

Ab initio protein structure assembly using continuous
optimized knowledge-based force field

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Assessing the accuracy of template-based structure prediction metaservers by comparison with structural genomics structures. <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 213-225.	1.2	10
2	The MULTICOM toolbox for protein structure prediction. <i>BMC Bioinformatics</i> , 2012, 13, 65.	2.6	30
3	Antimicrobial activity of recombinant Pg-AMP1, a glycine-rich peptide from guava seeds. <i>Peptides</i> , 2012, 37, 294-300.	2.4	48
5	Bioinformatics and variability in drug response: a protein structural perspective. <i>Journal of the Royal Society Interface</i> , 2012, 9, 1409-1437.	3.4	66
6	The attack of the phytopathogens and the trumpet solo: Identification of a novel plant antifungal peptide with distinct fold and disulfide bond pattern. <i>Biochimie</i> , 2013, 95, 1939-1948.	2.6	34
7	ClusCo: clustering and comparison of protein models. <i>BMC Bioinformatics</i> , 2013, 14, 62.	2.6	32
8	Segment assembly, structure alignment and iterative simulation in protein structure prediction. <i>BMC Biology</i> , 2013, 11, 44.	3.8	12
9	Structural and functional insights on folate receptor $\hat{\pm}$ (FR $\hat{\pm}$) by homology modeling, ligand docking and molecular dynamics. <i>Journal of Molecular Graphics and Modelling</i> , 2013, 44, 197-207.	2.4	22
10	Comparative analysis of interactions of RASSF1-10. <i>Advances in Biological Regulation</i> , 2013, 53, 190-201.	2.3	34
11	Structure and Dynamics of the N-Terminal Domain of the Cu(I) Binding Protein CusB. <i>Biochemistry</i> , 2013, 52, 6911-6923.	2.5	26
12	Analysis of Sry duplications on the <i>Rattus norvegicus</i> Y-chromosome. <i>BMC Genomics</i> , 2013, 14, 792.	2.8	18
13	Protein Depth Calculation and the Use for Improving Accuracy of Protein Fold Recognition. <i>Journal of Computational Biology</i> , 2013, 20, 805-816.	1.6	19
14	Toward optimal fragment generations for <i>ab initio</i> protein structure assembly. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 229-239.	2.6	191
15	Mass spectrometry investigation of glycosylation on the NXS/T sites in recombinant glycoproteins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1474-1483.	2.3	30
16	Peamaclein – A new peach allergenic protein: similarities, differences and misleading features compared to Pru p 3. <i>Clinical and Experimental Allergy</i> , 2013, 43, 128-140.	2.9	85
17	Molecular modelling and simulations in cancer research. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2013, 1836, 1-14.	7.4	39
18	Theoretical structural insights into the snakin/GASA family. <i>Peptides</i> , 2013, 44, 163-167.	2.4	55
19	Plant Coilin: Structural Characteristics and RNA-Binding Properties. <i>PLoS ONE</i> , 2013, 8, e53571.	2.5	32

#	ARTICLE	IF	CITATIONS
20	Probabilistic Search and Energy Guidance for Biased Decoy Sampling in Ab Initio Protein Structure Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 1162-1175.	3.0	36
21	Innovations in proteomic profiling of cancers: Alternative splice variants as a new class of cancer biomarker candidates and bridging of proteomics with structural biology. <i>Journal of Proteomics</i> , 2013, 90, 28-37.	2.4	30
22	Ab Initio structure prediction for Escherichia coli: towards genome-wide protein structure modeling and fold assignment. <i>Scientific Reports</i> , 2013, 3, 1895.	3.3	43
23	Dynamics of an Ultrafast Folding Subdomain in the Context of a Larger Protein Fold. <i>Journal of the American Chemical Society</i> , 2013, 135, 19260-19267.	13.7	18
24	Multi-Objective Stochastic Search for Sampling Local Minima in the Protein Energy Surface. , 2013, , .		34
25	Structure- and Modeling-based Identification of the Adenovirus E4orf4 Binding Site in the Protein Phosphatase 2A B55± Subunit. <i>Journal of Biological Chemistry</i> , 2013, 288, 13718-13727.	3.4	11
26	Mass Spectrometry Coupled Experiments and Protein Structure Modeling Methods. <i>International Journal of Molecular Sciences</i> , 2013, 14, 20635-20657.	4.1	9
27	An Evolution-Based Approach to De Novo Protein Design and Case Study on Mycobacterium tuberculosis. <i>PLoS Computational Biology</i> , 2013, 9, e1003298.	3.2	44
28	Strategies and molecular tools to fight antimicrobial resistance: resistome, transcriptome, and antimicrobial peptides. <i>Frontiers in Microbiology</i> , 2013, 4, 412.	3.5	51
29	CABS-fold: server for the de novo and consensus-based prediction of protein structure. <i>Nucleic Acids Research</i> , 2013, 41, W406-W411.	14.5	86
30	Application of the AMPLE cluster-and-truncate approach to NMR structures for molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2194-2201.	2.5	13
31	Elucidating the Interacting Domains of Chandipura Virus Nucleocapsid Protein. <i>Advances in Virology</i> , 2013, 2013, 1-9.	1.1	7
32	A novel spliced gene in alcelaphine herpesvirus 1 encodes a glycoprotein which is secreted in vitro. <i>Journal of General Virology</i> , 2013, 94, 2515-2523.	2.9	6
33	Off-lattice protein structure prediction with homologous crossover. , 2013, , .		28
34	Molecular Cloning and Characterization of Cystatin, a Cysteine Protease Inhibitor, from Bufo melanostictus. <i>Bioscience, Biotechnology and Biochemistry</i> , 2013, 77, 2077-2081.	1.3	3
35	Validating a Coarse-Grained Potential Energy Function through Protein Loop Modelling. <i>PLoS ONE</i> , 2013, 8, e65770.	2.5	14
36	Efficient Sampling in Fragment-Based Protein Structure Prediction Using an Estimation of Distribution Algorithm. <i>PLoS ONE</i> , 2013, 8, e68954.	2.5	22
37	Computational and Experimental Validation of B and T-Cell Epitopes of the In Vivo Immune Response to a Novel Malarial Antigen. <i>PLoS ONE</i> , 2013, 8, e71610.	2.5	45

#	ARTICLE	IF	CITATIONS
38	Detecting Protein Candidate Fragments Using a Structural Alphabet Profile Comparison Approach. PLoS ONE, 2013, 8, e80493.	2.5	14
39	Functional Environmental Screening of a Metagenomic Library Identifies <i>stlA</i> ; A Unique Salt Tolerance Locus from the Human Gut Microbiome. PLoS ONE, 2013, 8, e82985.	2.5	39
40	Antiviral potential of 4-hydroxy panduratin A, secondary metabolite of Fingerroot, <i>Boesenbergia pandurata</i> (Schult.), towards Japanese Encephalitis virus NS2B/NS3 prote. Bioinformatics, 2013, 9, 54-60.	0.5	19
41	AIDA: ab initio domain assembly server. Nucleic Acids Research, 2014, 42, W308-W313.	14.5	47
42	A Novel Highly Divergent Protein Family Identified from a Viviparous Insect by RNA-seq Analysis: A Potential Target for Tsetse Fly-Specific Abortifacients. PLoS Genetics, 2014, 10, e1003874.	3.5	46
43	Plant 4/1 protein: potential player in intracellular, cell-to-cell and long-distance signaling. Frontiers in Plant Science, 2014, 5, 26.	3.6	21
44	Nucleotide Variability at Its Limit? Insights into the Number and Evolutionary Dynamics of the Sex-Determining Specificities of the Honey Bee <i>Apis mellifera</i> . Molecular Biology and Evolution, 2014, 31, 272-287.	8.9	35
45	Molecular basis for the fold organization and sarcomeric targeting of the muscle atrogin MuRF1. Open Biology, 2014, 4, 130172.	3.6	17
46	Further experiments in biocomputational structural analysis of malware. , 2014, , .		8
47	Improved PEP-FOLD Approach for Peptide and Mini-protein Structure Prediction. Journal of Chemical Theory and Computation, 2014, 10, 4745-4758.	5.3	525
48	The expanded FindCore method for identification of a core atom set for assessment of protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2014, 82, 219-230.	2.6	20
49	Perforin-like protein PPLP2 permeabilizes the red blood cell membrane during egress of <i>Plasmodium falciparum</i> gametocytes. Cellular Microbiology, 2014, 16, 709-733.	2.1	106
50	Improving the orientation-dependent statistical potential using a reference state. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2383-2393.	2.6	9
51	From local structure to a global framework: recognition of protein folds. Journal of the Royal Society Interface, 2014, 11, 20131147.	3.4	11
52	Regulation of the <i>Rana sylvatica</i> brevinin-1SY antimicrobial peptide during development and in dorsal and ventral skin in response to freezing, anoxia, and dehydration. Journal of Experimental Biology, 2014, 217, 1392-401.	1.7	16
53	Computational modeling suggests dimerization of equine infectious anemia virus Rev is required for RNA binding. Retrovirology, 2014, 11, 115.	2.0	6
54	Interplay of I-TASSER and QUARK for template-based and ab initio protein structure prediction in CASP10. Proteins: Structure, Function and Bioinformatics, 2014, 82, 175-187.	2.6	98
55	Identification of multifunctional peptides from human milk. Peptides, 2014, 56, 84-93.	2.4	51

#	ARTICLE	IF	CITATIONS
56	Characterization of a New Bacteriocin from <i>Lactobacillus plantarum</i> LE5 and LE27 Isolated from Ensiled Corn. <i>Applied Biochemistry and Biotechnology</i> , 2014, 172, 3374-3389.	2.9	12
57	Improving fragment quality for de novo structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2240-2252.	2.6	10
58	Princeton_TIGRESS: Protein geometry refinement using simulations and support vector machines. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 794-814.	2.6	21
59	In-silico modelling and identification of a possible inhibitor of H1N1 virus. <i>Asian Pacific Journal of Tropical Disease</i> , 2014, 4, S467-S476.	0.5	5
60	MOLECULAR EVOLUTION OF GPCRS: Melanocortin/melanocortin receptors. <i>Journal of Molecular Endocrinology</i> , 2014, 52, T29-T42.	2.5	80
61	Signature Protein of the PVC Superphylum. <i>Applied and Environmental Microbiology</i> , 2014, 80, 440-445.	3.1	20
62	Protein folding and de novo protein design for biotechnological applications. <i>Trends in Biotechnology</i> , 2014, 32, 99-109.	9.3	127
63	FFAS-3D: improving fold recognition by including optimized structural features and template re-ranking. <i>Bioinformatics</i> , 2014, 30, 660-667.	4.1	97
64	HCV E2 core structures and mAbs: something is still missing. <i>Drug Discovery Today</i> , 2014, 19, 1964-1970.	6.4	27
65	One contact for every twelve residues allows robust and accurate topology-level protein structure modeling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 208-218.	2.6	87
66	Three-dimensional protein structure prediction: Methods and computational strategies. <i>Computational Biology and Chemistry</i> , 2014, 53, 251-276.	2.3	160
67	Structure of the VipA/B Type VI Secretion Complex Suggests a Contraction-State-Specific Recycling Mechanism. <i>Cell Reports</i> , 2014, 8, 20-30.	6.4	74
68	Emergence of structure through protein-protein interactions and pH changes in dually predicted coiled-coil and disordered regions of centrosomal proteins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 1808-1819.	2.3	9
69	Conserved and host-specific features of influenza virion architecture. <i>Nature Communications</i> , 2014, 5, 4816.	12.8	214
70	Molecular modeling and molecular dynamics simulations based structural analysis of the SG2NA protein variants. <i>BMC Research Notes</i> , 2014, 7, 446.	1.4	30
71	Evidence supporting the existence of a NUPR1-like family of helix-loop-helix chromatin proteins related to, yet distinct from, AT hook-containing HMG proteins. <i>Journal of Molecular Modeling</i> , 2014, 20, 2357.	1.8	15
72	A local landscape mapping method for protein structure prediction in the HP model. <i>Natural Computing</i> , 2014, 13, 309-319.	3.0	1
73	Predicting the molecular interactions of CRIP1a-cannabinoid 1 receptor with integrated molecular modeling approaches. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2014, 24, 1158-1165.	2.2	13

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74	Differentiation of <scp>DctA</scp> and <scp>DcuS</scp> function in the <scp>DctA</scp>/<scp>DcuS</scp> sensor complex of <scp><i>Escherichia coli</i></scp>: function of <scp>DctA</scp> as an activity switch and of <scp>DcuS</scp> as the <scp>C</scp>₄-dicarboxylate sensor. <i>Molecular Microbiology</i> , 2014, 94, 218-229.	2.5	24
75	Native and recombinant Pg-AMP1 show different antibacterial activity spectrum but similar folding behavior. <i>Peptides</i> , 2014, 55, 92-97.	2.4	8
76	Why Are the Truncated Cyclin Es More Effective CDK2 Activators than the Full-Length Isoforms?. <i>Biochemistry</i> , 2014, 53, 4612-4624.	2.5	16
77	Physics-based protein structure refinement through multiple molecular dynamics trajectories and structure averaging. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 196-207.	2.6	100
78	Bhageerath-H: A homology/ab initio hybrid server for predicting tertiary structures of monomeric soluble proteins. <i>BMC Bioinformatics</i> , 2014, 15, S7.	2.6	45
79	Evidence of recent interspecies horizontal gene transfer regarding nucleopolyhedrovirus infection of <i>Spodoptera frugiperda</i> . <i>BMC Genomics</i> , 2015, 16, 1008.	2.8	15
80	Protein Structure and Function Prediction Using I-TASSER. <i>Current Protocols in Bioinformatics</i> , 2015, 52, 5.8.1-5.8.15.	25.8	367
81	General overview on structure prediction of twilight-zone proteins. <i>Theoretical Biology and Medical Modelling</i> , 2015, 12, 15.	2.1	68
82	Identification of a novel dehydration responsive gene, <i>drp10</i>, from the African clawed frog, <i>Xenopus laevis</i>. <i>Journal of Experimental Zoology</i> , 2015, 323, 375-381.	1.2	4
84	A Novel Peptide-Binding Motifs Inference Approach to Understand Deoxynivalenol Molecular Toxicity. <i>Toxins</i> , 2015, 7, 1989-2005.	3.4	32
85	Extracellular matrix-associated proteins form an integral and dynamic system during <i>Pseudomonas aeruginosa</i> biofilm development. <i>Frontiers in Cellular and Infection Microbiology</i> , 2015, 5, 40.	3.9	48
86	A Multi-Objective Approach for Protein Structure Prediction Based on an Energy Model and Backbone Angle Preferences. <i>International Journal of Molecular Sciences</i> , 2015, 16, 15136-15149.	4.1	4
87	Advances in Understanding Carboxysome Assembly in <i>Prochlorococcus</i> and <i>Synechococcus</i> Implicate CsoS2 as a Critical Component. <i>Life</i> , 2015, 5, 1141-1171.	2.4	82
88	The Road to Metagenomics: From Microbiology to DNA Sequencing Technologies and Bioinformatics. <i>Frontiers in Genetics</i> , 2015, 6, 348.	2.3	252
89	Model-driven discovery of synergistic inhibitors against <i>E. coli</i> and <i>S. enterica</i> serovar Typhimurium targeting a novel synthetic lethal pair, <i>aldA</i> and <i>prpC</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 958.	3.5	8
90	Abundant Intergenic TAACTGA Direct Repeats and Putative Alternate RNA Polymerase β Subunits in Marine Beggiatoaceae Genomes: Possible Regulatory Roles and Origins. <i>Frontiers in Microbiology</i> , 2015, 6, 1397.	3.5	5
91	The Bactofilin Cytoskeleton Protein BacM of <i>Myxococcus xanthus</i> Forms an Extended β -Sheet Structure Likely Mediated by Hydrophobic Interactions. <i>PLoS ONE</i> , 2015, 10, e0121074.	2.5	18
92	Cysteine-Rich Atrial Secretory Protein from the Snail <i>Achatina achatina</i> : Purification and Structural Characterization. <i>PLoS ONE</i> , 2015, 10, e0138787.	2.5	5

