

Ziding Zhang

List of Publications by Year in descending order

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141
papers

6,550
citations

87888

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79698

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149
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149
docs citations

149
times ranked

8919
citing authors

#	ARTICLE	IF	CITATIONS
1	The zinc-finger bearing xenogeneic silencer MucR in $\hat{\pm}$ -proteobacteria balances adaptation and regulatory integrity. ISME Journal, 2022, 16, 738-749.	9.8	12
2	Computational design of a cutinase for plastic biodegradation by mining molecular dynamics simulations trajectories. Computational and Structural Biotechnology Journal, 2022, 20, 459-470.	4.1	27
3	Understanding the influence of AMG 510 on the structure of KRASG12C empowered by molecular dynamics simulation. Computational and Structural Biotechnology Journal, 2022, 20, 1056-1067.	4.1	5
4	Deep Learning-Powered Prediction of Human-Virus Protein-Protein Interactions. Frontiers in Microbiology, 2022, 13, 842976.	3.5	1
5	Proteome-wide prediction and analysis of the <i>Cryptosporidium parvum</i> protein-protein interaction network through integrative methods. Computational and Structural Biotechnology Journal, 2022, 20, 2322-2331.	4.1	2
6	Sympatric Recombination in Zoonotic <i>Cryptosporidium</i> Leads to Emergence of Populations with Modified Host Preference. Molecular Biology and Evolution, 2022, 39, .	8.9	10
7	Tobacco Necrosis Virus-A ^C Single Coat Protein Amino Acid Substitutions Determine Host-Specific Systemic Infections of <i>Nicotiana benthamiana</i> and Soybean. Molecular Plant-Microbe Interactions, 2021, 34, 49-61.	2.6	11
8	Comparative Analysis of Core and Accessory Genes in Coexpression Network. Methods in Molecular Biology, 2021, 2242, 45-58.	0.9	2
9	HVIDB: a comprehensive database for human-virus protein-protein interactions. Briefings in Bioinformatics, 2021, 22, 832-844.	6.5	48
10	Multi-scale Convolutional Neural Networks for the Prediction of Human-virus Protein Interactions. , 2021, , .		2
11	Current status and future perspectives of computational studies on human-virus protein-protein interactions. Briefings in Bioinformatics, 2021, 22, .	6.5	17
12	Comparative Study of Two Insulinlike Proteases in <i>Cryptosporidium parvum</i> . Microorganisms, 2021, 9, 861.	3.6	3
13	Insights into genomic evolution from the chromosomal and mitochondrial genomes of <i>Ustilaginoidea virens</i> . Phytopathology Research, 2021, 3, .	2.4	9
14	Lineage-Specific Rewiring of Core Pathways Predating Innovation of Legume Nodules Shapes Symbiotic Efficiency. MSystems, 2021, 6, .	3.8	11
15	Prp19-associated splicing factor Cwf15 regulates fungal virulence and development in the rice blast fungus. Environmental Microbiology, 2021, 23, 5901-5916.	3.8	11
16	Network-based analysis of virulence factors for uncovering <i>Aeromonas veronii</i> pathogenesis. BMC Microbiology, 2021, 21, 188.	3.3	5
17	Transfer learning via multi-scale convolutional neural layers for human-virus protein-protein interaction prediction. Bioinformatics, 2021, 37, 4771-4778.	4.1	33
18	Transcriptional Landscapes of Long Non-coding RNAs and Alternative Splicing in <i>Pyricularia oryzae</i> Revealed by RNA-Seq. Frontiers in Plant Science, 2021, 12, 723636.	3.6	3

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19	Three chromosome-level duck genome assemblies provide insights into genomic variation during domestication. <i>Nature Communications</i> , 2021, 12, 5932.	12.8	27
20	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
21	The hybrid protein interactome contributes to rice heterosis as epistatic effects. <i>Plant Journal</i> , 2020, 102, 116-128.	5.7	10
22	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
23	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
24	Isolation of SARS-CoV-2-related coronavirus from Malayan pangolins. <i>Nature</i> , 2020, 583, 286-289.	27.8	599
25	PlaPPISite: a comprehensive resource for plant protein-protein interaction sites. <i>BMC Plant Biology</i> , 2020, 20, 61.	3.6	25
26	Characterization of Three Calcium-Dependent Protein Kinases of <i>Cryptosporidium parvum</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 622203.	3.5	6
27	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
28	Human Gene Functional Network-Informed Prediction of HIV-1 Host Dependency Factors. <i>MSystems</i> , 2020, 5, .	3.8	4
29	Understanding Human-Virus Protein-Protein Interactions Using a Human Protein Complex-Based Analysis Framework. <i>MSystems</i> , 2019, 4, .	3.8	42
30	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
31	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
32	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
33	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
34	Special Issue on Plant Bioinformatics. <i>Current Bioinformatics</i> , 2019, 14, 564-565.	1.5	1
35	Prediction of Protein Ubiquitination Sites in <i>Arabidopsis thaliana</i> . <i>Current Bioinformatics</i> , 2019, 14, 614-620.	1.5	21
36	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

