a trypsin inhibitor from Putranjiva roxburghii seeds. Phytochemistry, 2008, 69, 2120-2126.	1.4	59
22	HumanÎ²-Glucuronidase: Structure, Function, and Application in Enzyme Replacement Therapy. Rejuvenation Research, 2013, 16, 352-363.	0.9	59
23	Therapeutic progress in amyotrophic lateral sclerosis-beginning to learning. European Journal of Medicinal Chemistry, 2016, 121, 903-917.	2.6	59
24	Evidence of vanillin binding to CAMKIV explains the anti-cancer mechanism in human hepatic carcinoma and neuroblastoma cells. Molecular and Cellular Biochemistry, 2018, 438, 35-45.	1.4	56
25	FNDC5/Irisin: Physiology and Pathophysiology. Molecules, 2022, 27, 1118.	1.7	56
26	Calcium/calmodulin-dependent protein kinase IV: A multifunctional enzyme and potential therapeutic target. Progress in Biophysics and Molecular Biology, 2016, 121, 54-65.	1.4	54
27	Structural Analysis and Conformational Dynamics of STN1 Gene Mutations Involved in Coat Plus Syndrome. Frontiers in Molecular Biosciences, 2019, 6, 41.	1.6	53
28	Probing the interaction of Rivastigmine Tartrate, an important Alzheimer's drug, with serum albumin: Attempting treatment of Alzheimer's disease. International Journal of Biological Macromolecules, 2020, 148, 533-542.	3.6	52
29	Functional annotation of putative hypothetical proteins from Candida dubliniensis. Gene, 2014, 543, 93-100.	1.0	51
30	Structural characterization of MG and pre-MG states of proteins by MD simulations, NMR, and other techniques. Journal of Biomolecular Structure and Dynamics, 2015, 33, 2267-2284.	2.0	51
31	Designing New Kinase Inhibitor Derivatives as Therapeutics Against Common Complex Diseases: Structural Basis of Microtubule Affinity-Regulating Kinase 4 (MARK4) Inhibition. OMICS A Journal of Integrative Biology, 2015, 19, 700-711.	1.0	50
32	Natural products can be used in therapeutic management of COVID-19: Probable mechanistic insights. Biomedicine and Pharmacotherapy, 2022, 147, 112658.	2.5	50
33	Inhibiting CDK6 Activity by Quercetin Is an Attractive Strategy for Cancer Therapy. ACS Omega, 2020, 5, 27480-27491.	1.6	48
34	Unraveling Binding Mechanism of Alzheimerâ€™s Drug Rivastigmine Tartrate with Human Transferrin: Molecular Docking and Multi-Spectroscopic Approach towards Neurodegenerative Diseases. Biomolecules, 2019, 9, 495.	1.8	46
35	Exploring molecular insights into the interaction mechanism of cholesterol derivatives with the Mce4A: A combined spectroscopic and molecular dynamic simulation studies. International Journal of Biological Macromolecules, 2018, 111, 548-560.	3.6	45
36	Amphiphilic nature of polyethylene glycols and their role in medical research. Polymer Testing, 2020, 82, 106316.	2.3	45

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37	Elucidating the Interaction of Human Ferritin with Quercetin and Naringenin: Implication of Natural Products in Neurodegenerative Diseases: Molecular Docking and Dynamics Simulation Insight. ACS Omega, 2021, 6, 7922-7930.	1.6	45
38	Protein aggregation, misfolding and consequential human neurodegenerative diseases. International Journal of Neuroscience, 2017, 127, 1047-1057.	0.8	44
39	Structureâ€based investigation of MARK4 inhibitory potential of Naringenin for therapeutic management of cancer and neurodegenerative diseases. Journal of Cellular Biochemistry, 2021, 122, 1445-1459.	1.2	44
40	Phytochemicals targeting NF-Î¹B signaling: Potential anti-cancer interventions. Journal of Pharmaceutical Analysis, 2022, 12, 394-405.	2.4	44
41	Stability of proteins in the presence of polyols estimated from their guanidinium chloride-induced transition curves at different pH values and 25 Â°C. Biophysical Chemistry, 2006, 119, 224-233.	1.5	43
42	2/3D-QSAR, molecular docking and MD simulation studies of FtsZ protein targeting benzimidazoles derivatives. Computational Biology and Chemistry, 2019, 78, 398-413.	1.1	43
43	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. Archives of Biochemistry and Biophysics, 2015, 584, 42-50.	1.4	42