#	ARTICLE	IF	CITATIONS
93	CCP4 Software Suite: history, evolution, content, challenges and future developments. <i>Arbor</i> , 2015, 191, a220.	0.3	4
94	Control of Ethanol Sensitivity of the Glycine Receptor $\alpha 3$ Subunit by Transmembrane 2, the Intracellular Splice Cassette and C-Terminal Domain. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2015, 353, 80-90.	2.5	16
95	Customised fragments libraries for protein structure prediction based on structural class annotations. <i>BMC Bioinformatics</i> , 2015, 16, 136.	2.6	20
96	Large-scale model quality assessment for improving protein tertiary structure prediction. <i>Bioinformatics</i> , 2015, 31, i116-i123.	4.1	55
97	Scaling Ab Initio Predictions of 3D Protein Structures in Microsoft Azure Cloud. <i>Journal of Grid Computing</i> , 2015, 13, 561-585.	3.9	30
98	A multiobjective approach for protein structure prediction using a steady-state genetic algorithm with phenotypic crowding. , 2015, , .		6
99	TMFoldWeb: a web server for predicting transmembrane protein fold class. <i>Biology Direct</i> , 2015, 10, 54.	4.6	8
100	Modeling three-dimensional structure of two closely related Ni-Fe hydrogenases. <i>Photosynthesis Research</i> , 2015, 125, 341-353.	2.9	5
101	Improving accuracy of protein contact prediction using balanced network deconvolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 485-496.	2.6	22
102	KECSA-Movable Type Implicit Solvation Model (KMTISM). <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 667-682.	5.3	19
103	AIDA: ab initio domain assembly for automated multi-domain protein structure prediction and domain-domain interaction prediction. <i>Bioinformatics</i> , 2015, 31, 2098-2105.	4.1	59
104	Optimized distance-dependent atom-pair-based potential DOOP for protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 881-890.	2.6	11
105	Molecular level biodegradation of phenol and its derivatives through dmp operon of <i>Pseudomonas putida</i> : A bio-molecular modeling and docking analysis. <i>Journal of Environmental Sciences</i> , 2015, 36, 144-151.	6.1	11
106	I-TASSER server: new development for protein structure and function predictions. <i>Nucleic Acids Research</i> , 2015, 43, W174-W181.	14.5	1,897
107	Temperature dependent dynamics of DegP-trimer: A molecular dynamics study. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 329-338.	4.1	3
108	Fusion of selected regions of mycobacterial antigens for enhancing sensitivity in serodiagnosis of tuberculosis. <i>Journal of Microbiological Methods</i> , 2015, 115, 104-111.	1.6	13
109	Exploring the speed and performance of molecular replacement with AMPLE using QUARK ab initio protein models. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 338-343.	2.5	25
110	The Complete Sequence of the First <i>Spodoptera frugiperda</i> Betabaculovirus Genome: A Natural Multiple Recombinant Virus. <i>Viruses</i> , 2015, 7, 394-421.	3.3	23

#	ARTICLE	IF	CITATIONS
111	Lipopolysaccharide-Binding Motif Derived Peptides Induce Cell Membrane Damages in Human Lung Cancer and Hepatoma Cell Lines. <i>International Journal of Peptide Research and Therapeutics</i> , 2015, 21, 313-324.	1.9	1
112	Predicting Three-Dimensional Conformations of Peptides Constructed of Only Glycine, Alanine, Aspartic Acid, and Valine. <i>Origins of Life and Evolution of Biospheres</i> , 2015, 45, 183-193.	1.9	11
113	Phylogeny and evolution of plant macrophage migration inhibitory factor/D-dopachrome tautomerase-like proteins. <i>BMC Evolutionary Biology</i> , 2015, 15, 64.	3.2	31
114	Identifying a potential receptor for the antibacterial peptide of sponge <i>Axinella donnani</i> endosymbiont. <i>Gene</i> , 2015, 566, 166-174.	2.2	3
115	Proteogenomic Discovery of a Small, Novel Protein in Yeast Reveals a Strategy for the Detection of Unannotated Short Open Reading Frames. <i>Journal of Proteome Research</i> , 2015, 14, 5038-5047.	3.7	25
116	Evolution Strategies for Exploring Protein Energy Landscapes. , 2015, , .		5
117	Did Convergent Protein Evolution Enable Phytoplasmata to Generate "Zombie Plants"? <i>Trends in Plant Science</i> , 2015, 20, 798-806.	8.8	28
118	Design of symmetric TIM barrel proteins from first principles. <i>BMC Biochemistry</i> , 2015, 16, 18.	4.4	24
119	Prediction Enhancement of Residue Real-Value Relative Accessible Surface Area in Transmembrane Helical Proteins by Solving the Output Preference Problem of Machine Learning-Based Predictors. <i>Journal of Chemical Information and Modeling</i> , 2015, 55, 2464-2474.	5.4	19
120	Accurate disulfide-bonding network predictions improve <i>ab initio</i> structure prediction of cysteine-rich proteins. <i>Bioinformatics</i> , 2015, 31, 3773-3781.	4.1	36
121	Zeta Inhibitory Peptide Disrupts Electrostatic Interactions That Maintain Atypical Protein Kinase C in Its Active Conformation on the Scaffold p62. <i>Journal of Biological Chemistry</i> , 2015, 290, 21845-21856.	3.4	33
122	Soft computing methods for the prediction of protein tertiary structures: A survey. <i>Applied Soft Computing Journal</i> , 2015, 35, 398-410.	7.2	24
123	Crystal structure of designed PX domain from cytokine-independent survival kinase and implications on evolution-based protein engineering. <i>Journal of Structural Biology</i> , 2015, 191, 197-206.	2.8	9
124	Expression, purification and structural characterization of the type 1-specific ATP binding site of IP 3 receptor (IP 3 RI-ATPA). <i>Process Biochemistry</i> , 2015, 50, 1600-1606.	3.7	1
125	Overview of computational vaccinology: vaccine development through information technology. <i>Journal of Applied Genetics</i> , 2015, 56, 381-391.	1.9	17
126	Evidence for α -Helices in the Large Intracellular Domain Mediating Modulation of the α -1-Glycine Receptor by Ethanol and G β γ . <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2015, 352, 148-155.	2.5	18
127	Identification of candidate antimicrobial peptides derived from abalone hemocyanin. <i>Developmental and Comparative Immunology</i> , 2015, 49, 96-102.	2.3	53
128	Secondary and Tertiary Structure Prediction of Proteins: A Bioinformatic Approach. <i>Studies in Fuzziness and Soft Computing</i> , 2015, , 541-569.	0.8	6

#	ARTICLE	IF	CITATIONS
129	Protein structure prediction provides comparable performance to crystallographic structures in docking-based virtual screening. <i>Methods</i> , 2015, 71, 77-84.	3.8	25
130	Hb Wilde and Hb Patagonia: two novel elongated beta-globin variants causing dominant beta-thalassemia. <i>European Journal of Haematology</i> , 2015, 94, 498-503.	2.2	4
131	Analysis of regulatory mechanism after ErbB4 gene mutation based on local modeling methodology. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.2	3
132	Ribosome-RelA structures reveal the mechanism of stringent response activation. <i>ELife</i> , 2016, 5, .	6.0	143
133	The Receptor-Binding Domain in the VP1u Region of Parvovirus B19. <i>Viruses</i> , 2016, 8, 61.	3.3	33
134	Development of Monoclonal Antibody and Diagnostic Test for Middle East Respiratory Syndrome Coronavirus Using Cell-Free Synthesized Nucleocapsid Antigen. <i>Frontiers in Microbiology</i> , 2016, 7, 509.	3.5	32
135	Comparative Analysis of Type IV Pilin in Desulfuromonadales. <i>Frontiers in Microbiology</i> , 2016, 7, 2080.	3.5	14
136	Influence of Cysteine and Tryptophan Substitution on DNA-Binding Activity on Maize \pm -Hairpinin Antimicrobial Peptide. <i>Molecules</i> , 2016, 21, 1062.	3.8	33
137	GPO.4 from bacteriophage T7: in silico characterisation of its structure and interaction with E. coli FtsZ. <i>BMC Research Notes</i> , 2016, 9, 343.	1.4	3
138	Computational methods in drug discovery. <i>Beilstein Journal of Organic Chemistry</i> , 2016, 12, 2694-2718.	2.2	418
139	UniCon3D: <i>de novo</i> protein structure prediction using united-residue conformational search via stepwise, probabilistic sampling. <i>Bioinformatics</i> , 2016, 32, 2791-2799.	4.1	40
140	Computational modeling of Repeat1 region of INI1/hSNF5: An evolutionary link with ubiquitin. <i>Protein Science</i> , 2016, 25, 1593-1604.	7.6	1
141	Template-based protein structure prediction in <i>CASP11</i> and retrospect of <i>ASSER</i> in the last decade. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 233-246.	2.6	48
142	Integration of <i>QUARK</i> and <i>ASSER</i> for Ab Initio Protein Structure Prediction in <i>CASP11</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 76-86.	2.6	63
143	Massive integration of diverse protein quality assessment methods to improve template based modeling in <i>CASP11</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 247-259.	2.6	26
144	Mutational analysis and interactions of HBV preS1 with asialoglycoprotein receptor. <i>Future Virology</i> , 2016, 11, 761-774.	1.8	2
145	Evaluation of a combined energy fitness function for a distributed memetic algorithm to tackle the 3D protein structure prediction problem. , 2016, , .		1
146	Amyloid-like ribbons of amelogenins in enamel mineralization. <i>Scientific Reports</i> , 2016, 6, 23105.	3.3	73

#	ARTICLE	IF	CITATIONS
147	Functional and structural characterization of a novel putative cysteine protease cell wall-modifying multi-domain enzyme selected from a microbial metagenome. <i>Scientific Reports</i> , 2016, 6, 38031.	3.3	9
148	MIB: Metal Ion-Binding Site Prediction and Docking Server. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 2287-2291.	5.4	185
149	The unexpected structure of the designed protein Octarellin V.1 forms a challenge for protein structure prediction tools. <i>Journal of Structural Biology</i> , 2016, 195, 19-30.	2.8	15
150	Molecular Evolution of Alternative Oxidase Proteins: A Phylogenetic and Structure Modeling Approach. <i>Journal of Molecular Evolution</i> , 2016, 82, 207-218.	1.8	27
151	Accurate Structure Prediction and Conformational Analysis of Cyclic Peptides with Residue-Specific Force Fields. <i>Journal of Physical Chemistry Letters</i> , 2016, 7, 1805-1810.	4.6	50
152	Type III polyketide synthase repertoire in Zingiberaceae: computational insights into the sequence, structure and evolution. <i>Development Genes and Evolution</i> , 2016, 226, 269-285.	0.9	5
153	The function of the two-pore channel TPC1 depends on dimerization of its carboxy-terminal helix. <i>Cellular and Molecular Life Sciences</i> , 2016, 73, 2565-2581.	5.4	28
154	Structural and dynamic insights into the C-terminal extension of cysteine proteinase B from <i>Leishmania amazonensis</i> . <i>Journal of Molecular Graphics and Modelling</i> , 2016, 70, 30-39.	2.4	2
155	Is unphosphorylated Rex, as multifunctional protein of HTLV-1, a fully intrinsically disordered protein? An in silico study. <i>Biochemistry and Biophysics Reports</i> , 2016, 8, 14-22.	1.3	2
156	Domain Organization in the 54-kDa Subunit of the Chloroplast Signal Recognition Particle. <i>Biophysical Journal</i> , 2016, 111, 1151-1162.	0.5	7
157	A population-based conformational optimal algorithm using replica-exchange in ab-initio protein structure prediction. , 2016, , .		2
158	Cofactors-loaded quaternary structure of lysine-specific demethylase 5C (KDM5C) protein: Computational model. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1797-1809.	2.6	7
159	Identification of 2-oxohistidine Interacting Proteins Using E. coli Proteome Chips. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3581-3593.	3.8	3
160	Using Crowding-Distance in a Multiobjective Genetic Algorithm for Protein Structure Prediction. , 2016, , .		4
161	The Ep152R ORF of African swine fever virus strain Georgia encodes for an essential gene that interacts with host protein BAG6. <i>Virus Research</i> , 2016, 223, 181-189.	2.2	23
162	Recent advances in sequence-based protein structure prediction: Table 1. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw070.	6.5	26
163	Coagulation Factor XIII A Subunit Missense Mutations Affect Structure and Function at the Various Steps of Factor XIII Action. <i>Human Mutation</i> , 2016, 37, 1030-1041.	2.5	17
164	Protein ligand-specific binding residue predictions by an ensemble classifier. <i>BMC Bioinformatics</i> , 2016, 17, 470.	2.6	25

