

# Ziding Zhang

## List of Publications by Year in descending order

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141  
papers

6,550  
citations

87888

38  
h-index

79698

73  
g-index

149  
all docs

149  
docs citations

149  
times ranked

8919  
citing authors

#	ARTICLE	IF	CITATIONS
1	Isolation of SARS-CoV-2-related coronavirus from Malayan pangolins. <i>Nature</i> , 2020, 583, 286-289.	27.8	599
2	SRAMP: prediction of mammalian N <sup>6</sup> -methyladenosine (m <sup>6</sup> A) sites based on sequence-derived features. <i>Nucleic Acids Research</i> , 2016, 44, e91-e91.	14.5	560
3	Toxicity of Ionic Liquids. <i>Clean - Soil, Air, Water</i> , 2007, 35, 42-48.	1.1	499
4	<i>Badh2</i> , Encoding Betaine Aldehyde Dehydrogenase, Inhibits the Biosynthesis of 2-Acetyl-1-Pyrroline, a Major Component in Rice Fragrance. <i>Plant Cell</i> , 2008, 20, 1850-1861.	6.6	267
5	Comparative Analysis of the Genomes of Two Field Isolates of the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>PLoS Genetics</i> , 2012, 8, e1002869.	3.5	167
6	Prediction of Ubiquitination Sites by Using the Composition of k-Spaced Amino Acid Pairs. <i>PLoS ONE</i> , 2011, 6, e22930.	2.5	162
7	Prediction of mucin-type O-glycosylation sites in mammalian proteins using the composition of k-spaced amino acid pairs. <i>BMC Bioinformatics</i> , 2008, 9, 101.	2.6	143
8	The <i>Bifidobacterium dentium</i> Bd1 Genome Sequence Reflects Its Genetic Adaptation to the Human Oral Cavity. <i>PLoS Genetics</i> , 2009, 5, e1000785.	3.5	141
9	MDP25, A Novel Calcium Regulatory Protein, Mediates Hypocotyl Cell Elongation by Destabilizing Cortical Microtubules in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2011, 23, 4411-4427.	6.6	106
10	Prediction of human-virus protein-protein interactions through a sequence embedding-based machine learning method. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 153-161.	4.1	98
11	hCKSAAP_UbSite: Improved prediction of human ubiquitination sites by exploiting amino acid pattern and properties. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1461-1467.	2.3	97
12	AtKC1 and CIPK23 Synergistically Modulate AKT1-Mediated Low-Potassium Stress Responses in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2016, 170, 2264-2277.	4.8	96
13	Genetic analysis and morphological identification of pilus-like structures in members of the genus <i>Bifidobacterium</i> . <i>Microbial Cell Factories</i> , 2011, 10, S16.	4.0	84
14	Binding specificity of locust odorant binding protein and its key binding site for initial recognition of alcohols. <i>Insect Biochemistry and Molecular Biology</i> , 2009, 39, 440-447.	2.7	80
15	Interaction of Positional Isomers of Quercetin Glucuronides with the Transporter ABCC2 (cMOAT). <i>Tj ETQq1</i> 1 0.784314 rgBT/Overlook	3.3	79
16	The prediction of protein-protein interaction networks in rice blast fungus. <i>BMC Genomics</i> , 2008, 9, 519.	2.8	77
17	Towards more accurate prediction of ubiquitination sites: a comprehensive review of current methods, tools and features. <i>Briefings in Bioinformatics</i> , 2015, 16, 640-657.	6.5	76
18	Polysaccharide-Induced Order-to-Order Transitions in Lyotropic Liquid Crystals. <i>Langmuir</i> , 2005, 21, 6165-6169.	3.5	73