44	Therapeutic Potential of Ursolic Acid in Cancer and Diabetic Neuropathy Diseases. International Journal of Molecular Sciences, 2021, 22, 12162.	1.8	42
45	Biophysical Analyses of Human Resistin: Oligomer Formation Suggests Novel Biological Function. Biochemistry, 2008, 47, 12457-12466.	1.2	39
46	Identification of Potential Inhibitors of Calcium/Calmodulin-Dependent Protein Kinase IV from Bioactive Phytoconstituents. Oxidative Medicine and Cellular Longevity, 2020, 2020, 1-14.	1.9	39
47	Macromolecular crowding induces molten globule state in the native myoglobin at physiological pH. International Journal of Biological Macromolecules, 2018, 106, 130-139.	3.6	38
48	A Unique Molten Globule State Occurs during Unfolding of Cytochrome c by LiClO4 Near Physiological pH and Temperature: Structural and Thermodynamic Characterization. Biochemistry, 2006, 45, 4695-4702.	1.2	37
49	Evaluation of pyrazolopyrimidine derivatives as microtubule affinity regulating kinase 4 inhibitors: Towards therapeutic management of Alzheimerâ€™s disease. Journal of Biomolecular Structure and Dynamics, 2020, 38, 3892-3907.	2.0	37
50	Structural and biochemical investigation of MARK4 inhibitory potential of cholic acid: Towards therapeutic implications in neurodegenerative diseases. International Journal of Biological Macromolecules, 2020, 161, 596-604.	3.6	37
51	Thermal Stabilization of Proteins by Mono- and Oligosaccharides: Measurement and Analysis in the Context of an Excluded Volume Model. Biochemistry, 2015, 54, 3594-3603.	1.2	35
52	First evidence of formation of pre-molten globule state in myoglobin: A macromolecular crowding approach towards protein folding in vivo. International Journal of Biological Macromolecules, 2019, 126, 1288-1294.	3.6	35
53	Structure guided design of potential inhibitors of human calciumâ€“calmodulin dependent protein kinase IV containing pyrimidine scaffold. Bioorganic and Medicinal Chemistry Letters, 2016, 26, 782-788.	1.0	34
54	Computing disease-linked SOD1 mutations: deciphering protein stability and patient-phenotype relations. Scientific Reports, 2017, 7, 4678.	1.6	34

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55	Chikungunya virus: recent advances in epidemiology, host pathogen interaction and vaccine strategies. Pathogens and Disease, 2016, 74, ftv119.	0.8	33
56	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. Journal of Biological Chemistry, 2017, 292, 505-511.	1.6	33
57	Targeting the Sphingosine Kinase/Sphingosine-1-Phosphate Signaling Axis in Drug Discovery for Cancer Therapy. Cancers, 2021, 13, 1898.	1.7	33
58	Investigation of deleterious effects of nsSNPs in the POT1 gene: a structural genomicsâ€based approach to understand the mechanism of cancer development. Journal of Cellular Biochemistry, 2019, 120, 10281-10294.	1.2	32
59	Virtual high-throughput screening of natural compounds in-search of potential inhibitors for protection of telomeres 1 (POT1). Journal of Biomolecular Structure and Dynamics, 2020, 38, 4625-4634.	2.0	32
60	Corona virus versus existence of human on the earth: A computational and biophysical approach. International Journal of Biological Macromolecules, 2020, 161, 271-281.	3.6	32
61	In vitro and in silico studies of urea-induced denaturation of yeast iso-1-cytochromecand its deletants at pH 6.0 and 25 Â°C. Journal of Biomolecular Structure and Dynamics, 2015, 33, 1493-1502.	2.0	31
62	Effect of pH on the structure, function, and stability of human calcium/calmodulin-dependent protein kinase IV: combined spectroscopic and MD simulation studies. Biochemistry and Cell Biology, 2016, 94, 221-228.	0.9	31
63	Mechanistic insights into the urea-induced denaturation of kinase domain of human integrin linked kinase. International Journal of Biological Macromolecules, 2018, 111, 208-218.	3.6	31