#	ARTICLE	IF	CITATIONS
165	The centrosomal Deubiquitylase USP21 regulates Gli1 transcriptional activity and stability.. Journal of Cell Science, 2016, 129, 4001-4013.	2.0	30
166	Solution structure of the microtubuleâ€targeting COS domain of MID1. FEBS Journal, 2016, 283, 3089-3102.	4.7	13
167	Structure models of G72, the product of a susceptibility gene to schizophrenia. Journal of Biochemistry, 2016, 161, mvw064.	1.7	3
168	A mutation in the atrial-specific myosin light chain gene (MYL4) causes familial atrial fibrillation. Nature Communications, 2016, 7, 11303.	12.8	106
169	LRFragLib: an effective algorithm to identify fragments for de novo protein structure prediction. Bioinformatics, 2017, 33, 677-684.	4.1	10
170	Simultaneous Optimization of Biomolecular Energy Functions on Features from Small Molecules and Macromolecules. Journal of Chemical Theory and Computation, 2016, 12, 6201-6212.	5.3	382
171	An anti-infective synthetic peptide with dual antimicrobial and immunomodulatory activities. Scientific Reports, 2016, 6, 35465.	3.3	105
172	Tertiary alphabet for the observable protein structural universe. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E7438-E7447.	7.1	60
173	Exploring Human Diseases and Biological Mechanisms by Protein Structure Prediction and Modeling. Advances in Experimental Medicine and Biology, 2016, 939, 39-61.	1.6	4
174	Folding and Stabilization of Native-Sequence-Reversed Proteins. Scientific Reports, 2016, 6, 25138.	3.3	6
175	Pseudocontact Shift-Driven Iterative Resampling for 3D Structure Determinations of Large Proteins. Journal of Molecular Biology, 2016, 428, 522-532.	4.2	26
176	Coarse-Grained Protein Models and Their Applications. Chemical Reviews, 2016, 116, 7898-7936.	47.7	721
177	The molecular organization of the beta-sheet region in Corneous beta-proteins (beta-keratins) of sauropsids explains its stability and polymerization into filaments. Journal of Structural Biology, 2016, 194, 282-291.	2.8	53
178	The phenotypic impact of the male-specific region of chromosome-Y in inbred mating: the role of genetic variants and gene duplications in multiple inbred rat strains. Biology of Sex Differences, 2016, 7, 10.	4.1	15
179	PEP-FOLD3: faster<i>de novo</i>structure prediction for linear peptides in solution and in complex. Nucleic Acids Research, 2016, 44, W449-W454.	14.5	703
180	Template based protein structure modeling by global optimization in <sc>CASP</sc>11. Proteins: Structure, Function and Bioinformatics, 2016, 84, 221-232.	2.6	28
181	Analysis of free modeling predictions by <sc>RBO</sc> aleph in <sc>CASP</sc>11. Proteins: Structure, Function and Bioinformatics, 2016, 84, 87-104.	2.6	9
182	Evaluation of free modeling targets in CASP11 and ROLL. Proteins: Structure, Function and Bioinformatics, 2016, 84, 51-66.	2.6	70

#	ARTICLE	IF	CITATIONS
183	Assessment of template-based modeling of protein structure in CASP11. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 200-220.	2.6	26
184	Looking into laminin receptor: critical discussion regarding the non-integrin 37/67 kDa laminin receptor/RPSA protein. <i>Biological Reviews</i> , 2016, 91, 288-310.	10.4	96
185	An Enhanced Genetic Algorithm for <i>Ab Initio</i> Protein Structure Prediction. <i>IEEE Transactions on Evolutionary Computation</i> , 2016, 20, 627-644.	10.0	29
186	A generative model for protein contact networks. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 1441-1454.	3.5	16
187	Guided macro-mutation in a graded energy based genetic algorithm for protein structure prediction. <i>Computational Biology and Chemistry</i> , 2016, 61, 162-177.	2.3	15
188	Structural characterization of ANGPTL8 (betatrophin) with its interacting partner lipoprotein lipase. <i>Computational Biology and Chemistry</i> , 2016, 61, 210-220.	2.3	41
189	Using a biomimetic membrane surface experiment to investigate the activity of the magnetite biomineralisation protein Mms6. <i>RSC Advances</i> , 2016, 6, 7356-7363.	3.6	32
190	Generating, Maintaining, and Exploiting Diversity in a Memetic Algorithm for Protein Structure Prediction. <i>Evolutionary Computation</i> , 2016, 24, 577-607.	3.0	38
191	The Use of Mn(II) Bound to His-tags as Genetically Encodable Spin-Label for Nanometric Distance Determination in Proteins. <i>Journal of Physical Chemistry Letters</i> , 2016, 7, 1072-1076.	4.6	22
192	A Novel Method Using Abstract Convex Underestimation in Ab-Initio Protein Structure Prediction for Guiding Search in Conformational Feature Space. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 887-900.	3.0	14
193	3DRobot: automated generation of diverse and well-packed protein structure decoys. <i>Bioinformatics</i> , 2016, 32, 378-387.	4.1	104
194	ResQ: An Approach to Unified Estimation of B-Factor and Residue-Specific Error in Protein Structure Prediction. <i>Journal of Molecular Biology</i> , 2016, 428, 693-701.	4.2	119
195	Enhancing Protein Conformational Space Sampling Using Distance Profile-Guided Differential Evolution. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 1288-1301.	3.0	35
196	Balancing exploration and exploitation in population-based sampling improves fragment-based <i>de novo</i> protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 852-858.	2.6	20
197	Electrostatic Stabilization Plays a Central Role in Autoinhibitory Regulation of the Na ⁺ ,K ⁺ -ATPase. <i>Biophysical Journal</i> , 2017, 112, 288-299.	0.5	22
198	Molecular modeling in the age of clinical genomics, the enterprise of the next generation. <i>Journal of Molecular Modeling</i> , 2017, 23, 75.	1.8	39
199	In-silico screening, identification and validation of a novel vaccine candidate in the fight against <i>Plasmodium falciparum</i> . <i>Parasitology Research</i> , 2017, 116, 1293-1305.	1.6	13
200	The genome of <i>Chenopodium quinoa</i> . <i>Nature</i> , 2017, 542, 307-312.	27.8	569

#	ARTICLE	IF	CITATIONS
201	VoroMQA: Assessment of protein structure quality using interatomic contact areas. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1131-1145.	2.6	149
202	Computational tools for exploring sequence databases as a resource for antimicrobial peptides. <i>Biotechnology Advances</i> , 2017, 35, 337-349.	11.7	111
203	Disclosing the Interaction of Carbonic Anhydrase IX with Cullin-Associated NEDD8-Dissociated Protein 1 by Molecular Modeling and Integrated Binding Measurements. <i>ACS Chemical Biology</i> , 2017, 12, 1460-1465.	3.4	17
204	Prediction of Protein Function from Theoretical Models. , 2017, , 467-498.		3
205	Identification of a conserved 8 aa insert in the PIP5K protein in the <i>Saccharomycetaceae</i> family of fungi and the molecular dynamics simulations and structural analysis to investigate its potential functional role. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1454-1467.	2.6	22
206	COFACTOR: improved protein function prediction by combining structure, sequence and protein-protein interaction information. <i>Nucleic Acids Research</i> , 2017, 45, W291-W299.	14.5	424
207	The myosin mesa and the basis of hypercontractility caused by hypertrophic cardiomyopathy mutations. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 525-533.	8.2	164
208	Protein structural motifs in prediction and design. <i>Current Opinion in Structural Biology</i> , 2017, 44, 161-167.	5.7	41
209	Structural investigation of a C-terminal EphA2 receptor mutant: Does mutation affect the structure and interaction properties of the Sam domain?. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1095-1104.	2.3	3
210	Validation of protein structure models using network similarity score. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1759-1776.	2.6	14
211	Antimicrobial activity predictors benchmarking analysis using shuffled and designed synthetic peptides. <i>Journal of Theoretical Biology</i> , 2017, 426, 96-103.	1.7	51
212	PTHrP(12-48) Modulates the Bone Marrow Microenvironment and Suppresses Human Osteoclast Differentiation and Lifespan. <i>Journal of Bone and Mineral Research</i> , 2017, 32, 1421-1431.	2.8	17
213	NeBcon: protein contact map prediction using neural network training coupled with naïve Bayes classifiers. <i>Bioinformatics</i> , 2017, 33, 2296-2306.	4.1	71
214	Block-restraining of residual dipolar couplings to allow fluctuating relative alignments of molecular subdomains. <i>Progress in Biophysics and Molecular Biology</i> , 2017, 128, 133-141.	2.9	0
215	Hierarchical Assembly of Tough Bioelastomeric Egg Capsules is Mediated by a Bundling Protein. <i>Biomacromolecules</i> , 2017, 18, 931-942.	5.4	4
216	Protein interaction evolution from promiscuity to specificity with reduced flexibility in an increasingly complex network. <i>Scientific Reports</i> , 2017, 7, 44948.	3.3	40
217	Computational protein structure refinement: almost there, yet still so far to go. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2017, 7, e1307.	14.6	57
218	Delineating distinct heme-scavenging and -binding functions of domains in MF6p/helminth defense molecule (HDM) proteins from parasitic flatworms. <i>Journal of Biological Chemistry</i> , 2017, 292, 8667-8682.	3.4	15

#	ARTICLE	IF	CITATIONS
219	Systems-level understanding of ethanol-induced stresses and adaptation in <i>E. coli</i> . <i>Scientific Reports</i> , 2017, 7, 44150.	3.3	43
220	Biogenic manganese oxide nanoparticle formation by a multimeric multicopper oxidase Mnx. <i>Nature Communications</i> , 2017, 8, 746.	12.8	65
221	Structures of transcription pre-initiation complex with TFIID and Mediator. <i>Nature</i> , 2017, 551, 204-209.	27.8	219
222	A conserved degron containing an amphipathic helix regulates the cholesterol-mediated turnover of human squalene monooxygenase, a rate-limiting enzyme in cholesterol synthesis. <i>Journal of Biological Chemistry</i> , 2017, 292, 19959-19973.	3.4	51
223	Double estimation of distribution guided sampling algorithm for de-novo protein structure prediction. , 2017, , .		1
224	Improving protein fold recognition by extracting fold-specific features from predicted residue-residue contacts. <i>Bioinformatics</i> , 2017, 33, 3749-3757.	4.1	47
225	Chemical Synthesis of the Highly Hydrophobic Antiviral Membrane-Associated Protein IFITM3 and Modified Variants. <i>Angewandte Chemie</i> , 2017, 129, 12813-12817.	2.0	11
226	Chemical Synthesis of the Highly Hydrophobic Antiviral Membrane-Associated Protein IFITM3 and Modified Variants. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 12639-12643.	13.8	35
227	Publisher's note. <i>Journal of Molecular Graphics and Modelling</i> , 2017, 77, 280.	2.4	1
228	Novel Organelles with Elements of Bacterial and Eukaryotic Secretion Systems Weaponize Parasites of <i>Drosophila</i> . <i>Current Biology</i> , 2017, 27, 2869-2877.e6.	3.9	37
229	Expanding the genetic heterogeneity of intellectual disability. <i>Human Genetics</i> , 2017, 136, 1419-1429.	3.8	122
230	Probing Medin Monomer Structure and its Amyloid Nucleation Using ¹³ C-Direct Detection NMR in Combination with Structural Bioinformatics. <i>Scientific Reports</i> , 2017, 7, 45224.	3.3	13
231	FOXP2 variation in great ape populations offers insight into the evolution of communication skills. <i>Scientific Reports</i> , 2017, 7, 16866.	3.3	27
232	Measuring the Conformational Distance of GPCR-related Proteins Using a Joint-based Descriptor. <i>Scientific Reports</i> , 2017, 7, 15205.	3.3	1
233	Conformational Space Sampling Method Using Multi-Subpopulation Differential Evolution for De novo Protein Structure Prediction. <i>IEEE Transactions on Nanobioscience</i> , 2017, 16, 618-633.	3.3	8
234	A bacterial negative transcription regulator binding on an inverted repeat in the promoter for epothilone biosynthesis. <i>Microbial Cell Factories</i> , 2017, 16, 92.	4.0	8
235	A Plastid Protein That Evolved from Ubiquitin and Is Required for Apicoplast Protein Import in <i>Toxoplasma gondii</i> . <i>MBio</i> , 2017, 8, .	4.1	25
236	KDF1, encoding keratinocyte differentiation factor 1, is mutated in a multigenerational family with ectodermal dysplasia. <i>Human Genetics</i> , 2017, 136, 99-105.	3.8	18

#	ARTICLE	IF	CITATIONS
237	Mapping of Functional Subdomains in the Terminal Protein Domain of Hepatitis B Virus Polymerase. <i>Journal of Virology</i> , 2017, 91, .	3.4	13
238	Performance of ZDOCK and IRAD in CAPRI rounds 28-34. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 408-416.	2.6	13
239	PGLa-H tandem-repeat peptides active against multidrug resistant clinical bacterial isolates. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2017, 1859, 228-237.	2.6	23
240	A protein structure refinement method using bi-objective particle swarm optimization algorithm. , 2017, , .		1
241	Protein structure prediction on 2D square HP lattice with revised fitness function. , 2017, , .		3
242	Using an aggregation tree to arrange energy function terms for protein structure prediction. , 2017, , .		1
243	The Protein-Protein Interactions of Cannabinoid Receptor Interacting Protein 1a (CRIP1a) and Cannabinoid 1 Receptor: The Molecular Mechanism Study Through an Integrated Molecular Modeling Approach. , 2017, , 680-690.		0
244	An in silico and in vitro approach to elucidate the impact of residues flanking the cleavage scissile bonds of FVIII. <i>PLoS ONE</i> , 2017, 12, e0180456.	2.5	3
245	A preference-based multi-objective evolutionary strategy for Ab initio prediction of proteins. , 2017, , .		1
246	The association between an endothelial nitric oxide synthase gene polymorphism and coronary heart disease in young people and the underlying mechanism. <i>Molecular Medicine Reports</i> , 2018, 17, 3928-3934.	2.4	13
247	In silico optimization of a guava antimicrobial peptide enables combinatorial exploration for peptide design. <i>Nature Communications</i> , 2018, 9, 1490.	12.8	179
249	The D5 region of the intelectin domain is a new type of carbohydrate recognition domain in the intelectin gene family. <i>Developmental and Comparative Immunology</i> , 2018, 85, 150-160.	2.3	7
250	ALMOES: Archive information assisted multi-objective evolutionary strategy for ab initio protein structure prediction. <i>Knowledge-Based Systems</i> , 2018, 146, 58-72.	7.1	46
251	Structural and functional modeling of viral protein 5 of Infectious Bursal Disease Virus. <i>Virus Research</i> , 2018, 247, 55-60.	2.2	7
252	Prediction of Protein Configurational Entropy (Popcoen). <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 1811-1819.	5.3	11
253	The alpha helix 1 from the first conserved region of HIV1 gp120 is reconstructed in the short NQ21 peptide. <i>Archives of Biochemistry and Biophysics</i> , 2018, 638, 66-75.	3.0	9
254	Enhancing Evolutionary Couplings with Deep Convolutional Neural Networks. <i>Cell Systems</i> , 2018, 6, 65-74.e3.	6.2	97
255	Where Informatics Lags Chemistry Leads. <i>Biochemistry</i> , 2018, 57, 503-506.	2.5	18