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19	PhosphoPredict: A bioinformatics tool for prediction of human kinase-specific phosphorylation substrates and sites by integrating heterogeneous feature selection. <i>Scientific Reports</i> , 2017, 7, 6862.	3.3	72
20	Accurate in silico identification of species-specific acetylation sites by integrating protein sequence-derived and functional features. <i>Scientific Reports</i> , 2014, 4, 5765.	3.3	71
21	Characterization of the Serpin-Encoding Gene of <i>Bifidobacterium breve</i> 210B. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3206-3219.	3.1	66
22	Functional characterization and immunolocalization of odorant binding protein 1 in the lucerne plant bug, <i>Adelphocoris lineolatus</i> (GOEZE). <i>Archives of Insect Biochemistry and Physiology</i> , 2011, 77, 81-99.	1.5	66
23	Computational Identification of Protein Pupylation Sites by Using Profile-Based Composition of k-Spaced Amino Acid Pairs. <i>PLoS ONE</i> , 2015, 10, e0129635.	2.5	65
24	Revealing Shared and Distinct Gene Network Organization in Arabidopsis Immune Responses by Integrative Analysis. <i>Plant Physiology</i> , 2015, 167, 1186-1203.	4.8	62
25	<i>Ornithorhynchus anatinus</i> (Platypus) Links the Evolution of Immunoglobulin Genes in Eutherian Mammals and Nonmammalian Tetrapods. <i>Journal of Immunology</i> , 2009, 183, 3285-3293.	0.8	59
26	GANNPhos: a new phosphorylation site predictor based on a genetic algorithm integrated neural network. <i>Protein Engineering, Design and Selection</i> , 2007, 20, 405-412.	2.1	56
27	BEAN 2.0: an integrated web resource for the identification and functional analysis of type III secreted effectors. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav064.	3.0	56
28	Exploiting <i>Bifidobacterium</i> genomes: The molecular basis of stress response. <i>International Journal of Food Microbiology</i> , 2007, 120, 13-24.	4.7	55
29	Molecular Characterization of hsp20, Encoding a Small Heat Shock Protein of <i>Bifidobacterium breve</i> UCC2003. <i>Applied and Environmental Microbiology</i> , 2007, 73, 4695-4703.	3.1	51
30	Coordinated regulation of core and accessory genes in the multipartite genome of <i>Sinorhizobium fredii</i> . <i>PLoS Genetics</i> , 2018, 14, e1007428.	3.5	50
31	How high G+C Gram-positive bacteria and in particular bifidobacteria cope with heat stress: protein players and regulators. <i>FEMS Microbiology Reviews</i> , 2006, 30, 734-759.	8.6	48
32	HVIDB: a comprehensive database for human-virus protein-protein interactions. <i>Briefings in Bioinformatics</i> , 2021, 22, 832-844.	6.5	48
33	Critical assessment and performance improvement of plant-pathogen protein-protein interaction prediction methods. <i>Briefings in Bioinformatics</i> , 2019, 20, 274-287.	6.5	47
34	Prediction of protein (domain) structural classes based on amino-acid index. <i>FEBS Journal</i> , 1999, 266, 1043-1049.	0.2	46
35	Similarity networks of protein binding sites. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 470-478.	2.6	46
36	Understanding Human-Virus Protein-Protein Interactions Using a Human Protein Complex-Based Analysis Framework. <i>MSystems</i> , 2019, 4, .	3.8	42