64	Carbohydrate-Based Macromolecular Crowding-Induced Stabilization of Proteins: Towards Understanding the Significance of the Size of the Crowder. Biomolecules, 2019, 9, 477.	1.8	31
65	Effect of pH on structure, function, and stability of mitochondrial carbonic anhydrase VA. Journal of Biomolecular Structure and Dynamics, 2017, 35, 449-461.	2.0	29
66	Impact of Gln94Glu mutation on the structure and function of protection of telomere 1, a cause of cutaneous familial melanoma. Journal of Biomolecular Structure and Dynamics, 2020, 38, 1514-1524.	2.0	29
67	PKR-inhibitor binds efficiently with human microtubule affinity-regulating kinase 4. Journal of Molecular Graphics and Modelling, 2015, 62, 245-252.	1.3	28
68	Molecular basis of the structural stability of hemochromatosis factor <scp>E</scp>: A combined molecular dynamic simulation and GdmClâ€induced denaturation study. Biopolymers, 2016, 105, 133-142.	1.2	28
69	Design, synthesis, and biological evaluation of pyrimidine derivatives as potential inhibitors of human calcium/calmodulinâ€dependent protein kinase <scp>IV</scp>. Chemical Biology and Drug Design, 2017, 89, 741-754.	1.5	28
70	Sequence Analysis of Hypothetical Proteins fromHelicobacter pylori26695 to Identify Potential Virulence Factors. Genomics and Informatics, 2016, 14, 125.	0.4	28
71	Evidence of non-coincidence of normalized sigmoidal curves of two different structural properties for two-state protein folding/unfolding. Journal of Chemical Thermodynamics, 2013, 58, 351-358.	1.0	27
72	Structure-based functional annotation of hypothetical proteins from Candida dubliniensis: a quest for potential drug targets. 3 Biotech, 2015, 5, 561-576.	1.1	27

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73	Effect of 1,4-bis(3-dodecylimidazolium-1-yl) butane bromide on channel form of gramicidin vesicles. Colloids and Surfaces A: Physicochemical and Engineering Aspects, 2016, 508, 150-158.	2.3	27
74	Characterization of intermediate state of myoglobin in the presence of PEG 10 under physiological conditions. International Journal of Biological Macromolecules, 2017, 99, 241-248.	3.6	27
75	Effect of sequential deletion of extra N-terminal residues on the structure and stability of yeast iso-1-cytochrome-c. Journal of Biomolecular Structure and Dynamics, 2014, 32, 2005-2016.	2.0	26
76	Evaluation of Binding of Rosmarinic Acid with Human Transferrin and Its Impact on the Protein Structure: Targeting Polyphenolic Acid-Induced Protection of Neurodegenerative Disorders. Oxidative Medicine and Cellular Longevity, 2020, 2020, 1-14.	1.9	26
77	Interactions Under Crowding Milieu: Chemical-Induced Denaturation of Myoglobin is Determined by the Extent of Heme Dissociation on Interaction with Crowders. Biomolecules, 2020, 10, 490.	1.8	26
78	Interaction of polyethylene glycol with cytochrome c investigated via in vitro and in silico approaches. Scientific Reports, 2021, 11, 6475.	1.6	26
79	Probing the interaction of memantine, an important Alzheimer's drug, with human serum albumin: In silico and in vitro approach. Journal of Molecular Liquids, 2021, 340, 116888.	2.3	26
80	Myricetin inhibits breast and lung cancer cells proliferation via inhibiting MARK4. Journal of Cellular Biochemistry, 2022, 123, 359-374.	1.2	26
81	Cloning, Expression, Purification and Refolding of Microtubule Affinity-Regulating Kinase 4 Expressed in Escherichia coli. Applied Biochemistry and Biotechnology, 2014, 172, 2838-2848.	1.4	25
82	Structural insight into C9orf72 hexanucleotide repeat expansions: Towards new therapeutic targets in FTD-ALS. Neurochemistry International, 2016, 100, 11-20.	1.9	25
83	Urea-induced denaturation of human calcium/calmodulin-dependent protein kinase IV: a combined spectroscopic and MD simulation studies. Journal of Biomolecular Structure and Dynamics, 2017, 35, 463-475.	2.0	25
84	Characterization of folding intermediates during urea-induced denaturation of human carbonic anhydrase II. International Journal of Biological Macromolecules, 2017, 95, 881-887.	3.6	25