#	ARTICLE	IF	CITATIONS
256	Familial and Somatic <i>BAP1</i> Mutations Inactivate ASXL1/2-Mediated Allosteric Regulation of BAP1 Deubiquitinase by Targeting Multiple Independent Domains. <i>Cancer Research</i> , 2018, 78, 1200-1213.	0.9	24
257	Structural mechanisms of centromeric nucleosome recognition by the kinetochore protein CENP-N. <i>Science</i> , 2018, 359, 339-343.	12.6	98
258	Exploring the association of rs10490924 polymorphism with age-related macular degeneration: An in silico approach. <i>Journal of Molecular Graphics and Modelling</i> , 2018, 80, 52-58.	2.4	2
259	Assessment of data-assisted prediction by inclusion of crosslinking/mass spectrometry and small angle X-ray scattering data in the 12 th Critical Assessment of protein Structure Prediction experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 215-227.	2.6	4
260	DNCON2: improved protein contact prediction using two-level deep convolutional neural networks. <i>Bioinformatics</i> , 2018, 34, 1466-1472.	4.1	148
261	Protein structure prediction. <i>International Journal of Modern Physics B</i> , 2018, 32, 1840009.	2.0	50
262	Prosystemin, a prohormone that modulates plant defense barriers, is an intrinsically disordered protein. <i>Protein Science</i> , 2018, 27, 620-632.	7.6	16
263	Chemical shift-based methods in NMR structure determination. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2018, 106-107, 1-25.	7.5	44
264	Interaction of N-terminal peptide analogues of the Na ⁺ ,K ⁺ -ATPase with membranes. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2018, 1860, 1282-1291.	2.6	26
265	Principal component analysis in protein tertiary structure prediction. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1850005.	0.8	4
266	Guiding exploration in conformational feature space with Lipschitz underestimation for ab-initio protein structure prediction. <i>Computational Biology and Chemistry</i> , 2018, 73, 105-119.	2.3	4
267	Antibacterial Activity Affected by the Conformational Flexibility in Glycine-Lysine Based α -Helical Antimicrobial Peptides. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 2924-2936.	6.4	48
268	High-throughput statistical screening of anti-infective peptides from natural antibacterial protein repertoire: Chemometric prediction, molecular modeling, and susceptibility analysis. <i>Journal of Chemometrics</i> , 2018, 32, e3026.	1.3	1
269	A Memetic Algorithm for 3D Protein Structure Prediction Problem. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 690-704.	3.0	24
270	Molecular dynamics recipes for genome research. <i>Briefings in Bioinformatics</i> , 2018, 19, 853-862.	6.5	23
271	Incorporation of Solvent Effect into Multi-Objective Evolutionary Algorithm for Improved Protein Structure Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1365-1378.	3.0	68
272	Finding the needle in the haystack: towards solving the protein-folding problem computationally. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2018, 53, 1-28.	5.2	31
273	Three-dimensional protein structure prediction based on memetic algorithms. <i>Computers and Operations Research</i> , 2018, 91, 160-177.	4.0	18

#	ARTICLE	IF	CITATIONS
274	Template-based and free modeling of IÄTASSER and QUARK pipelines using predicted contact maps in CASP12. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 136-151.	2.6	86
275	Nsp3 of coronaviruses: Structures and functions of a large multi-domain protein. <i>Antiviral Research</i> , 2018, 149, 58-74.	4.1	542
276	Identification of protein W, the elusive sixth subunit of the <i>Rhodospseudomonas palustris</i> reaction center-light harvesting 1 core complex. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2018, 1859, 119-128.	1.0	19
277	Inserting Co-Evolution Information from Contact Maps into a Multiobjective Genetic Algorithm for Protein Structure Prediction. , 2018, , .		3
278	Expression of a novel surfactant protein gene is associated with sites of extrapulmonary respiration in a lungless salamander. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20181589.	2.6	4
279	clustQ. , 2018, , .		8
280	Community Detection for Decoy Selection in Template-free Protein Structure Prediction. , 2018, , .		2
281	An Energy Landscape Treatment of Decoy Selection in Template-Free Protein Structure Prediction. <i>Computation</i> , 2018, 6, 39.	2.0	13
282	Towards Building a Coordinate Clustered Library for Template-Based Modeling of Protein Structures. , 2018, , .		1
283	Step IIIa: Biological Hit Discovery Through High-Throughput Screening (HTS): Random Approaches and Rational Design. , 2018, , 77-113.		0
284	Atomistic Details of Chymotrypsin Conformational Changes upon Adsorption on Silica. <i>ACS Biomaterials Science and Engineering</i> , 2018, 4, 4036-4050.	5.2	15
285	Study of specific nanoenvironments containing Î±-helices in all-Î± and (Î±+Î²)+(Î±/Î²) proteins. <i>PLoS ONE</i> , 2018, 13, e0200018.	2.5	2
286	Modification Targeting the "Rana Box" Motif of a Novel Nigrocin Peptide From <i>Hylarana latouchii</i> Enhances and Broadens Its Potency Against Multiple Bacteria. <i>Frontiers in Microbiology</i> , 2018, 9, 2846.	3.5	22
287	The translation of non-canonical open reading frames controls mucosal immunity. <i>Nature</i> , 2018, 564, 434-438.	27.8	159
288	THE-DB: a threading model database for comparative protein structure analysis of the <i>E. coli</i> K12 and human proteomes. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, , .	3.0	6
289	Systematic Comparison of Amber and Rosetta Energy Functions for Protein Structure Evaluation. <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 6015-6025.	5.3	20
290	Designed peptide with a flexible central motif from ranatuerins adapts its conformation to bacterial membranes. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2018, 1860, 2655-2668.	2.6	8
291	Modeling the Tertiary Structure of a Multi-domain Protein. , 2018, , .		0

#	ARTICLE	IF	CITATIONS
292	Structural Bioinformatics: Life Through The 3D Glasses. , 2018, , 191-253.		0
293	Selection and structural analysis of the NY25 peptide – A vaccine candidate from hemagglutinin of swine-origin Influenza H1N1. Microbial Pathogenesis, 2018, 125, 72-83.	2.9	3
294	Adoption of an improved PSO to explore a compound multi-objective energy function in protein structure prediction. Applied Soft Computing Journal, 2018, 72, 539-551.	7.2	26
295	Exploiting distant homologues for phasing through the generation of compact fragments, local fold refinement and partial solution combination. Acta Crystallographica Section D: Structural Biology, 2018, 74, 290-304.	2.3	30
296	Improved fragment-based protein structure prediction by redesign of search heuristics. Scientific Reports, 2018, 8, 13694.	3.3	12
297	Methods for Determining and Understanding Serpin Structure and Function: X-Ray Crystallography. Methods in Molecular Biology, 2018, 1826, 9-39.	0.9	2
298	Sequential search leads to faster, more efficient fragment-based <i>de novo</i> protein structure prediction. Bioinformatics, 2018, 34, 1132-1140.	4.1	12
299	Interactive structural analysis of TrCP1 and PER2 phosphoswitch binding through dynamics simulation assay. Archives of Biochemistry and Biophysics, 2018, 651, 34-42.	3.0	5
300	In Silico Characterization and Structural Modeling of Dermacentor andersoni p36 Immunosuppressive Protein. Advances in Bioinformatics, 2018, 2018, 1-12.	5.7	6
301	A Novel Method for Drug Screen to Regulate G Protein-Coupled Receptors in the Metabolic Network of Alzheimer’s Disease. BioMed Research International, 2018, 2018, 1-10.	1.9	2
302	The Hyr1 protein from the fungus Candida albicans is a cross kingdom immunotherapeutic target for Acinetobacter bacterial infection. PLoS Pathogens, 2018, 14, e1007056.	4.7	43
303	New insights into the structural dynamics of the kinase JNK3. Scientific Reports, 2018, 8, 9435.	3.3	24
304	Prediction of Cell-Penetrating Potential of Modified Peptides Containing Natural and Chemically Modified Residues. Frontiers in Microbiology, 2018, 9, 725.	3.5	58
305	From Extraction of Local Structures of Protein Energy Landscapes to Improved Decoy Selection in Template-Free Protein Structure Prediction. Molecules, 2018, 23, 216.	3.8	29
306	Employing immuno-affinity for the analysis of various microbial metabolites of the mycotoxin deoxynivalenol. Journal of Chromatography A, 2018, 1556, 81-87.	3.7	4
307	ARCIMBOLDO on coiled coils. Acta Crystallographica Section D: Structural Biology, 2018, 74, 194-204.	2.3	41
308	Evolutionary Analysis of the Lysine-Rich N-terminal Cytoplasmic Domains of the Gastric H ⁺ ,K ⁺ -ATPase and the Na ⁺ ,K ⁺ -ATPase. Journal of Membrane Biology, 2018, 251, 653-666.	2.1	13
309	Structural and Evolutionary Insights within the Polysaccharide Deacetylase Gene Family of Bacillus anthracis and Bacillus cereus. Genes, 2018, 9, 386.	2.4	14

#	ARTICLE	IF	CITATIONS
310	Specific binding between <i>Bacillus thuringiensis</i> Cry9Aa and Vip3Aa toxins synergizes their toxicity against Asiatic rice borer (<i>Chilo suppressalis</i>). <i>Journal of Biological Chemistry</i> , 2018, 293, 11447-11458.	3.4	33
311	Establishing the role of PLVAP in protein-losing enteropathy: a homozygous missense variant leads to an attenuated phenotype. <i>Journal of Medical Genetics</i> , 2018, 55, 779-784.	3.2	14
312	Antimicrobial and structural insights of a new snak-in-like peptide isolated from <i>Peltophorum dubium</i> (Fabaceae). <i>Amino Acids</i> , 2018, 50, 1245-1259.	2.7	25
313	Amino acid content of beta strands and alpha helices depends on their flanking secondary structure elements. <i>BioSystems</i> , 2018, 168, 45-54.	2.0	11
314	Structural basis of meiotic chromosome synapsis through SYCP1 self-assembly. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 557-569.	8.2	67
315	Joker: An algorithm to insert patterns into sequences for designing antimicrobial peptides. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 2043-2052.	2.4	53
316	Protein Structural Bioinformatics: An Overview. , 2019, , 445-459.		23
317	Ab initio Protein Structure Prediction. , 2019, , 62-76.		0
318	Cloud-Based Molecular Modeling Systems. , 2019, , 261-264.		0
319	Computational Tools for Structural Analysis of Proteins. , 2019, , 539-549.		0
320	Protein Three-Dimensional Structure Prediction. , 2019, , 497-511.		4
321	Mutations in RABL3 alter KRAS prenylation and are associated with hereditary pancreatic cancer. <i>Nature Genetics</i> , 2019, 51, 1308-1314.	21.4	47
322	Advances in protein structure prediction and design. <i>Nature Reviews Molecular Cell Biology</i> , 2019, 20, 681-697.	37.0	489
323	TOM40 Targets Atg2 to Mitochondria-Associated ER Membranes for Phagophore Expansion. <i>Cell Reports</i> , 2019, 28, 1744-1757.e5.	6.4	84
324	Anti-mullerian hormone receptor type II as a Potential Target for Antineoplastic Therapy. <i>Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry</i> , 2019, 13, 202-213.	0.4	3
325	Structural Mapping of Missense Mutations in the Pex1/Pex6 Complex. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3756.	4.1	15
326	The molecular nature of the 17 β -Estradiol binding site in the voltage- and Ca ²⁺ -activated K ⁺ (BK) channel β 1 subunit. <i>Scientific Reports</i> , 2019, 9, 9965.	3.3	14
327	Protein structure prediction using sparse NOE and RDC restraints with Rosetta in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1341-1350.	2.6	11

#	ARTICLE	IF	CITATIONS
328	Assembling multidomain protein structures through analogous global structural alignments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15930-15938.	7.1	104
329	Deep learning contact map guided protein structure prediction in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1149-1164.	2.6	180
330	Loop Enhanced Conformational Resampling Method for Protein Structure Prediction. <i>IEEE Transactions on Nanobioscience</i> , 2019, 18, 567-577.	3.3	0
331	Redirecting the immune response towards immunoprotective domains of a DNABII protein resolves experimental otitis media. <i>Npj Vaccines</i> , 2019, 4, 43.	6.0	28
332	Detecting distant-homology protein structures by aligning deep neural-network based contact maps. <i>PLoS Computational Biology</i> , 2019, 15, e1007411.	3.2	45
333	Reliable Generation of Native-Like Decoys Limits Predictive Ability in Fragment-Based Protein Structure Prediction. <i>Biomolecules</i> , 2019, 9, 612.	4.0	0
334	The mitoribosome-specific protein mS38 is preferentially required for synthesis of cytochrome c oxidase subunits. <i>Nucleic Acids Research</i> , 2019, 47, 5746-5760.	14.5	18
335	A new approach to biomining: Bioengineering surfaces for metal recovery from aqueous solutions. <i>Scientific Reports</i> , 2019, 9, 16422.	3.3	16
336	AngularQA: Protein Model Quality Assessment with LSTM Networks. <i>Computational and Mathematical Biophysics</i> , 2019, 7, 1-9.	1.1	33
337	Fueling ab initio folding with marine metagenomics enables structure and function predictions of new protein families. <i>Genome Biology</i> , 2019, 20, 229.	8.8	28
338	Unevolved De Novo Proteins Have Innate Tendencies to Bind Transition Metals. <i>Life</i> , 2019, 9, 8.	2.4	8
339	Applications of Molecular Dynamics Simulation in Structure Prediction of Peptides and Proteins. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 1162-1170.	4.1	73
340	Protein model accuracy estimation based on local structure quality assessment using 3D convolutional neural network. <i>PLoS ONE</i> , 2019, 14, e0221347.	2.5	28
341	Structure-function relationship of an Urokinase Receptor-derived peptide which inhibits the Formyl Peptide Receptor type 1 activity. <i>Scientific Reports</i> , 2019, 9, 12169.	3.3	11
342	Mechanism of stimulation of DNA binding of the transcription factors by human apurinic/aprimidinic endonuclease 1, APE1. <i>DNA Repair</i> , 2019, 82, 102698.	2.8	24
343	Structural and dynamic studies reveal that the Ala-rich region of ataxin-7 initiates α -helix formation of the polyQ tract but suppresses its aggregation. <i>Scientific Reports</i> , 2019, 9, 7481.	3.3	13
344	The Arginines in the N-Terminus of the Porcine Circovirus 2 Virus-like Particles Are Responsible for Disrupting the Membranes at Neutral and Acidic pH. <i>Journal of Molecular Biology</i> , 2019, 431, 3261-3274.	4.2	4
345	Redesigning Arenicin-1, an Antimicrobial Peptide from the Marine Polychaeta <i>Arenicola marina</i> , by Strand Rearrangement or Branching, Substitution of Specific Residues, and Backbone Linearization or Cyclization. <i>Marine Drugs</i> , 2019, 17, 376.	4.6	28