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37	The ClgR Protein Regulates Transcription of the clpP Operon in <i>Bifidobacterium breve</i> UCC 2003. <i>Journal of Bacteriology</i> , 2005, 187, 8411-8426.	2.2	41
38	Crystal structure of the <i>Locusta migratoria</i> odorant binding protein. <i>Biochemical and Biophysical Research Communications</i> , 2015, 456, 737-742.	2.1	41
39	The clpB gene of <i>Bifidobacterium breve</i> UCC 2003: transcriptional analysis and first insights into stress induction. <i>Microbiology (United Kingdom)</i> , 2005, 151, 2861-2872.	1.8	40
40	Predicting Residue-Residue Contacts and Helix-Helix Interactions in Transmembrane Proteins Using an Integrative Feature-Based Random Forest Approach. <i>PLoS ONE</i> , 2011, 6, e26767.	2.5	39
41	MucR Is Required for Transcriptional Activation of Conserved Ion Transporters to Support Nitrogen Fixation of <i>Sinorhizobium fredii</i> in Soybean Nodules. <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 352-361.	2.6	39
42	Machine-Learning-Based Predictor of Human Bacteria Protein-Protein Interactions by Incorporating Comprehensive Host-Network Properties. <i>Journal of Proteome Research</i> , 2019, 18, 2195-2205.	3.7	39
43	An improved prediction of catalytic residues in enzyme structures. <i>Protein Engineering, Design and Selection</i> , 2008, 21, 295-302.	2.1	38
44	Network-Based Comparative Analysis of <i>Arabidopsis</i> Immune Responses to <i>Golovinomyces orontii</i> and <i>Botrytis cinerea</i> Infections. <i>Scientific Reports</i> , 2016, 6, 19149.	3.3	37
45	Prediction of protein-protein interactions between <i>Ralstonia solanacearum</i> and <i>Arabidopsis thaliana</i> . <i>Amino Acids</i> , 2012, 42, 2363-2371.	2.7	36
46	Using Weakly Conserved Motifs Hidden in Secretion Signals to Identify Type-III Effectors from Bacterial Pathogen Genomes. <i>PLoS ONE</i> , 2013, 8, e56632.	2.5	36
47	Crysalis: an integrated server for computational analysis and design of protein crystallization. <i>Scientific Reports</i> , 2016, 6, 21383.	3.3	35
48	Cyanidin-3-o-glucoside directly binds to ER $\alpha$ and inhibits EGFR-positive triple-negative breast cancer. <i>Oncotarget</i> , 2016, 7, 68864-68882.	1.8	34
49	Descriptor-based protein remote homology identification. <i>Protein Science</i> , 2005, 14, 431-444.	7.6	33
50	ZincExplorer: an accurate hybrid method to improve the prediction of zinc-binding sites from protein sequences. <i>Molecular BioSystems</i> , 2013, 9, 2213.	2.9	33
51	Transfer learning via multi-scale convolutional neural layers for human-virus protein-protein interaction prediction. <i>Bioinformatics</i> , 2021, 37, 4771-4778.	4.1	33
52	Computational Studies of Ligand-Receptor Interactions in Bitter Taste Receptors. <i>Journal of Receptor and Signal Transduction Research</i> , 2006, 26, 611-630.	2.5	32
53	A New Approach to Predict the Helix/Strand Content of Globular Proteins. <i>Journal of Theoretical Biology</i> , 2001, 208, 65-78.	1.7	31
54	Prediction of the helix/strand content of globular proteins based on their primary sequences. <i>Protein Engineering, Design and Selection</i> , 1998, 11, 971-979.	2.1	30