85	Sequence, structure and evolutionary analysis of cold shock domain proteins, a member of OB fold family. Journal of Evolutionary Biology, 2018, 31, 1903-1917.	0.8	25
86	Mixture of Macromolecular Crowding Agents Has a Non-additive Effect on the Stability of Proteins. Applied Biochemistry and Biotechnology, 2019, 188, 927-941.	1.4	25
87	Formation of molten globule state in horse heart cytochrome c under physiological conditions: Importance of soft interactions and spectroscopic approach in crowded milieu. International Journal of Biological Macromolecules, 2020, 148, 192-200.	3.6	25
88	MAP/Microtubule Affinity Regulating Kinase 4 Inhibitory Potential of Irisin: A New Therapeutic Strategy to Combat Cancer and Alzheimerâ€™s Disease. International Journal of Molecular Sciences, 2021, 22, 10986.	1.8	25
89	Characterization of pre-molten globule state of yeast iso-1-cytochrome c and its deletants at pH 6.0 and 25 Â°C. International Journal of Biological Macromolecules, 2015, 72, 1406-1418.	3.6	24
90	Refolding of urea denatured cytochrome c : Role of hydrophobic tail of the cationic gemini surfactants. Journal of Colloid and Interface Science, 2016, 484, 205-212.	5.0	24

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91	Ubiquitin-associated domain of MARK4 provides stability at physiological pH. International Journal of Biological Macromolecules, 2016, 93, 1147-1154.	3.6	24
92	Structural Features of Nucleoprotein CST/Shelterin Complex Involved in the Telomere Maintenance and Its Association with Disease Mutations. Cells, 2020, 9, 359.	1.8	24
93	Cooperative Unfolding of Residual Structure in Heat Denatured Proteins by Urea and Guanidinium Chloride. PLoS ONE, 2015, 10, e0128740.	1.1	24
94	Atypical PKC phosphorylates microtubule affinity-regulating kinase 4 in vitro. Molecular and Cellular Biochemistry, 2015, 410, 223-228.	1.4	23
95	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
96	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. Biomedicine and Pharmacotherapy, 2017, 94, 265-279.	2.5	23
97	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
98	Biophysical Elucidation of Fibrillation Inhibition by Sugar Osmolytes in Î±-Lactalbumin: Multispectroscopic and Molecular Docking Approaches. ACS Omega, 2020, 5, 26871-26882.	1.6	23
99	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
100	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
101	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
102	Sugar osmolytes-induced stabilization of RNase A in macromolecular crowded cellular environment. International Journal of Biological Macromolecules, 2018, 115, 349-357.	3.6	22
103	Identification of high-affinity inhibitors of pyruvate dehydrogenase kinase-3: towards therapeutic management of cancer. Journal of Biomolecular Structure and Dynamics, 2021, 39, 586-594.	2.0	22
104	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
105	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
106	Circulation of single serotype of Dengue Virus (DENV-3) in New Delhi, India during 2016: A change in the epidemiological trend. Journal of Infection and Public Health, 2019, 12, 49-56.	1.9	21
107	Effects of Ethylene Glycol on the Structure and Stability of Myoglobin Using Spectroscopic, Interaction, and In Silico Approaches: Monomer Is Different from Those of Its Polymers. ACS Omega, 2020, 5, 13840-13850.	1.6	21
108	Mechanistic insight into the binding of graphene oxide with human serum albumin: Multispectroscopic and molecular docking approach. Spectrochimica Acta - Part A: Molecular and Biomolecular Spectroscopy, 2021, 256, 119750.	2.0	21

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109	Guanidinium chloride and urea denaturations of Î²-Lactoglobulin A at pH 2.0 and 25ÂÂ°C: The equilibrium intermediate contains non-native structures (helix, tryptophan and hydrophobic patches). Biophysical Chemistry, 2007, 127, 140-148.	1.5	20