#	ARTICLE	IF	CITATIONS
346	Mode-of-Action-Guided, Molecular Modeling-Based Toxicity Prediction: A Novel Approach for In Silico Predictive Toxicology. Challenges and Advances in Computational Chemistry and Physics, 2019, , 99-118.	0.6	2
347	A Meta-proteogenomic Approach to Peptide Identification Incorporating Assembly Uncertainty and Genomic Variation. Molecular and Cellular Proteomics, 2019, 18, S183-S192.	3.8	17
348	A novel biallelic loss-of-function mutation in <i>TMCO1</i> gene confirming and expanding the phenotype spectrum of cerebrofaciothoracic dysplasia. American Journal of Medical Genetics, Part A, 2019, 179, 1338-1345.	1.2	9
349	Balancing multiple objectives in conformation sampling to control decoy diversity in template-free protein structure prediction. BMC Bioinformatics, 2019, 20, 211.	2.6	20
350	Computational structural enzymology methodologies for the study and engineering of fatty acid synthases, polyketide synthases and nonribosomal peptide synthetases. Methods in Enzymology, 2019, 622, 375-409.	1.0	11
351	End-to-End Differentiable Learning of Protein Structure. Cell Systems, 2019, 8, 292-301.e3.	6.2	278
352	Molecular architecture, polar targeting and biogenesis of the Legionella Dot/Icm T4SS. Nature Microbiology, 2019, 4, 1173-1182.	13.3	80
353	Performance comparison of ab initio protein structure prediction methods. Ain Shams Engineering Journal, 2019, 10, 713-719.	6.1	7
354	I-TASSER gateway: A protein structure and function prediction server powered by XSEDE. Future Generation Computer Systems, 2019, 99, 73-85.	7.5	80
355	Epidemic Clostridioides difficile Ribotype 027 Lineages: Comparisons of Texas Versus Worldwide Strains. Open Forum Infectious Diseases, 2019, 6, ofz013.	0.9	14
356	Graph-Based Community Detection for Decoy Selection in Template-Free Protein Structure Prediction. Molecules, 2019, 24, 854.	3.8	9
357	Educational Material about Influenza Viruses. Viruses, 2019, 11, 231.	3.3	6
358	Variants in DOCK3 cause developmental delay and hypotonia. European Journal of Human Genetics, 2019, 27, 1225-1234.	2.8	15
359	Simulation Studies of Amyloidogenic Polypeptides and Their Aggregates. Chemical Reviews, 2019, 119, 6956-6993.	47.7	138
360	Constructing effective energy functions for protein structure prediction through broadening attraction-basin and reverse Monte Carlo sampling. BMC Bioinformatics, 2019, 20, 135.	2.6	1
361	β -Sheet Super-Secondary Motifs: Sequence, Structural Overview, and Pursuit of Potential Autonomously Folding Sequences from β -TIM Barrels. Methods in Molecular Biology, 2019, 1958, 221-236.	0.9	2
362	Learning Organizations of Protein Energy Landscapes: An Application on Decoy Selection in Template-Free Protein Structure Prediction. Methods in Molecular Biology, 2019, 1958, 147-171.	0.9	2
363	Modeling of Disordered Protein Structures Using Monte Carlo Simulations and Knowledge-Based Statistical Force Fields. International Journal of Molecular Sciences, 2019, 20, 606.	4.1	45

#	ARTICLE	IF	CITATIONS
364	Generation and characterization of a specific single-chain antibody against DSPP as a prostate cancer biomarker: Involvement of bioinformatics-based design of novel epitopes. <i>International Immunopharmacology</i> , 2019, 69, 217-224.	3.8	4
365	Exploration of inositol 1,4,5-trisphosphate (IP3) regulated dynamics of N-terminal domain of IP3 receptor reveals early phase molecular events during receptor activation. <i>Scientific Reports</i> , 2019, 9, 2454.	3.3	8
366	Divergent Evolution of E1A CR3 in Human Adenovirus Species D. <i>Viruses</i> , 2019, 11, 143.	3.3	3
367	A combined computational strategy of sequence and structural analysis predicts the existence of a functional eicosanoid pathway in <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2019, 14, e0211897.	2.5	25
368	Non-Negative Matrix Factorization for Selection of Near-Native Protein Tertiary Structures. , 2019, , .		6
369	Building maps of protein structure spaces in template-free protein structure prediction. <i>Journal of Bioinformatics and Computational Biology</i> , 2019, 17, 1940013.	0.8	3
370	Structure determination of the CAMP factor of <i>Streptococcus agalactiae</i> with the aid of an MBP tag and insights into membrane-surface attachment. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 772-781.	2.3	7
371	Structural and Functional Analysis of human lung cancer risk associated hOGG1 variant Ser326Cys in DNA repair gene by molecular dynamics simulation. <i>Non-coding RNA Research</i> , 2019, 4, 109-119.	4.6	5
372	Enhanced GROMACS: toward a better numerical simulation framework. <i>Journal of Molecular Modeling</i> , 2019, 25, 355.	1.8	43
373	Molecular Interaction between Distal C-Terminal Domain of the CB ₁ Cannabinoid Receptor and Cannabinoid Receptor Interacting Proteins (CRIP1a/CRIP1b). <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 5294-5303.	5.4	4
374	GRSA Enhanced for Protein Folding Problem in the Case of Peptides. <i>Axioms</i> , 2019, 8, 136.	1.9	2
375	ABC ATPases Involved in Protein Synthesis, Ribosome Assembly and Antibiotic Resistance: Structural and Functional Diversification across the Tree of Life. <i>Journal of Molecular Biology</i> , 2019, 431, 3568-3590.	4.2	90
376	Identification and Verification of Ubiquitin-Activated Bacterial Phospholipases. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	9
377	Metallochaperone function of the self-subunit swapping chaperone involved in the maturation of subunit-cobalt nitrile hydratase. <i>Biotechnology and Bioengineering</i> , 2019, 116, 481-489.	3.3	11
378	Changing the Apoptosis Pathway through Evolutionary Protein Design. <i>Journal of Molecular Biology</i> , 2019, 431, 825-841.	4.2	16
379	Cadmium-induced conformational changes in type 2 metallothionein of medicinal plant <i>Coptis japonica</i> : insights from molecular dynamics studies of apo, partially and fully metalated forms. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 1520-1533.	3.5	12
380	Secondary Structure and Contact Guided Differential Evolution for Protein Structure Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 1068-1081.	3.0	29
381	Artificial intelligence-based multi-objective optimization protocol for protein structure refinement. <i>Bioinformatics</i> , 2020, 36, 437-448.	4.1	21

#	ARTICLE	IF	CITATIONS
382	Two-Stage Distance Feature-based Optimization Algorithm for De novo Protein Structure Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 2119-2130.	3.0	3
383	Polarity of the ATP binding site of the Na ⁺ ,K ⁺ -ATPase, gastric H ⁺ ,K ⁺ -ATPase and sarcoplasmic reticulum Ca ²⁺ -ATPase. Biochimica Et Biophysica Acta - Biomembranes, 2020, 1862, 183138.	2.6	10
384	CGLFold: a contact-assisted de novo protein structure prediction using global exploration and loop perturbation sampling algorithm. Bioinformatics, 2020, 36, 2443-2450.	4.1	36
385	Enhancement of metallomacrocyclic-based oxygen reduction catalysis through immobilization in a tunable silk-protein scaffold. Journal of Inorganic Biochemistry, 2020, 204, 110960.	3.5	3
386	CATHER: a novel threading algorithm with predicted contacts. Bioinformatics, 2020, 36, 2119-2125.	4.1	11
387	Competitive ubiquitination activates the tumor suppressor p53. Cell Death and Differentiation, 2020, 27, 1807-1818.	11.2	27
388	Characterization of p53 Family Homologs in Evolutionary Remote Branches of Holozoa. International Journal of Molecular Sciences, 2020, 21, 6.	4.1	40
389	Recent Perspectives on COVID-19 and Computer-Aided Virtual Screening of Natural Compounds for the Development of Therapeutic Agents Towards SARS-CoV-2. Methods in Pharmacology and Toxicology, 2020, , 433-471.	0.2	5
390	Interdomain Flexibility within NADPH Oxidase Suggested by SANS Using LMNG Stealth Carrier. Biophysical Journal, 2020, 119, 605-618.	0.5	9
391	Fast and Flexible Protein Design Using Deep Graph Neural Networks. Cell Systems, 2020, 11, 402-411.e4.	6.2	121
392	Mutations in the phosphorylation sites of SARS-CoV-2 encoded nucleocapsid protein and structure model of sequestration by protein 14-3-3. Biochemical and Biophysical Research Communications, 2020, 532, 134-138.	2.1	35
393	In silico modelling and virtual screening for identification of inhibitors for spore wall protein-5 in Nosema bombycis. Journal of Biomolecular Structure and Dynamics, 2022, 40, 1748-1763.	3.5	1
394	Unravelling the unfolding pathway of human Fas-activated serine/threonine kinase induced by urea. Journal of Biomolecular Structure and Dynamics, 2021, 39, 5516-5525.	3.5	1
395	Structural Requirements of the Phytoplasma Effector Protein SAP54 for Causing Homeotic Transformation of Floral Organs. Molecular Plant-Microbe Interactions, 2020, 33, 1129-1141.	2.6	9
396	DNA Binding Reorganizes the Intrinsically Disordered C-Terminal Region of PSC in Drosophila PRC1. Journal of Molecular Biology, 2020, 432, 4856-4871.	4.2	6
397	Optimization of Molecular Dynamics Simulations of c-MYC1-88 An Intrinsically Disordered System. Life, 2020, 10, 109.	2.4	10
398	In Silico Analysis and In Vitro Characterization of the Bioactive Profile of Three Novel Peptides Identified from 19 kDa Zein Sequences of Maize. Molecules, 2020, 25, 5405.	3.8	13
399	Protein storytelling through physics. Science, 2020, 370, .	12.6	49

#	ARTICLE	IF	CITATIONS
400	A New Protocol for Atomic-Level Protein Structure Modeling and Refinement Using Low-to-Medium Resolution Cryo-EM Density Maps. <i>Journal of Molecular Biology</i> , 2020, 432, 5365-5377.	4.2	26
401	Functional Pangenome Analysis Shows Key Features of E Protein Are Preserved in SARS and SARS-CoV-2. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 405.	3.9	40
402	Molecular characterisation of ILRUN, a novel inhibitor of proinflammatory and antimicrobial cytokines. <i>Heliyon</i> , 2020, 6, e04115.	3.2	15
403	Structural signatures in EPR3 define a unique class of plant carbohydrate receptors. <i>Nature Communications</i> , 2020, 11, 3797.	12.8	31
404	Structure of fish Toll-like receptors (TLR) and NOD-like receptors (NLR). <i>International Journal of Biological Macromolecules</i> , 2020, 161, 1602-1617.	7.5	99
405	A highly potential cleavable linker for tumor targeting antibody-chemokines. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, , 1-11.	3.5	10
406	KOBRA: a fluctuating elastic rod model for slender biological macromolecules. <i>Soft Matter</i> , 2020, 16, 7544-7555.	2.7	4
407	A Poplar Rust Effector Protein Associates with Protein Disulfide Isomerase and Enhances Plant Susceptibility. <i>Biology</i> , 2020, 9, 294.	2.8	8
408	A Completely <i>De Novo</i> ATPase from Combinatorial Protein Design. <i>Journal of the American Chemical Society</i> , 2020, 142, 15230-15234.	13.7	9
409	Sequence-based protein structure optimization using enhanced simulated annealing algorithm on a coarse-grained model. <i>Journal of Molecular Modeling</i> , 2020, 26, 250.	1.8	2
410	Overproduction of the AlgT Sigma Factor Is Lethal to Mucoid <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	4
411	Structural basis of client specificity in mitochondrial membrane-protein chaperones. <i>Science Advances</i> , 2020, 6, .	10.3	21
412	Decoy selection for protein structure prediction via extreme gradient boosting and ranking. <i>BMC Bioinformatics</i> , 2020, 21, 189.	2.6	5
413	The VP1u of Human Parvovirus B19: A Multifunctional Capsid Protein with Biotechnological Applications. <i>Viruses</i> , 2020, 12, 1463.	3.3	7
414	The cytoplasmic tail of influenza A/H1N1 virus hemagglutinin is β -structural. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 4642-4661.	3.5	5
415	Enhancing fragment-based protein structure prediction by customising fragment cardinality according to local secondary structure. <i>BMC Bioinformatics</i> , 2020, 21, 170.	2.6	7
416	Cathelicidin-DM is an Antimicrobial Peptide from <i>Duttaphrynus melanostictus</i> and Has Wound-Healing Therapeutic Potential. <i>ACS Omega</i> , 2020, 5, 9301-9310.	3.5	24
417	Reducing Ensembles of Protein Tertiary Structures Generated De Novo via Clustering. <i>Molecules</i> , 2020, 25, 2228.	3.8	6