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37	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
38	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
39	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
40	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
41	An Important Role for Purifying Selection in Archaeal Genome Evolution. <i>MSystems</i> , 2017, 2, .	3.8	5
42	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
43	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
44	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
45	Cyanidin-3-o-glucoside directly binds to ER α and inhibits EGFR-positive triple-negative breast cancer. <i>Oncotarget</i> , 2016, 7, 68864-68882.	1.8	34
46	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
47	AtKC1 and CIPK23 Synergistically Modulate AKT1-Mediated Low-Potassium Stress Responses in Arabidopsis. <i>Plant Physiology</i> , 2016, 170, 2264-2277.	4.8	96
48	Crysalis: an integrated server for computational analysis and design of protein crystallization. <i>Scientific Reports</i> , 2016, 6, 21383.	3.3	35
49	Network-Based Comparative Analysis of Arabidopsis Immune Responses to <i>Golovinomyces orontii</i> and <i>Botrytis cinerea</i> Infections. <i>Scientific Reports</i> , 2016, 6, 19149.	3.3	37
50	Identification of WD40 repeats by secondary structure-aided profile-profile alignment. <i>Journal of Theoretical Biology</i> , 2016, 398, 122-129.	1.7	7
51	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
52	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
53	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
54	AraPPISite: a database of fine-grained protein-protein interaction site annotations for Arabidopsis thaliana. <i>Plant Molecular Biology</i> , 2016, 92, 105-116.	3.9	11

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55	SRAMP: prediction of mammalian N ⁶ -methyladenosine (m ⁶ A) sites based on sequence-derived features. <i>Nucleic Acids Research</i> , 2016, 44, e91-e91.	14.5	560
56	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
57	Competition-cooperation relationship networks characterize the competition and cooperation between proteins. <i>Scientific Reports</i> , 2015, 5, 11619.	3.3	3
58	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
59	MAPalyzer: a novel online tool for analyzing microtubule-associated proteins. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	3.0	23
60	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
61	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
62	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
63	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
64	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
65	Operating Mechanism and Molecular Dynamics of Pheromone-Binding Protein ASP1 as Influenced by pH. <i>PLoS ONE</i> , 2014, 9, e110565.	2.5	9
66	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
67	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
68	GPCRserver: an accurate and novel G protein-coupled receptor predictor. <i>Molecular BioSystems</i> , 2014, 10, 2495-2504.	2.9	10
69	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
70	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
71	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
72	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

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73	Functional Characteristics of a Novel Chemosensory Protein in the Cotton Bollworm <i>Helicoverpa armigera</i> (H&A14bner). <i>Journal of Integrative Agriculture</i> , 2013, 12, 853-861.	3.5	29
74	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
75	Structural Propensities of Human Ubiquitination Sites: Accessibility, Centrality and Local Conformation. <i>PLoS ONE</i> , 2013, 8, e83167.	2.5	10
76	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
77	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
78	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
79	Quantitative structure&A146activity relationship study on antitumour activity of a series of flavonoids. <i>Molecular Simulation</i> , 2012, 38, 38-44.	2.0	6
80	COMPUTATIONAL ENZYME DESIGN APPROACHES WITH SIGNIFICANT BIOLOGICAL OUTCOMES: PROGRESS AND CHALLENGES. <i>Computational and Structural Biotechnology Journal</i> , 2012, 2, e201209007.	4.1	21
81	Can simple codon pair usage predict protein&A146protein interaction?. <i>Molecular BioSystems</i> , 2012, 8, 1396.	2.9	28
82	Structure, Binding Characteristics, and 3D Model Prediction of a Newly Identified Odorant-Binding Protein from the Cotton Bollworm, <i>Helicoverpa armigera</i> (H&A14bner). <i>Journal of Integrative Agriculture</i> , 2012, 11, 430-438.	3.5	11
83	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
84	Prediction of protein&A146protein interactions between <i>Ralstonia solanacearum</i> and <i>Arabidopsis thaliana</i> . <i>Amino Acids</i> , 2012, 42, 2363-2371.	2.7	36
85	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
86	A predicted protein&A146protein interaction network of the filamentous fungus <i>Neurospora crassa</i> . <i>Molecular BioSystems</i> , 2011, 7, 2278.	2.9	29
87	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
88	Prediction of Ubiquitination Sites by Using the Composition of k-Spaced Amino Acid Pairs. <i>PLoS ONE</i> , 2011, 6, e22930.	2.5	162
89	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
90	Comprehensive analysis of tandem amino acid repeats from ten angiosperm genomes. <i>BMC Genomics</i> , 2011, 12, 632.	2.8	12