110	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
111	Testing the dependence of stabilizing effect of osmolytes on the fractional increase in the accessible surface area on thermal and chemical denaturations of proteins. Archives of Biochemistry and Biophysics, 2016, 591, 7-17.	1.4	19
112	Effect of pH on the stability of hemochromatosis factor E: a combined spectroscopic and molecular dynamics simulation-based study. Journal of Biomolecular Structure and Dynamics, 2017, 35, 1582-1598.	2.0	19
113	Estimation of thermodynamic stability of human carbonic anhydrase IX from urea-induced denaturation and MD simulation studies. International Journal of Biological Macromolecules, 2017, 105, 183-189.	3.6	19
114	Insight into the binding of PEG-400 with eye protein alpha-crystallin: Multi spectroscopic and computational approach: possible therapeutics targeting eye diseases. Journal of Biomolecular Structure and Dynamics, 2022, 40, 4496-4506.	2.0	19
115	Protein folding: Molecular dynamics simulations and in vitro studies for probing mechanism of urea- and guanidinium chloride-induced unfolding of horse cytochrome-c. International Journal of Biological Macromolecules, 2019, 122, 695-704.	3.6	18
116	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. International Journal of Biological Macromolecules, 2020, 150, 1238-1248.	3.6	18
117	Investigation of conformational dynamics of Tyr89Cys mutation in protection of telomeres 1 gene associated with familial melanoma. Journal of Biomolecular Structure and Dynamics, 2021, 39, 35-44.	2.0	18
118	Structural genomics approach to investigate deleterious impact of nsSNPs in conserved telomere maintenance component 1. Scientific Reports, 2021, 11, 10202.	1.6	18
119	Investigating architecture and structure-function relationships in cold shock DNA-binding domain family using structural genomics-based approach. International Journal of Biological Macromolecules, 2019, 133, 484-494.	3.6	17
120	Glossary of phytoconstituents: Can these be repurposed against SARS CoV-2? A quick in silico screening of various phytoconstituents from plant Glycyrrhiza glabra with SARS CoV-2 main protease. Food and Chemical Toxicology, 2021, 150, 112057.	1.8	17
121	Heterogeneity of Equilibrium Molten Globule State of Cytochrome c Induced by Weak Salt Denaturants under Physiological Condition. PLoS ONE, 2015, 10, e0120465.	1.1	16
122	GdnHCl-induced unfolding intermediate in the mitochondrial carbonic anhydrase VA. International Journal of Biological Macromolecules, 2016, 91, 1151-1160.	3.6	16
123	Human microtubule affinity-regulating kinase 4 is stable at extremes of pH. Journal of Biomolecular Structure and Dynamics, 2016, 34, 1241-1251.	2.0	16
124	Evaluation of human microtubule affinity-regulating kinase 4 inhibitors: fluorescence binding studies, enzyme, and cell assays. Journal of Biomolecular Structure and Dynamics, 2017, 35, 3194-3203.	2.0	16
125	Effect of pH on the structure and function of pyruvate dehydrogenase kinase 3: Combined spectroscopic and MD simulation studies. International Journal of Biological Macromolecules, 2020, 147, 768-777.	3.6	16
126	Structural and thermodynamic characterisation of L94F mutant of horse cytochrome c. International Journal of Biological Macromolecules, 2016, 92, 202-212.	3.6	15

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127	Unravelling the unfolding mechanism of human integrin linked kinase by GdmCl-induced denaturation. International Journal of Biological Macromolecules, 2018, 117, 1252-1263.	3.6	15
128	Structural Characterization, Homology Modeling and Docking Studies of ARG674 Mutation in MyH8 Gene Associated with Trismus-Pseudocamptodactyly Syndrome. Letters in Drug Design and Discovery, 2014, 11, 1177-1187.	0.4	15