#	ARTICLE	IF	CITATIONS
418	Molecular, Evolutionary, and Structural Analysis of the Terminal Protein Domain of Hepatitis B Virus Polymerase, a Potential Drug Target. <i>Viruses</i> , 2020, 12, 570.	3.3	10
419	Selenoprotein T: An Essential Oxidoreductase Serving as a Guardian of Endoplasmic Reticulum Homeostasis. <i>Antioxidants and Redox Signaling</i> , 2020, 33, 1257-1275.	5.4	34
420	Structure-guided rational design of the substrate specificity and catalytic activity of an enzyme. <i>Methods in Enzymology</i> , 2020, 643, 181-202.	1.0	4
421	Incorporating a multiobjective knowledge-based energy function into differential evolution for protein structure prediction. <i>Information Sciences</i> , 2020, 540, 69-88.	6.9	15
422	Performance of human and server prediction in <scp>CAPRI</scp> rounds 38â€45. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1110-1120.	2.6	6
423	In silico structure prediction of full-length cotton cellulose synthase protein (GhCESA1) and its hierarchical complexes. <i>Cellulose</i> , 2020, 27, 5597-5616.	4.9	13
424	Monoclonal IgM Antibodies Targeting <i>Candida albicans</i> Hyr1 Provide Cross-Kingdom Protection Against Gram-Negative Bacteria. <i>Frontiers in Immunology</i> , 2020, 11, 76.	4.8	11
425	Pervasive functional translation of noncanonical human open reading frames. <i>Science</i> , 2020, 367, 1140-1146.	12.6	400
426	De novo Protein Structure Prediction by Coupling Contact With Distance Profile. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 395-406.	3.0	10
427	Alzheimerâ€™s disease: unraveling APOE4 binding to amyloid-beta peptide and lipids with molecular dynamics and quantum mechanics. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 5026-5032.	3.5	3
428	Structural Determinants of Insulin Release: Disordered N-Terminal Tail of Kir6.2 Affects Potassium Channel Dynamics through Interactions with Sulfonyleurea Binding Region in a SUR1 Partner. <i>Journal of Physical Chemistry B</i> , 2020, 124, 6198-6211.	2.6	11
429	Characterization and Optimization of the Novel Transient Receptor Potential Melastatin 2 Antagonist tatM2NX. <i>Molecular Pharmacology</i> , 2020, 97, 102-111.	2.3	11
430	Exploring the high selectivity of 3-D protein structures using distributed memetic algorithms. <i>Journal of Computational Science</i> , 2020, 41, 101087.	2.9	3
431	Structural proteomics, electron cryo-microscopy and structural modeling approaches in bacteriaâ€™human protein interactions. <i>Medical Microbiology and Immunology</i> , 2020, 209, 265-275.	4.8	13
432	Complement C9 binding site and the anti-microbial activity of caprine vitronectin are localized in close proximity in the N-terminal region of the protein. <i>Microbial Pathogenesis</i> , 2020, 149, 104111.	2.9	3
433	Hyper-phosphorylation of nsp2-related proteins of porcine reproductive and respiratory syndrome virus. <i>Virology</i> , 2020, 543, 63-75.	2.4	3
434	SPECS: Integration of side-chain orientation and global distance-based measures for improved evaluation of protein structural models. <i>PLoS ONE</i> , 2020, 15, e0228245.	2.5	5
435	Hup-Type Hydrogenases of Purple Bacteria: Homology Modeling and Computational Assessment of Biotechnological Potential. <i>International Journal of Molecular Sciences</i> , 2020, 21, 366.	4.1	4

#	ARTICLE	IF	CITATIONS
436	Transit of Procaspase-9 towards its activation. New mechanistic insights from molecular dynamics simulations. <i>Journal of Molecular Modeling</i> , 2020, 26, 24.	1.8	2
437	In silico Studies on Antimicrobial Peptide (AMP) in Leeches. <i>International Journal of Peptide Research and Therapeutics</i> , 2020, 26, 2253-2267.	1.9	2
438	Rational Design Principles of Attenuated Cationic Lytic Peptides for Intracellular Delivery of Biomacromolecules. <i>Molecular Pharmaceutics</i> , 2020, 17, 2175-2185.	4.6	15
439	Multifunctional Acidocin 4356 Combats <i>Pseudomonas aeruginosa</i> through Membrane Perturbation and Virulence Attenuation: Experimental Results Confirm Molecular Dynamics Simulation. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	5
440	Protein assembly systems in natural and synthetic biology. <i>BMC Biology</i> , 2020, 18, 35.	3.8	44
441	Functional characterization of an unknown soybean intrinsically disordered protein in vitro and in <i>Escherichia coli</i> . <i>International Journal of Biological Macromolecules</i> , 2021, 166, 538-549.	7.5	4
442	<i>CSU57</i> encodes a novel repressor of sorbose utilization in opportunistic human fungal pathogen <i>Candida albicans</i> . <i>Yeast</i> , 2021, 38, 222-238.	1.7	5
443	Electrostatic Potentials around the Proteins Preferably Crystallized by Ammonium Sulfate. <i>Crystal Growth and Design</i> , 2021, 21, 297-305.	3.0	5
444	Optogenetic control of <i>Neisseria meningitidis</i> Cas9 genome editing using an engineered, light-switchable anti-CRISPR protein. <i>Nucleic Acids Research</i> , 2021, 49, e29-e29.	14.5	25
445	Evaluation of a peptide motif designed for protein tethering to polymer surfaces. <i>Journal of Biomaterials Science, Polymer Edition</i> , 2021, 32, 76-92.	3.5	2
446	Protein Structure Prediction Using Population-Based Algorithm Guided by Information Entropy. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 697-707.	3.0	6
449	Oxidative Damage? Not a Problem! The Characterization of Humanin-like Mitochondrial Peptide in Anoxia Tolerant Freshwater Turtles. <i>Protein Journal</i> , 2021, 40, 87-107.	1.6	5
450	Computational Methods for the Elucidation of Protein Structure and Interactions. <i>Methods in Molecular Biology</i> , 2021, 2305, 23-52.	0.9	1
451	Molecular basis of tail-anchored integral membrane protein recognition by the cochaperone Sgt2. <i>Journal of Biological Chemistry</i> , 2021, 296, 100441.	3.4	15
452	Protein Analysis: From Sequence to Structure. , 2021, , 59-82.		0
453	ProMod3: A versatile homology modelling toolbox. <i>PLoS Computational Biology</i> , 2021, 17, e1008667.	3.2	161
454	Searching for an Identity: Functional Characterization of Taxonomically Restricted Genes in Grain Amaranth. <i>Compendium of Plant Genomes</i> , 2021, , 97-124.	0.5	5
456	In silico identification of novel open reading frames in <i>Plasmodium falciparum</i> oocyte and salivary gland sporozoites using proteogenomics framework. <i>Malaria Journal</i> , 2021, 20, 71.	2.3	1

#	ARTICLE	IF	CITATIONS
457	The evolutionary conserved iron-sulfur protein TCR controls P700 oxidation in photosystem I. <i>IScience</i> , 2021, 24, 102059.	4.1	3
458	Highly sensitive clinical diagnostic method for PTPRZ1-MET and the characteristic protein structure contributing to ligand-independent MET activation. <i>CNS Neuroscience and Therapeutics</i> , 2021, 27, 617-628.	3.9	7
459	Effect of the p53 P72R Polymorphism on Mutant TP53 Allele Selection in Human Cancer. <i>Journal of the National Cancer Institute</i> , 2021, 113, 1246-1257.	6.3	16
460	Exploring Obscurin and SPEG Kinase Biology. <i>Journal of Clinical Medicine</i> , 2021, 10, 984.	2.4	12
461	Molecular Characterization of the Von Willebrand Factor Type D Domain of Vitellogenin from <i>Takifugu flavidus</i> . <i>Marine Drugs</i> , 2021, 19, 181.	4.6	7
462	Development of new vaccine target against SARS-CoV2 using envelope (E) protein: An evolutionary, molecular modeling and docking based study. <i>International Journal of Biological Macromolecules</i> , 2021, 172, 74-81.	7.5	12
464	Structural and functional characterization of a putative de novo gene in <i>Drosophila</i> . <i>Nature Communications</i> , 2021, 12, 1667.	12.8	40
465	Phenotypic characterization and predictive analysis of p.Asp47Asn LDL receptor mutation associated with Familial Hypercholesterolemia in a Chilean population. <i>Journal of Clinical Lipidology</i> , 2021, 15, 366-374.e1.	1.5	0
466	Purification and characterization of a novel and conserved TPR-domain protein that binds both Hsp90 and Hsp70 and is expressed in all developmental stages of <i>Leishmania major</i> . <i>Biochimie</i> , 2021, 182, 51-60.	2.6	2
467	Remodelling structure-based drug design using machine learning. <i>Emerging Topics in Life Sciences</i> , 2021, 5, 13-27.	2.6	6
469	Protein Structure Refinement Using Multi-Objective Particle Swarm Optimization with Decomposition Strategy. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4408.	4.1	1
470	The Nesprin-1/2 ortholog ANC-1 regulates organelle positioning in <i>C. elegans</i> independently from its KASH or actin-binding domains. <i>ELife</i> , 2021, 10, .	6.0	21
472	A Peptides Prediction Methodology for Tertiary Structure Based on Simulated Annealing. <i>Mathematical and Computational Applications</i> , 2021, 26, 39.	1.3	3
473	Current directions in combining simulation-based macromolecular modeling approaches with deep learning. <i>Expert Opinion on Drug Discovery</i> , 2021, 16, 1025-1044.	5.0	8
476	Simulation of the Positive Inotropic Peptide S100A1ct in Aqueous Environment by Gaussian Accelerated Molecular Dynamics. <i>Journal of Physical Chemistry B</i> , 2021, 125, 4654-4666.	2.6	3
477	Fisetin inhibits tau aggregation by interacting with the protein and preventing the formation of β^2 -strands. <i>International Journal of Biological Macromolecules</i> , 2021, 178, 381-393.	7.5	27
478	Genetic analysis of sinonasal undifferentiated carcinoma discovers recurrent SWI/SNF alterations and a novel PGAP3-SRPK1 fusion gene. <i>BMC Cancer</i> , 2021, 21, 636.	2.6	9
479	Crystal and solution structures reveal oligomerization of individual capsid homology domains of <i>Drosophila</i> Arc. <i>PLoS ONE</i> , 2021, 16, e0251459.	2.5	7

#	ARTICLE	IF	CITATIONS
480	Deep template-based protein structure prediction. <i>PLoS Computational Biology</i> , 2021, 17, e1008954.	3.2	19
481	Antibacterial effects assessment on some livestock pathogens, thermal stability and proposing a probable reason for different levels of activity of thanatin. <i>Scientific Reports</i> , 2021, 11, 10890.	3.3	3
482	Protein Predictive Modeling and Simulation of Mutations of Presenilin-1 Familial Alzheimer's Disease on the Orthosteric Site. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 649990.	3.5	3
483	The stabilization of yes-associated protein by TGF β -activated kinase 1 regulates the self-renewal and oncogenesis of gastric cancer stem cells. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 6584-6601.	3.6	5
484	Deep learning techniques have significantly impacted protein structure prediction and protein design. <i>Current Opinion in Structural Biology</i> , 2021, 68, 194-207.	5.7	77
485	A unique view of SARS-CoV-2 through the lens of ORF8 protein. <i>Computers in Biology and Medicine</i> , 2021, 133, 104380.	7.0	48
486	SLX4IP promotes RAP1 SUMOylation by PIAS1 to coordinate telomere maintenance through NF- κ B and Notch signaling. <i>Science Signaling</i> , 2021, 14, .	3.6	17
487	Crystal and solution structures of a novel antimicrobial peptide from <i>Chrysomya megacephala</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 894-903.	2.3	0
488	Identification of a protein unique to the genus <i>Plasmodium</i> that contains a WD40 repeat domain and extensive low-complexity sequence. <i>Parasitology Research</i> , 2021, 120, 2617-2629.	1.6	0
489	TopDomain: Exhaustive Protein Domain Boundary Metaprediction Combining Multisource Information and Deep Learning. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 4599-4613.	5.3	5
490	Computational generation of proteins with predetermined three-dimensional shapes using ProteinSolver. <i>STAR Protocols</i> , 2021, 2, 100505.	1.2	5
491	Notable sequence homology of the ORF10 protein introspects the architecture of SARS-CoV-2. <i>International Journal of Biological Macromolecules</i> , 2021, 181, 801-809.	7.5	36
492	Computational Methods and Tools in Antimicrobial Peptide Research. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 3172-3196.	5.4	51
495	Computational Simulation of Holin S105 in Membrane Bilayer and Its Dimerization Through a Helix-Turn-Helix Motif. <i>Journal of Membrane Biology</i> , 2021, 254, 397-407.	2.1	1
496	MMpred: a distance-assisted multimodal conformation sampling for <i>de novo</i> protein structure prediction. <i>Bioinformatics</i> , 2021, 37, 4350-4356.	4.1	22
497	Structure of the dihydrolipoamide succinyltransferase (E2) component of the human alpha-ketoglutarate dehydrogenase complex (hKGDHc) revealed by cryo-EM and cross-linking mass spectrometry: Implications for the overall hKGDHc structure. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2021, 1865, 129889.	2.4	23
498	Complementing sequence-derived features with structural information extracted from fragment libraries for protein structure prediction. <i>BMC Bioinformatics</i> , 2021, 22, 351.	2.6	1
499	Identification of promiscuous T cell epitopes on Mayaro virus structural proteins using immunoinformatics, molecular modeling, and QM:MM approaches. <i>Infection, Genetics and Evolution</i> , 2021, 91, 104826.	2.3	4

#	ARTICLE	IF	CITATIONS
500	Cryo-EM structure of the human ELMO1-DOCK5-Rac1 complex. <i>Science Advances</i> , 2021, 7, .	10.3	17
501	Development and structural characterisation of human scFv targeting MDM2 spliced variant MDM215kDa. <i>Molecular Immunology</i> , 2021, 135, 191-203.	2.2	3
502	A sequential niche multimodal conformational sampling algorithm for protein structure prediction. <i>Bioinformatics</i> , 2021, 37, 4357-4365.	4.1	11
503	Toward the solution of the protein structure prediction problem. <i>Journal of Biological Chemistry</i> , 2021, 297, 100870.	3.4	73
504	Integrative Structural Biology in the Era of Accurate Structure Prediction. <i>Journal of Molecular Biology</i> , 2021, 433, 167127.	4.2	36
505	Protein structure prediction using deep learning distance and hydrogen bonding restraints in <sc>CASP14</sc>. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1734-1751.	2.6	53
506	The bacteriophage LUZ24 œlygœ peptide inhibits the <i>Pseudomonas</i> DNA gyrase. <i>Cell Reports</i> , 2021, 36, 109567.	6.4	15
507	Improving fragment-based ab initio protein structure assembly using low-accuracy contact-map predictions. <i>Nature Communications</i> , 2021, 12, 5011.	12.8	44
508	Activation of the Type VI Secretion System in the Squid Symbiont <i>Vibrio fischeri</i> Requires the Transcriptional Regulator TasR and the Structural Proteins TssM and TssA. <i>Journal of Bacteriology</i> , 2021, 203, e0039921.	2.2	11
509	Distance-guided protein folding based on generalized descent direction. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	3
510	A <i>de novo</i> protein structure prediction by iterative partition sampling, topology adjustment and residue-level distance deviation optimization. <i>Bioinformatics</i> , 2021, 38, 99-107.	4.1	8
511	A variant ECE1 allele contributes to reduced pathogenicity of <i>Candida albicans</i> during vulvovaginal candidiasis. <i>PLoS Pathogens</i> , 2021, 17, e1009884.	4.7	35
513	PAK1-Dependent Antitumor Effect of AAC-11œ Derived Peptides on Sœzary Syndrome Malignant CD4+ T Lymphocytes. <i>Journal of Investigative Dermatology</i> , 2021, 141, 2261-2271.e5.	0.7	3
514	Green biomanufacturing promoted by automatic retrobiosynthesis planning and computational enzyme design. <i>Chinese Journal of Chemical Engineering</i> , 2022, 41, 6-21.	3.5	1
515	Assessment of IsPETase-Assisted Depolymerization of Terephthalate Aromatic Polyesters and the Effect of the Thioredoxin Fusion Domain. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 8315.	2.5	6
516	Silencing of a <i>Pseudoœnitzschia arenysensis</i> lipoxygenase transcript leads to reduced oxylipin production and impaired growth. <i>New Phytologist</i> , 2022, 233, 809-822.	7.3	4
517	Improved 3-D Protein Structure Predictions using Deep ResNet Model. <i>Protein Journal</i> , 2021, 40, 669-681.	1.6	4
518	In-silico evidence for enhancement of avian influenza virus H9N2 virulence by modulation of its hemagglutinin (HA) antigen function and stability during co-infection with infectious bronchitis virus in chickens. <i>VirusDisease</i> , 2021, 32, 548-558.	2.0	1