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55	DescFold: A web server for protein fold recognition. <i>BMC Bioinformatics</i> , 2009, 10, 416.	2.6	30
56	A new class of anti-thrombosis hexahydropyrazino-[1,2,2',6']pyrido-[3,4-b]-indole-1,4-dions: Design, synthesis, logK determination, and QSAR analysis. <i>Bioorganic and Medicinal Chemistry</i> , 2007, 15, 5672-5693.	3.0	29
57	A predicted protein-protein interaction network of the filamentous fungus <i>Neurospora crassa</i> . <i>Molecular BioSystems</i> , 2011, 7, 2278.	2.9	29
58	Functional Characteristics of a Novel Chemosensory Protein in the Cotton Bollworm <i>Helicoverpa armigera</i> (H&A1/4bner). <i>Journal of Integrative Agriculture</i> , 2013, 12, 853-861.	3.5	29
59	Prediction of the secondary structure content of globular proteins based on structural classes. <i>The Protein Journal</i> , 1996, 15, 775-786.	1.1	28
60	Can simple codon pair usage predict protein-protein interaction?. <i>Molecular BioSystems</i> , 2012, 8, 1396.	2.9	28
61	PredPPCrys: Accurate Prediction of Sequence Cloning, Protein Production, Purification and Crystallization Propensity from Protein Sequences Using Multi-Step Heterogeneous Feature Fusion and Selection. <i>PLoS ONE</i> , 2014, 9, e105902.	2.5	27
62	Three chromosome-level duck genome assemblies provide insights into genomic variation during domestication. <i>Nature Communications</i> , 2021, 12, 5932.	12.8	27
63	Computational design of a cutinase for plastic biodegradation by mining molecular dynamics simulations trajectories. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 459-470.	4.1	27
64	Title is missing!. <i>Biotechnology Letters</i> , 1999, 13, 781-786.	0.5	26
65	Studies on logP, retention time and QSAR of 2-substituted phenylnitronyl nitroxides as free radical scavengers. <i>European Journal of Medicinal Chemistry</i> , 2007, 42, 955-965.	5.5	26
66	Prediction of the secondary structure contents of globular proteins based on three structural classes. <i>The Protein Journal</i> , 1998, 17, 261-272.	1.1	25
67	N-[2-(5,5-Dimethyl-1,3-dioxane-2-yl)ethyl]amino acids: Their synthesis, anti-inflammatory evaluation and QSAR analysis. <i>European Journal of Medicinal Chemistry</i> , 2008, 43, 8-18.	5.5	25
68	SPAR: a random forest-based predictor for self-interacting proteins with fine-grained domain information. <i>Amino Acids</i> , 2016, 48, 1655-1665.	2.7	25
69	Differential Coexpression Analysis Reveals Extensive Rewiring of Arabidopsis Gene Coexpression in Response to <i>Pseudomonas syringae</i> Infection. <i>Scientific Reports</i> , 2016, 6, 35064.	3.3	25
70	PlaPPISite: a comprehensive resource for plant protein-protein interaction sites. <i>BMC Plant Biology</i> , 2020, 20, 61.	3.6	25
71	Deciphering the Arabidopsis Floral Transition Process by Integrating a Protein-Protein Interaction Network and Gene Expression Data. <i>Plant Physiology</i> , 2010, 153, 1492-1505.	4.8	24
72	An Integrative Computational Framework Based on a Two-Step Random Forest Algorithm Improves Prediction of Zinc-Binding Sites in Proteins. <i>PLoS ONE</i> , 2012, 7, e49716.	2.5	24