129	Structureâ€“function studies of Murraya koenigii trypsin inhibitor revealed a stable core beta sheet structure surrounded by Î±-helices with a possible role for Î±-helix in inhibitory function. International Journal of Biological Macromolecules, 2007, 41, 410-414.	3.6	14
130	Discovery of 4-(2-(dimethylamino)ethoxy)benzohydrazide derivatives as prospective microtubule affinity regulating kinase 4 inhibitors. RSC Advances, 2020, 10, 20129-20137.	1.7	14
131	Cloning, expression, purification and characterization of human mitochondrial carbonic anhydrase VA. 3 Biotech, 2016, 6, 16.	1.1	13
132	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
133	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
134	Multispectroscopic and Molecular Docking Insight into Elucidating the Interaction of Irisin with Rivastigmine Tartrate: A Combinational Therapy Approach to Fight Alzheimerâ€™s Disease. ACS Omega, 2021, 6, 7910-7921.	1.6	13
135	An Insight Into Mitochondrial Dysfunction and its Implications in Neurological Diseases. Current Drug Targets, 2021, 22, 1585-1595.	1.0	13
136	Investigating single amino acid substitutions in PIM1 kinase: A structural genomics approach. PLoS ONE, 2021, 16, e0258929.	1.1	13
137	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
138	Purification and structural characterization of Mce4A from Mycobacterium tuberculosis. International Journal of Biological Macromolecules, 2016, 93, 235-241.	3.6	12
139	Probing pH sensitivity of Î±C-phycoerythrin and its natural truncant: A comparative study. International Journal of Biological Macromolecules, 2016, 86, 18-27.	3.6	12
140	Denatured states of yeast cytochromecinduced by heat and guanidinium chloride are structurally and thermodynamically different. Journal of Biomolecular Structure and Dynamics, 2017, 35, 1420-1435.	2.0	12
141	Ionic Liquid Green Assembly-Mediated Migration of Piperine from Calf-Thymus DNA: A New Possibility of the Tunable Drug Delivery System. ACS Omega, 2019, 4, 21005-21017.	1.6	12
142	Investigation of guanidinium chloride-induced unfolding pathway of sphingosine kinase 1. International Journal of Biological Macromolecules, 2020, 147, 177-186.	3.6	12
143	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
144	Aurora B kinase: a potential drug target for cancer therapy. Journal of Cancer Research and Clinical Oncology, 2021, 147, 2187-2198.	1.2	12

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145	Investigating binding mechanism of thymoquinone to human transferrin, targeting Alzheimer's disease therapy. Journal of Cellular Biochemistry, 2022, 123, 1381-1393.	1.2	12
146	Heme-iron ligand (M80-Fe) in cytochrome c is destabilizing: combined inÂvitro and in silico 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
147	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
148	Trehalose Restrains the Fibril Load towards Î±-Lactalbumin Aggregation and Halts Fibrillation in a Concentration-Dependent Manner. Biomolecules, 2021, 11, 414.	1.8	11
149	Impact of single amino acid substitution on the structure and function of TANKâ€binding kinaseâ€1. Journal of Cellular Biochemistry, 2021, 122, 1475-1490.	1.2	11
150	Effect of pH on the structure and stability of irisin, a multifunctional protein: Multispectroscopic and molecular dynamics simulation approach. Journal of Molecular Structure, 2022, 1252, 132141.	1.8	11
151	Characterization of a Neutral and Thermostable Glucoamylase from the Thermophilic Mold Thermomucor indicae-seudaticae: Activity, Stability, and Structural Correlation. Applied Biochemistry and Biotechnology, 2010, 160, 879-890.	1.4	10
152	Purification and characterization of Ras related protein, Rab5a from Tinospora cordifolia. International Journal of Biological Macromolecules, 2016, 82, 471-479.	3.6	10
153	Counteraction of the deleterious effects of urea on structure and stability of mammalian kidney proteins by osmolytes. International Journal of Biological Macromolecules, 2018, 107, 1659-1667.	3.6	10
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