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91	Comparison of linear gap penalties and profile-based variable gap penalties in profile-profile alignments. <i>Computational Biology and Chemistry</i> , 2011, 35, 308-318.	2.3	6
92	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
93	Characterization of the MHC class II β -chain gene in ducks. <i>Immunogenetics</i> , 2011, 63, 667-678.	2.4	16
94	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
95	Outer membrane proteins can be simply identified using secondary structure element alignment. <i>BMC Bioinformatics</i> , 2011, 12, 76.	2.6	16
96	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
97	Evaluation of Protein Phosphorylation Site Predictors. <i>Protein and Peptide Letters</i> , 2010, 17, 64-69.	0.9	15
98	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
99	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
100	An Overview of the De Novo Prediction of Enzyme Catalytic Residues (Supplementary file). <i>Current Bioinformatics</i> , 2009, 4, 197-206.	1.5	4
101	DescFold: A web server for protein fold recognition. <i>BMC Bioinformatics</i> , 2009, 10, 416.	2.6	30
102	TIM-Finder: A new method for identifying TIM-barrel proteins. <i>BMC Structural Biology</i> , 2009, 9, 73.	2.3	13
103	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
104	Exploring the sequence-structure protein landscape in the glycosyltransferase family. <i>Protein Science</i> , 2009, 12, 2291-2302.	7.6	13
105	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
106	<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
107	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
108	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

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109	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
110	The prediction of protein-protein interaction networks in rice blast fungus. <i>BMC Genomics</i> , 2008, 9, 519.	2.8	77
111	<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
112	An improved prediction of catalytic residues in enzyme structures. <i>Protein Engineering, Design and Selection</i> , 2008, 21, 295-302.	2.1	38
113	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
114	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
115	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
116	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
117	Interaction of Positional Isomers of Quercetin Glucuronides with the Transporter ABCC2 (cMOAT). <i>Journal of Pharmaceutical Sciences</i> , 2007, 96, 1073-1083.	3.3	79
118	Toxicity of Ionic Liquids. <i>Clean - Soil, Air, Water</i> , 2007, 35, 42-48.	1.1	499
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	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
121	A new class of anti-thrombosis hexahydropyrazino-[1,6]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
122	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
123	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
124	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
125	Comparison of a homology model and the crystallographic structure of human 11 β -hydroxysteroid dehydrogenase type 1 (11 β HSD1) in a structure-based identification of inhibitors. <i>Journal of Computer-Aided Molecular Design</i> , 2006, 20, 67-81.	2.9	20
126	Descriptor-based protein remote homology identification. <i>Protein Science</i> , 2005, 14, 431-444.	7.6	33

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127	Similarity networks of protein binding sites. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 470-478.	2.6	46
128	The <i>clpB</i> 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
129	The <i>ClgR</i> Protein Regulates Transcription of the <i>clpP</i> Operon in <i>Bifidobacterium breve</i> UCC 2003. <i>Journal of Bacteriology</i> , 2005, 187, 8411-8426.	2.2	41
130	Polysaccharide-Induced Order-to-Order Transitions in Lyotropic Liquid Crystals. <i>Langmuir</i> , 2005, 21, 6165-6169.	3.5	73
131	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
132	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
133	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
134	Kinetic study of thermal inactivation for native and methoxypolyethylene glycol modified trypsin. <i>Process Biochemistry</i> , 2000, 35, 1235-1240.	3.7	17
135	Prediction of protein (domain) structural classes based on amino-acid index. <i>FEBS Journal</i> , 1999, 266, 1043-1049.	0.2	46
136	Solvation energy and thermal stability of hydrophilization-modified alpha-chymotrypsin. <i>The Protein Journal</i> , 1999, 18, 557-564.	1.1	10
137	Title is missing!. <i>Biotechnology Letters</i> , 1999, 13, 781-786.	0.5	26
138	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
139	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
140	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
141	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