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73	Network Analysis Reveals a Common Host–Pathogen Interaction Pattern in Arabidopsis Immune Responses. <i>Frontiers in Plant Science</i> , 2017, 8, 893.	3.6	24
74	MAPanalyzer: a novel online tool for analyzing microtubule-associated proteins. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	3.0	23
75	Systems understanding of plant–pathogen interactions through genome-wide protein–protein interaction networks. <i>Frontiers of Agricultural Science and Engineering</i> , 2016, 3, 102.	1.4	23
76	Transcriptome analysis reveals physiological characteristics required for magnetosome formation in <i>Magnetospirillum gryphiswaldense</i> MSR-1. <i>Environmental Microbiology Reports</i> , 2016, 8, 371-381.	2.4	22
77	Pathogenicity Genes in <i>Ustilagoidea virescens</i> Revealed by a Predicted Protein–Protein Interaction Network. <i>Journal of Proteome Research</i> , 2017, 16, 1193-1206.	3.7	22
78	COMPUTATIONAL ENZYME DESIGN APPROACHES WITH SIGNIFICANT BIOLOGICAL OUTCOMES: PROGRESS AND CHALLENGES. <i>Computational and Structural Biotechnology Journal</i> , 2012, 2, e201209007.	4.1	21
79	Prediction of protein–protein interactions between fungus ( <i>Magnaporthe grisea</i> ) and rice ( <i>Oryza</i> ) Tj ETQq1 1 0.784314 rgBT /Overl 6.5 21	6.5	21
80	Prediction of Protein Ubiquitination Sites in <i>Arabidopsis thaliana</i> . <i>Current Bioinformatics</i> , 2019, 14, 614-620.	1.5	21
81	Comparison of a homology model and the crystallographic structure of human 11 $\beta$ -hydroxysteroid dehydrogenase type 1 (11 $\beta$ HSD1) in a structure-based identification of inhibitors. <i>Journal of Computer-Aided Molecular Design</i> , 2006, 20, 67-81.	2.9	20
82	Expression patterns and ligand binding characterization of Plus-C odorant-binding protein 14 from <i>Adelphocoris lineolatus</i> (Goeze). <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2019, 227, 75-82.	1.6	20
83	Stabilization mechanism of MPEG modified trypsin based on thermal inactivation kinetic analysis and molecular modeling computation. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2001, 14, 85-94.	1.8	19
84	The AtMAP65-1 Cross-Bridge Between Microtubules is Formed by One Dimer. <i>Plant and Cell Physiology</i> , 2007, 48, 866-874.	3.1	19
85	Physiological characteristics of <i>Magnetospirillum gryphiswaldense</i> MSR-1 that control cell growth under high-iron and low-oxygen conditions. <i>Scientific Reports</i> , 2017, 7, 2800.	3.3	19
86	PlaD: A Transcriptomics Database for Plant Defense Responses to Pathogens, Providing New Insights into Plant Immune System. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 283-293.	6.9	19
87	Potential for Dramatic Improvement in Sequence Alignment against Structures of Remote Homologous Proteins by Extracting Structural Information from Multiple Structure Alignment. <i>Journal of Molecular Biology</i> , 2003, 332, 127-142.	4.2	18
88	Kinetic study of thermal inactivation for native and methoxypolyethylene glycol modified trypsin. <i>Process Biochemistry</i> , 2000, 35, 1235-1240.	3.7	17
89	Current status and future perspectives of computational studies on human–virus protein–protein interactions. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	17
90	MetalExplorer, a Bioinformatics Tool for the Improved Prediction of Eight Types of Metal-Binding Sites Using a Random Forest Algorithm with Two- Step Feature Selection. <i>Current Bioinformatics</i> , 2017, 12, .	1.5	17