#	ARTICLE	IF	CITATIONS
519	Immunoinformatics based designing and simulation of multi-epitope vaccine against multi-drug resistant <i>Stenotrophomonas maltophilia</i> . <i>Journal of Molecular Liquids</i> , 2021, 340, 116899.	4.9	5
520	Computational Modeling of Protein Three-Dimensional Structure: Methods and Resources. , 2021, , 155-178.		4
521	Differential genotypic signatures of Toll-like receptor polymorphisms among dengue-chikungunya mono- and co-infected Eastern Indian patients. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2021, 40, 1369-1381.	2.9	7
522	MO4: A Many-Objective Evolutionary Algorithm for Protein Structure Prediction. <i>IEEE Transactions on Evolutionary Computation</i> , 2022, 26, 417-430.	10.0	48
523	Improved Protein Decoy Selection via Non-Negative Matrix Factorization. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, PP, 1-1.	3.0	1
524	Vaccine Design and Immunoinformatics. , 2021, , 137-149.		1
525	Annotation of Alternatively Spliced Proteins and Transcripts with Protein-Folding Algorithms and Isoform-Level Functional Networks. <i>Methods in Molecular Biology</i> , 2017, 1558, 415-436.	0.9	2
526	Ab Initio Protein Structure Prediction. , 2017, , 3-35.		53
527	EcDBS1R6: A novel cationic antimicrobial peptide derived from a signal peptide sequence. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129633.	2.4	12
528	A glance into the evolution of template-free protein structure prediction methodologies. <i>Biochimie</i> , 2020, 175, 85-92.	2.6	24
529	Composition and in silico structural analysis of fibroin from liquid silk of non-mulberry silkworm <i>Antheraea assamensis</i> . <i>International Journal of Biological Macromolecules</i> , 2020, 163, 1947-1958.	7.5	7
530	Computational insight into the three-dimensional structure of ADP ribosylation factor like protein 15, a novel susceptibility gene for rheumatoid arthritis. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 4626-4641.	3.5	17
546	Production and Characterization of Synthetic Carboxysome Shells with Incorporated Luminal Proteins. <i>Plant Physiology</i> , 2016, 170, 1868-77.	4.8	64
547	Routine phasing of coiled-coil protein crystal structures with <i>AMPLE</i> . <i>IUCr</i> , 2015, 2, 198-206.	2.2	24
548	Solving coiled-coil protein structures. <i>IUCr</i> , 2015, 2, 164-165.	2.2	8
549	Distributed computing for macromolecular crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 143-151.	2.3	54
550	Recent developments in <i>MrBUMP</i> : better search-model preparation, graphical interaction with search models, and solution improvement and assessment. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 167-182.	2.3	35
551	Molecular replacement using structure predictions from databases. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 1051-1062.	2.3	15

#	ARTICLE	IF	CITATIONS
552	<i>SEQUENCE SLIDER</i>: expanding polyalanine fragments for phasing with multiple side-chain hypotheses. Acta Crystallographica Section D: Structural Biology, 2020, 76, 221-237.	2.3	10
553	A Systematic Review on the Use of AI and ML for Fighting the COVID-19 Pandemic. IEEE Transactions on Artificial Intelligence, 2020, 1, 258-270.	4.7	50
554	Deep Ranking in Template-free Protein Structure Prediction. , 2020, , .		5
555	Phosphorylation stateâ€“dependent modulation of spinal glycine receptors alleviates inflammatory pain. Journal of Clinical Investigation, 2016, 126, 2547-2560.	8.2	49
556	Fragger: a protein fragment picker for structural queries. F1000Research, 2017, 6, 1722.	1.6	2
557	Principles and Overview of Sampling Methods for Modeling Macromolecular Structure and Dynamics. PLoS Computational Biology, 2016, 12, e1004619.	3.2	188
558	A Probabilistic Fragment-Based Protein Structure Prediction Algorithm. PLoS ONE, 2012, 7, e38799.	2.5	40
559	eThread: A Highly Optimized Machine Learning-Based Approach to Meta-Threading and the Modeling of Protein Tertiary Structures. PLoS ONE, 2012, 7, e50200.	2.5	32
560	The SHOCT Domain: A Widespread Domain Under-Represented in Model Organisms. PLoS ONE, 2013, 8, e57848.	2.5	6
561	Low-Resolution Structure of the Full-Length Barley (<i>Hordeum vulgare</i>) SGT1 Protein in Solution, Obtained Using Small-Angle X-Ray Scattering. PLoS ONE, 2014, 9, e93313.	2.5	9
562	Addressing the Role of Conformational Diversity in Protein Structure Prediction. PLoS ONE, 2016, 11, e0154923.	2.5	14
563	Critical Features of Fragment Libraries for Protein Structure Prediction. PLoS ONE, 2017, 12, e0170131.	2.5	20
564	Sequence statistics of tertiary structural motifs reflect protein stability. PLoS ONE, 2017, 12, e0178272.	2.5	26
565	In silico analysis of protein toxin and bacteriocins from <i>Lactobacillus paracasei</i> SD1 genome and available online databases. PLoS ONE, 2017, 12, e0183548.	2.5	26
566	<i>Fasciola</i> spp: Mapping of the MF6 epitope and antigenic analysis of the MF6p/HDM family of heme-binding proteins. PLoS ONE, 2017, 12, e0188520.	2.5	11
567	Biophysical insights from a single chain camelid antibody directed against the Disrupted-in-Schizophrenia 1 protein. PLoS ONE, 2018, 13, e0191162.	2.5	7
568	A Constraint Solver for Flexible Protein Model. Journal of Artificial Intelligence Research, 0, 48, 953-1000.	7.0	7
569	A Survey of Computational Treatments of Biomolecules by Robotics-Inspired Methods Modeling Equilibrium Structure and Dynamic. Journal of Artificial Intelligence Research, 0, 57, 509-572.	7.0	20

#	ARTICLE	IF	CITATIONS
570	Homology modeling of the spatial structure of HydSL hydrogenase from purple sulphur bacterium <i>Thiocapsa roseopersicina</i> BBS. <i>Computer Research and Modeling</i> , 2013, 5, 737-747.	0.3	4
571	An Improved Integration of Template-Based and Template-Free Protein Structure Modeling Methods and its Assessment in CASP11. <i>Protein and Peptide Letters</i> , 2015, 22, 586-593.	0.9	11
572	Target Based Drug Design - A Reality in Virtual Sphere. <i>Current Medicinal Chemistry</i> , 2015, 22, 1603-1630.	2.4	29
573	Current Advances in the Identification and Characterization of Putative Drug and Vaccine Targets in the Bacterial Genomes. <i>Current Topics in Medicinal Chemistry</i> , 2015, 16, 1040-1069.	2.1	35
574	Rosetta and the Journey to Predict Proteinsâ€™ Structures, 20 Years on. <i>Current Bioinformatics</i> , 2020, 15, 611-628.	1.5	9
575	Molecular Dynamics Simulations for Biological Systems. , 2017, , 1044-1071.		1
576	Protein Structure Prediction. <i>Advances in Bioinformatics and Biomedical Engineering Book Series</i> , 2018, , 48-79.	0.4	3
577	Discovering Novel Anti-Malarial Peptides from the Not-coding Genome - A Working Hypothesis. <i>Current Synthetic and Systems Biology</i> , 2013, 01, .	0.3	2
578	A Hybrid Monte Carlo Ant Colony Optimization Approach for Protein Structure Prediction in the HP Model. <i>Electronic Proceedings in Theoretical Computer Science, EPTCS</i> , 0, 130, 61-69.	0.8	3
579	Protein structure prediction. <i>Wuli Xuebao/Acta Physica Sinica</i> , 2016, 65, 178701.	0.5	3
580	Super Spy variants implicate flexibility in chaperone action. <i>ELife</i> , 2014, 3, e01584.	6.0	48
581	Malaria parasite LIMP protein regulates sporozoite gliding motility and infectivity in mosquito and mammalian hosts. <i>ELife</i> , 2017, 6, .	6.0	27
582	Structure of the human epithelial sodium channel by cryo-electron microscopy. <i>ELife</i> , 2018, 7, .	6.0	141
583	The evolution of logic circuits for the purpose of protein contact map prediction. <i>PeerJ</i> , 2017, 5, e3139.	2.0	5
584	From molecular dynamics to quantum mechanics of misfolded proteins and amyloid-like macroaggregates applied to neurodegenerative diseases. <i>Journal of Molecular Graphics and Modelling</i> , 2022, 110, 108046.	2.4	6
585	Overexpression of Rice OsS1Fa1 Gene Confers Drought Tolerance in Arabidopsis. <i>Plants</i> , 2021, 10, 2181.	3.5	1
587	In-silico behavior of dissolved prolamins under electric field effect applied by electrospinning process using molecular dynamics simulation. <i>Journal of Molecular Liquids</i> , 2021, 344, 117778.	4.9	11
588	Formal Model of 3D Protein Structures for Functional Genomics, Comparative Bioinformatics, and Molecular Modeling. <i>SpringerBriefs in Computer Science</i> , 2014, , 1-23.	0.2	0

#	ARTICLE	IF	CITATIONS
589	Non-Linear and Misleading Template Scoring Criteria: Root Cause of Protein Modelling Inaccuracies. Current Synthetic and Systems Biology, 2015, 03, .	0.3	1
590	Cloud-Based Computing Architectures for Solving Hot Issues in Structural Bioinformatics. Advances in Systems Analysis, Software Engineering, and High Performance Computing Book Series, 2015, , 294-314.	0.5	2
591	Molecular Dynamics Simulations for Biological Systems. Advances in Bioinformatics and Biomedical Engineering Book Series, 2016, , 286-313.	0.4	3
592	Insights from the docked DoxDA Model with Thiosulphate. Bioinformation, 2016, 12, 69-73.	0.5	0
593	Rational Designing of Novel Proteins Through Computational Approaches. SpringerBriefs in Applied Sciences and Technology, 2017, , 61-83.	0.4	2
594	Fragger: a protein fragment picker for structural queries. F1000Research, 2017, 6, 1722.	1.6	2
596	Cloud Services for Efficient Ab Initio Predictions of 3D Protein Structures. Computational Biology, 2018, , 103-134.	0.2	0
597	Formal Model of 3D Protein Structures for Functional Genomics, Comparative Bioinformatics, and Molecular Modeling. Computational Biology, 2018, , 3-27.	0.2	0
598	End-to-End Differentiable Learning of Protein Structure. SSRN Electronic Journal, 0, , .	0.4	2
603	Protein Structure Prediction. , 2019, , 156-184.		0
604	Cloud-Based Computing Architectures for Solving Hot Issues in Structural Bioinformatics. , 2019, , 322-343.		0
605	Supersecondary Structures and Fragment Libraries. Methods in Molecular Biology, 2019, 1958, 283-295.	0.9	0
606	Combinatorial Designing of Novel Lead Molecules Towards the Putative Drug Targets of Extreme Drug-Resistant Mycobacterium tuberculosis: A Future Insight for Molecular Medicine. , 2019, , 233-281.		0
607	Prediction and Analysis of Three-Dimensional Structure of the p7- Transactivated Protein1 of Hepatitis C Virus. Infectious Disorders - Drug Targets, 2019, 19, 55-66.	0.8	2
609	Protein Structure Prediction with Parallel Algorithms Orthogonal to Parallel Platforms. , 2019, 17, .	0.0	0
611	Allosteric changes in HDM2 by the ATM phosphomimetic S395D mutation: implications on HDM2 function. Biochemical Journal, 2019, 476, 3401-3411.	3.7	3
613	Computational Methods Used in Prediction of Protein Structure. Algorithms for Intelligent Systems, 2020, , 119-133.	0.6	1
618	A Novel In Silico Benchmarked Pipeline Capable of Complete Protein Analysis: A Possible Tool for Potential Drug Discovery. Biology, 2021, 10, 1113.	2.8	6

#	ARTICLE	IF	CITATIONS
619	Critical Review of Synthesis, Toxicology and Detection of Acyclovir. <i>Molecules</i> , 2021, 26, 6566.	3.8	18
620	Improved Protein Structure Prediction Using a New Multi-scale Network and Homologous Templates. <i>Advanced Science</i> , 2021, 8, e2102592.	11.2	65
621	Protein Decoy Generation via Adaptive Stochastic Optimization for Protein Structure Determination. , 2020, , .		1
622	Structural and functional impacts of E5 genetic variants of human papillomavirus type 31. <i>Virus Research</i> , 2020, 290, 198143.	2.2	1
624	A tale of solving two computational challenges in protein science: neoantigen prediction and protein structure prediction. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	7
625	In Silico Designing of Vaccines: Methods, Tools, and Their Limitations. , 2020, , 245-277.		0
626	Orientation-dependent toxic effect of human papillomavirus type 33 long control region DNA in <i>Escherichia coli</i> cells. <i>Virus Genes</i> , 2020, 56, 298-305.	1.6	2
631	Variational Autoencoders for Protein Structure Prediction. , 2020, , .		6
632	From Interatomic Distances to Protein Tertiary Structures with a Deep Convolutional Neural Network. , 2020, , .		0
633	Structural Plasticity of EAK-16 Peptide Inducing Vesicle Membrane Leakage. <i>Protein and Peptide Letters</i> , 2020, 27, 801-807.	0.9	0
636	Structural and functional analysis of protein. , 2022, , 189-206.		0
637	Seq-SetNet: directly exploiting multiple sequence alignment for protein secondary structure prediction. <i>Bioinformatics</i> , 2022, 38, 990-996.	4.1	1
638	The trRosetta server for fast and accurate protein structure prediction. <i>Nature Protocols</i> , 2021, 16, 5634-5651.	12.0	290
639	Structural Predictive Model of Presenilin-2 Protein and Analysis of Structural Effects of Familial Alzheimer's Disease Mutations. <i>Biochemistry Research International</i> , 2021, 2021, 1-20.	3.3	6
640	An inductive transfer learning force field (ITLFF) protocol builds protein force fields in seconds. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	5
641	Transactivation domain of Adenovirus Early Region 1A (E1A): Investigating folding dynamics and aggregation. <i>Current Research in Structural Biology</i> , 2022, 4, 29-40.	2.2	1
643	DeepUMQA: ultrafast shape recognition-based protein model quality assessment using deep learning. <i>Bioinformatics</i> , 2022, 38, 1895-1903.	4.1	25
644	GPU-I-TASSER: a GPU accelerated I-TASSER protein structure prediction tool. <i>Bioinformatics</i> , 2022, 38, 1754-1755.	4.1	6