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91	Characterization of the MHC class II $\beta$ -chain gene in ducks. <i>Immunogenetics</i> , 2011, 63, 667-678.	2.4	16
92	Outer membrane proteins can be simply identified using secondary structure element alignment. <i>BMC Bioinformatics</i> , 2011, 12, 76.	2.6	16
93	Computational characterization of parallel dimeric and trimeric coiled-coils using effective amino acid indices. <i>Molecular BioSystems</i> , 2015, 11, 354-360.	2.9	16
94	Large-scale transcriptome analysis reveals arabidopsis metabolic pathways are frequently influenced by different pathogens. <i>Plant Molecular Biology</i> , 2017, 94, 453-467.	3.9	16
95	A new class of analgesic agents toward prostacyclin receptor inhibition: Synthesis, biological studies and QSAR analysis of 1-hydroxyl-2-substituted phenyl-4,4,5,5-tetramethylimidazolines. <i>European Journal of Medicinal Chemistry</i> , 2008, 43, 1048-1058.	5.5	15
96	Evaluation of Protein Phosphorylation Site Predictors. <i>Protein and Peptide Letters</i> , 2010, 17, 64-69.	0.9	15
97	TIM-Finder: A new method for identifying TIM-barrel proteins. <i>BMC Structural Biology</i> , 2009, 9, 73.	2.3	13
98	Exploring the sequence-structure protein landscape in the glycosyltransferase family. <i>Protein Science</i> , 2009, 12, 2291-2302.	7.6	13
99	Comprehensive analysis of tandem amino acid repeats from ten angiosperm genomes. <i>BMC Genomics</i> , 2011, 12, 632.	2.8	12
100	The zinc-finger bearing xenogeneic silencer MucR in $\beta$ -proteobacteria balances adaptation and regulatory integrity. <i>ISME Journal</i> , 2022, 16, 738-749.	9.8	12
101	Identification of Catalytic Residues Using a Novel Feature that Integrates the Microenvironment and Geometrical Location Properties of Residues. <i>PLoS ONE</i> , 2012, 7, e41370.	2.5	12
102	Structure, Binding Characteristics, and 3D Model Prediction of a Newly Identified Odorant-Binding Protein from the Cotton Bollworm, <i>Helicoverpa armigera</i> (H $\beta$ bner). <i>Journal of Integrative Agriculture</i> , 2012, 11, 430-438.	3.5	11
103	AraPPISite: a database of fine-grained protein-protein interaction site annotations for <i>Arabidopsis thaliana</i> . <i>Plant Molecular Biology</i> , 2016, 92, 105-116.	3.9	11
104	Prediction and analysis of human-herpes simplex virus type 1 protein-protein interactions by integrating multiple methods. <i>Quantitative Biology</i> , 2020, 8, 312-324.	0.5	11
105	Tobacco Necrosis Virus-A <sup>C</sup> Single Coat Protein Amino Acid Substitutions Determine Host-Specific Systemic Infections of <i>Nicotiana benthamiana</i> and Soybean. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 49-61.	2.6	11
106	Lineage-Specific Rewiring of Core Pathways Predating Innovation of Legume Nodules Shapes Symbiotic Efficiency. <i>MSystems</i> , 2021, 6, .	3.8	11
107	Prp19-associated splicing factor Cwf15 regulates fungal virulence and development in the rice blast fungus. <i>Environmental Microbiology</i> , 2021, 23, 5901-5916.	3.8	11
108	Solvation energy and thermal stability of hydrophilization-modified alpha-chymotrypsin. <i>The Protein Journal</i> , 1999, 18, 557-564.	1.1	10

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109	Two distinct sites are essential for virulent infection and support of variant satellite RNA replication in spontaneous beet black scorch virus variants. <i>Journal of General Virology</i> , 2012, 93, 2718-2728.	2.9	10
110	GPCRserver: an accurate and novel G protein-coupled receptor predictor. <i>Molecular BioSystems</i> , 2014, 10, 2495-2504.	2.9	10
111	The hybrid protein interactome contributes to rice heterosis as epistatic effects. <i>Plant Journal</i> , 2020, 102, 116-128.	5.7	10
112	Structural Propensities of Human Ubiquitination Sites: Accessibility, Centrality and Local Conformation. <i>PLoS ONE</i> , 2013, 8, e83167.	2.5	10
113	The MERS-CoV Receptor DPP4 as a Candidate Binding Target of the SARS-CoV-2 Spike. <i>SSRN Electronic Journal</i> , 0, , .	0.4	10
114	Sympatric Recombination in Zoonotic <i>Cryptosporidium</i> Leads to Emergence of Populations with Modified Host Preference. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	10
115	Operating Mechanism and Molecular Dynamics of Pheromone-Binding Protein ASP1 as Influenced by pH. <i>PLoS ONE</i> , 2014, 9, e110565.	2.5	9
116	Insights into genomic evolution from the chromosomal and mitochondrial genomes of <i>Ustilaginoidea virens</i> . <i>Phytopathology Research</i> , 2021, 3, .	2.4	9
117	Aspartic acid at residue 185 modulates the capacity of HP-PRRSV nsp4 to antagonize IFN-I expression. <i>Virology</i> , 2020, 546, 79-87.	2.4	9
118	Characterization of Calcium-Dependent Protein Kinases 3, a Protein Involved in Growth of <i>Cryptosporidium parvum</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 907.	3.5	8
119	Novel 1-oxyl-2-substitutedphenyl-4,4,5,5-tetramethylimidazolines: Synthesis, selectively analgesic action, and QSAR analysis. <i>Bioorganic and Medicinal Chemistry</i> , 2007, 15, 2815-2826.	3.0	7
120	Identification of WD40 repeats by secondary structure-aided profileâ€“profile alignment. <i>Journal of Theoretical Biology</i> , 2016, 398, 122-129.	1.7	7
121	Comparison of linear gap penalties and profile-based variable gap penalties in profileâ€“profile alignments. <i>Computational Biology and Chemistry</i> , 2011, 35, 308-318.	2.3	6
122	Quantitative structureâ€“activity relationship study on antitumour activity of a series of flavonoids. <i>Molecular Simulation</i> , 2012, 38, 38-44.	2.0	6
123	Characterization of Three Calcium-Dependent Protein Kinases of <i>Cryptosporidium parvum</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 622203.	3.5	6
124	An Important Role for Purifying Selection in Archaeal Genome Evolution. <i>MSystems</i> , 2017, 2, .	3.8	5
125	Network-based analysis of virulence factors for uncovering <i>Aeromonas veronii</i> pathogenesis. <i>BMC Microbiology</i> , 2021, 21, 188.	3.3	5
126	Understanding the influence of AMG 510 on the structure of KRASG12C empowered by molecular dynamics simulation. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1056-1067.	4.1	5



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127	Genome-Wide Analysis of Enzyme Structure-Function Combination Across Three Domains of Life. <i>Protein and Peptide Letters</i> , 2007, 14, 291-297.	0.9	4
128	An Overview of the De Novo Prediction of Enzyme Catalytic Residues (Supplementary file). <i>Current Bioinformatics</i> , 2009, 4, 197-206.	1.5	4
129	Human Gene Functional Network-Informed Prediction of HIV-1 Host Dependency Factors. <i>MSystems</i> , 2020, 5, .	3.8	4
130	Prediction of outer membrane proteins by combining the position- and composition-based features of sequence profiles. <i>Molecular BioSystems</i> , 2014, 10, 1004.	2.9	3
131	Competition-cooperation relationship networks characterize the competition and cooperation between proteins. <i>Scientific Reports</i> , 2015, 5, 11619.	3.3	3
132	Comparative Study of Two Insulinlike Proteases in <i>Cryptosporidium parvum</i> . <i>Microorganisms</i> , 2021, 9, 861.	3.6	3
133	Transcriptional Landscapes of Long Non-coding RNAs and Alternative Splicing in <i>Pyricularia oryzae</i> Revealed by RNA-Seq. <i>Frontiers in Plant Science</i> , 2021, 12, 723636.	3.6	3
134	Identifying Coevolution Between Amino Acid Residues in Protein Families: Advances in the Improvement and Evaluation of Correlated Mutation Algorithms. <i>Current Bioinformatics</i> , 2013, 8, 148-160.	1.5	3
135	Comparative Analysis of Core and Accessory Genes in Coexpression Network. <i>Methods in Molecular Biology</i> , 2021, 2242, 45-58.	0.9	2
136	Multi-scale Convolutional Neural Networks for the Prediction of Human-virus Protein Interactions. , 2021, , .		2
137	Proteome-wide prediction and analysis of the <i>Cryptosporidium parvum</i> protein-protein interaction network through integrative methods. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2322-2331.	4.1	2
138	Combination of specific single chain antibody variable fragment and siRNA has a synergistic inhibitory effect on the propagation of avian influenza virus H5N1 in chicken cells. <i>Virology Journal</i> , 2014, 11, 208.	3.4	1
139	Special Issue on Plant Bioinformatics. <i>Current Bioinformatics</i> , 2019, 14, 564-565.	1.5	1
140	Deep Learning-Powered Prediction of Human-Virus Protein-Protein Interactions. <i>Frontiers in Microbiology</i> , 2022, 13, 842976.	3.5	1
141	Critical roles of amino acids Ser231, His107 and Asp156 of <i>Staphylococcus sciuri</i> exfoliative toxin C (ExhC) in the induction of skin exfoliations in neonate mice. <i>Biologia (Poland)</i> , 2011, 66, 1189-1195.	1.5	0