#	ARTICLE	IF	CITATIONS
646	The importance of the compact disordered state in the fuzzy interactions between intrinsically disordered proteins. <i>Chemical Science</i> , 2022, 13, 2363-2377.	7.4	7
647	Modeling the MreB-CbtA Interaction to Facilitate the Prediction and Design of Candidate Antibacterial Peptides. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 814935.	3.5	0
648	Methods and applications of machine learning in structure-based drug discovery. , 2022, , 405-437.		2
649	Visualising Viruses. <i>Journal of General Virology</i> , 2022, 103, .	2.9	6
651	Decoding the link of microbiome niches with homologous sequences enables accurately targeted protein structure prediction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	12
653	Structural Insights into the Catalytic Cycle of a Bacterial Multidrug ABC Efflux Pump. <i>SSRN Electronic Journal</i> , 0, , .	0.4	2
654	A Conserved Receptor-Binding Domain in the VP1u of Primate Erythroparvoviruses Determines the Marked Tropism for Erythroid Cells. <i>Viruses</i> , 2022, 14, 420.	3.3	2
655	VHH Structural Modelling Approaches: A Critical Review. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3721.	4.1	9
656	Construct a variable-length fragment library for de novo protein structure prediction. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	4
657	Dimerization Activity of a Disordered N-Terminal Domain from <i>Drosophila</i> CLAMP Protein. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3862.	4.1	6
658	A Benchmark Dataset for Evaluating Practical Performance of Model Quality Assessment of Homology Models. <i>Bioengineering</i> , 2022, 9, 118.	3.5	1
659	Performance of Novel Antimicrobial Protein Bg_9562 and In Silico Predictions on Its Properties with Reference to Its Antimicrobial Efficiency against <i>Rhizoctonia solani</i> . <i>Antibiotics</i> , 2022, 11, 363.	3.7	1
660	Unheeded SARS-CoV-2 proteins? A deep look into negative-sense RNA. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	15
661	Computational vaccinology guided design of multi-epitope subunit vaccine against a neglected arbovirus of the Americas. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 3321-3338.	3.5	4
662	Structural Insights into the Catalytic Cycle of a Bacterial Multidrug ABC Efflux Pump. <i>Journal of Molecular Biology</i> , 2022, 434, 167541.	4.2	13
663	Structural insight into proteinâ€“protein interactions between intestinal microbiome and host. <i>Current Opinion in Structural Biology</i> , 2022, 74, 102354.	5.7	2
665	Modeling a unit cell: crystallographic refinement procedure using the biomolecular MD simulation platform <i>Amber</i> . <i>IUCr</i> , 2022, 9, 114-133.	2.2	4
666	Adjusting Local Conformational Sampling For Fragment Assembly Protein Structure Prediction Based On Secondary Structure Complexity. , 2021, , .		0

#	ARTICLE	IF	CITATIONS
667	Empirical Study of Protein Feature Representation on Deep Belief Networks Trained With Small Data for Secondary Structure Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 955-966.	3.0	1
677	Anisaxins, helical antimicrobial peptides from marine parasites, kill resistant bacteria by lipid extraction and membrane disruption. <i>Acta Biomaterialia</i> , 2022, 146, 131-144.	8.3	15
678	proANP Metabolism Provides New Insights Into Sacubitril/Valsartan Mode of Action. <i>Circulation Research</i> , 2022, 130, 101161CIRCRESAHA122320882.	4.5	5
679	<i>MrParse</i> : finding homologues in the PDB and the EBI AlphaFold database for molecular replacement and more. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 553-559.	2.3	12
680	In silico study predicts a key role of <i>RNA</i> binding domains 3 and 4 in <i>nucleolin</i> miRNA interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 1837-1850.	2.6	1
681	Recognizing protein-metal ion ligands binding residues by random forest algorithm with adding orthogonal properties. <i>Computational Biology and Chemistry</i> , 2022, 98, 107693.	2.3	2
682	In-silico zein/tannic acid colloidal nanoparticles and their activity at oil and water interface of Pickering emulsion using molecular dynamics simulation. <i>Journal of Molecular Liquids</i> , 2022, 359, 119321.	4.9	4
683	Progressive assembly of multi-domain protein structures from cryo-EM density maps. <i>Nature Computational Science</i> , 2022, 2, 265-275.	8.0	25
684	Different methods, techniques and their limitations in protein structure prediction: A review. <i>Progress in Biophysics and Molecular Biology</i> , 2022, 173, 72-82.	2.9	12
685	Constraint Guided Neighbor Generation for Protein Structure Prediction. <i>IEEE Access</i> , 2022, 10, 54991-55001.	4.2	3
687	Deep learning geometrical potential for high-accuracy ab initio protein structure prediction. <i>IScience</i> , 2022, 25, 104425.	4.1	7
688	Unattained geometric configurations of secondary structure elements in protein structural space. <i>Journal of Structural Biology</i> , 2022, 214, 107870.	2.8	1
689	Protein structural bioinformatics: An overview. <i>Computers in Biology and Medicine</i> , 2022, 147, 105695.	7.0	15
690	Integration of physicochemical, molecular dynamics, and in vitro evaluation of electrosprayed β -oryzanol-loaded gliadin nanoparticles. <i>Food Chemistry</i> , 2022, 395, 133589.	8.2	10
691	Computational Design of Peptide-Based Binders to Therapeutic Targets. <i>ACS Symposium Series</i> , 0, , 55-102.	0.5	0
693	I-TASSER-MTD: a deep-learning-based platform for multi-domain protein structure and function prediction. <i>Nature Protocols</i> , 2022, 17, 2326-2353.	12.0	104
695	Computational Methods for Peptide Macrocyclic Drug Design. <i>AAPS Advances in the Pharmaceutical Sciences Series</i> , 2022, , 79-161.	0.6	1
696	Coiled-coil structure of meiosis protein TEX12 and conformational regulation by its C-terminal tip. <i>Communications Biology</i> , 2022, 5, .	4.4	4

#	ARTICLE	IF	CITATIONS
697	Functional Testing of Bone Morphogenetic Protein (BMP) Pathway Variants Identified on Whole-Exome Sequencing in a Patient with Delayed-Onset Fibrodysplasia Ossificans Progressiva (FOP) Using ACVR1R206H-Specific Human Cellular and Zebrafish Models. <i>Journal of Bone and Mineral Research</i> , 2020, 37, 2058-2076.	2.8	2
698	Fast and accurate Ab Initio Protein structure prediction using deep learning potentials. <i>PLoS Computational Biology</i> , 2022, 18, e1010539.	3.2	9
699	Constraint Guided Beta-Sheet Refinement for Protein Structure Prediction. <i>Computational Biology and Chemistry</i> , 2022, 101, 107773.	2.3	1
700	Phylogenetic Characterization of HIV-1 Sub-Subtype A1 in Karachi, Pakistan. <i>Viruses</i> , 2022, 14, 2307.	3.3	0
701	CADD, AI and ML in drug discovery: A comprehensive review. <i>European Journal of Pharmaceutical Sciences</i> , 2023, 181, 106324.	4.0	30
702	Tools for protein structure prediction and for molecular docking applied to enzyme active site analysis: A case study using a BAHD hydroxycinnamoyltransferase. <i>Methods in Enzymology</i> , 2022, , .	1.0	0
704	Artificial intelligence for template-free protein structure prediction: a comprehensive review. <i>Artificial Intelligence Review</i> , 2023, 56, 7665-7732.	15.7	2
705	Improved model quality assessment using sequence and structural information by enhanced deep neural networks. <i>Briefings in Bioinformatics</i> , 2023, 24, .	6.5	13
706	Proteogenomic Approaches to Understand Gene Mutations and Protein Structural Alterations in Colon Cancer. <i>Physiologia</i> , 2023, 3, 11-29.	2.2	2
707	De novo protein fold design through sequence-independent fragment assembly simulations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	7.1	7
708	Protective Efficacy of Anti-Hyr1p Monoclonal Antibody against Systemic Candidiasis Due to Multi-Drug-Resistant <i>Candida auris</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 103.	3.5	3
709	Molecular interaction modeling of carbon nanotubes and fullerene toward prioritized targets of SARS-CoV-2 by computer-aided screening and docking studies. , 2023, , 157-179.		0
710	Electrospun zein/C-phycoerythrin composite: Simulation, characterization and therapeutic application. <i>Food Hydrocolloids</i> , 2023, 140, 108638.	10.7	7
711	Modelling and Simulation of Proteins. , 2021, , 394-411.		0
712	Structural Insights into ATP-Sensitive Potassium Channel Mechanics: A Role of Intrinsically Disordered Regions. <i>Journal of Chemical Information and Modeling</i> , 2023, 63, 1806-1818.	5.4	2
713	Hope toward potent drug target using tertiary topological instances of Mycobacterial transmembrane protein. <i>Journal of Bacteriology & Mycology Open Access</i> , 2022, 10, 69-75.	0.2	0
714	Protein structure prediction using the evolutionary algorithm <sc>USPEX</sc>. <i>Proteins: Structure, Function and Bioinformatics</i> , 2023, 91, 933-943.	2.6	0
715	Binding by calmodulin is coupled to transient unfolding of the third <sc>FF</sc> domain of <sc>Prp40A</sc>. <i>Protein Science</i> , 2023, 32, .	7.6	2

#	ARTICLE	IF	CITATIONS
716	Computational strategies and tools for protein tertiary structure prediction. , 2023, , 225-242.		0
717	Exploring microbial functional biodiversity at the protein family levelâ€”From metagenomic sequence reads to annotated protein clusters. <i>Frontiers in Bioinformatics</i> , 0, 3, .	2.1	2
718	Before and after AlphaFold2: An overview of protein structure prediction. <i>Frontiers in Bioinformatics</i> , 0, 3, .	2.1	32
719	Ab Initio Modelling of the Structure of ToxA-like and MAX Fungal Effector Proteins. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6262.	4.1	4
720	Assessing structure and disorder prediction tools for de novo emerged proteins in the age of machine learning. <i>F1000Research</i> , 0, 12, 347.	1.6	6
721	Protein Structure Prediction: Challenges, Advances, and the Shift of Research Paradigms. <i>Genomics, Proteomics and Bioinformatics</i> , 2023, , .	6.9	2
722	In silico analysis of the possible crosstalk between O-linked Î²-GlcNAcylation and phosphorylation sites of Disabled 1 adaptor protein in vertebrates. <i>Amino Acids</i> , 0, , .	2.7	0
723	Relating Molecular Dynamics Simulations to Functional Activity for Gly-Rich Membranolytic Helical Kiadin Peptides. <i>Pharmaceutics</i> , 2023, 15, 1433.	4.5	1
724	Exploring the â€”N-terminal armâ€™ & â€”Convex surfaceâ€™ Binding Interfaces of the T3SS Chaperone-Translocator Complexes from <i>P. Aeruginosa</i> . <i>Journal of Molecular Biology</i> , 2023, 435, 168146.	4.2	0
725	PLIN5 interacts with FATP4 at membrane contact sites to promote lipid droplet-to-mitochondria fatty acid transport. <i>Developmental Cell</i> , 2023, 58, 1250-1265.e6.	7.0	13
726	Host Cell Membrane Capture by the SARS-CoV-2 Spike Protein Fusion Intermediate. <i>ACS Central Science</i> , 2023, 9, 1213-1228.	11.3	2
727	Somatic mutations of CADM1 in aldosterone-producing adenomas and gap junction-dependent regulation of aldosterone production. <i>Nature Genetics</i> , 2023, 55, 1009-1021.	21.4	10
728	Improved structure-related prediction for insufficient homologous proteins using MSA enhancement and pre-trained language model. <i>Briefings in Bioinformatics</i> , 2023, 24, .	6.5	3
729	A de novo evolved gene contributes to rice grain shape difference between indica and japonica. <i>Nature Communications</i> , 2023, 14, .	12.8	4
730	Application of Computational Techniques in Antibody Fc-Fused Molecule Design for Therapeutics. <i>Molecular Biotechnology</i> , 0, , .	2.4	0
731	Predictive Modeling and Structure Analysis of Genetic Variants in Familial Hypercholesterolemia: Implications for Diagnosis and Protein Interaction Studies. <i>Current Atherosclerosis Reports</i> , 2023, 25, 839-859.	4.8	2
732	Identification of p53-R175H Q167 and R248 as Residues Most Involved in Its Interaction with Plakoglobin. <i>Re:GEN Open</i> , 2023, 3, 40-51.	0.2	0
733	Discovery of a Novel Intron in US10/US11/US12 of HSV-1 Strain 17. <i>Viruses</i> , 2023, 15, 2144.	3.3	1

#	ARTICLE	IF	CITATIONS
734	Transcriptome analysis of <i>Corvus splendens</i> reveals a repertoire of antimicrobial peptides. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
735	New fraternine analogues: Evaluation of the antiparkinsonian effect in the model of Parkinson's disease. <i>Neuropeptides</i> , 2024, 103, 102390.	2.2	0
736	Discovery and Identification of a Novel Tag of HlyA60 for Protein Active Aggregate Formation in <i>Escherichia coli</i> . <i>Journal of Agricultural and Food Chemistry</i> , 0, , .	5.2	0
737	Recent Advances and Challenges in Protein Structure Prediction. <i>Journal of Chemical Information and Modeling</i> , 0, , .	5.4	1
738	Protein Homology Modeling in the Low Sequence Similarity Regime. <i>Black Sea Journal of Engineering and Science</i> , 2024, 7, 165-174.	0.6	0
740	Navigating the Frontiers of Machine Learning in Neurodegenerative Disease Therapeutics. <i>Pharmaceuticals</i> , 2024, 17, 158.	3.8	0
741	<i>In-vitro</i> antimicrobial activity of AF-DP protein and <i>in-silico</i> approach of cell membrane disruption. <i>Journal of Biomolecular Structure and Dynamics</i> , 0, , 1-18.	3.5	0
742	An intramolecular cross-talk in D29 mycobacteriophage endolysin governs the lytic cycle and phage-host population dynamics. <i>Science Advances</i> , 2024, 10, .	10.3	0
743	Recent Progress of Protein Tertiary Structure Prediction. <i>Molecules</i> , 2024, 29, 832.	3.8	0
744	Application of electrospinning to fabricate phycocyanin- and <i>Spirulina</i> extract-loaded gliadin fibers for active food packaging. <i>Food Chemistry: X</i> , 2024, 22, 101275.	4.3	0