Jiangning Song

List of Publications by Year
in descending order

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212 papers	8,168 citations	47 h-index	78 g-index
		47006	66911
225 all docs	225 docs citations	225 times ranked	6599 citing authors

#	Article	IF	Citations
1	MAResNet: predicting transcription factor binding sites by combining multi-scale bottom-up and top-down attention and residual network. Briefings in Bioinformatics, 2022, 23, .	6.5	7
2	T4SEfinder: a bioinformatics tool for genome-scale prediction of bacterial type IV secreted effectors using pre-trained protein language model. Briefings in Bioinformatics, 2022, 23, .	6.5	12
3	Positive-unlabeled learning in bioinformatics and computational biology: a brief review. Briefings in Bioinformatics, 2022, 23, .	6.5	26
4	Critical assessment of computational tools for prokaryotic and eukaryotic promoter prediction. Briefings in Bioinformatics, 2022, 23, .	6.5	11
5	A polytherapy based approach to combat antimicrobial resistance using cubosomes. Nature Communications, 2022, 13, 343.	12.8	31
6	Personalized On-Device E-Health Analytics With Decentralized Block Coordinate Descent. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 2778-2786.	6.3	5
7	ASPIRER: a new computational approach for identifying non-classical secreted proteins based on deep learning. Briefings in Bioinformatics, 2022, 23, .	6.5	11
8	Polymyxin Induces Significant Transcriptomic Perturbations of Cellular Signalling Networks in Human Lung Epithelial Cells. Antibiotics, 2022, 11, 307.	3.7	0
9	Deep Ensemble Machine Learning Framework for the Estimation of PM2.5 Concentrations. Environmental Health Perspectives, 2022, 130, 37004.	6.0	14
10	Enhancing Characteristic Gene Selection and Tumor Classification by the Robust Laplacian Supervised Discriminative Sparse PCA. Journal of Chemical Information and Modeling, 2022, , .	5.4	2
11	Prediction of disease-associated nsSNPs by integrating multi-scale ResNet models with deep feature fusion. Briefings in Bioinformatics, 2022, 23, .	6.5	13
12	RBP-TSTL is a two-stage transfer learning framework for genome-scale prediction of RNA-binding proteins. Briefings in Bioinformatics, 2022, 23, .	6.5	6
13	Performing protein fold recognition by exploiting a stack convolutional neural network with the attention mechanism. Analytical Biochemistry, 2022, 651, 114695.	2.4	1
14	iFeatureOmega:an integrative platform for engineering, visualization and analysis of features from molecular sequences, structural and ligand data sets. Nucleic Acids Research, 2022, 50, W434-W447.	14.5	24
15	PERISCOPE-Opt: Machine learning-based prediction of optimal fermentation conditions and yields of recombinant periplasmic protein expressed in Escherichia coli. Computational and Structural Biotechnology Journal, 2022, 20, 2909-2920.	4.1	6
16	Response to â€œComment on â€˜Deep Ensemble Machine Learning Framework for the Estimation of PM2.5 Concentrationsâ€™â€• Environmental Health Perspectives, 2022, 130, .	6.0	0
17	Cell graph neural networks enable the precise prediction of patient survival in gastric cancer. Npj Precision Oncology, 2022, 6, .	5.4	22
18	PScL-DDCFPred: an ensemble deep learning-based approach for characterizing multiclass subcellular localization of human proteins from bioimage data. Bioinformatics, 2022, 38, 4019-4026.	4.1	6

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19	DeepGenGrep: a general deep learning-based predictor for multiple genomic signals and regions. Bioinformatics, 2022, 38, 4053-4061.	4.1	6
20	Formator: Predicting Lysine Formylation Sites Based on the Most Distant Undersampling and Safe-Level Synthetic Minority Oversampling. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1937-1945.	3.0	17
21	DeepBL: a deep learning-based approach for in silico discovery of beta-lactamases. Briefings in Bioinformatics, 2021, 22, .	6.5	9
22	Computational identification of eukaryotic promoters based on cascaded deep capsule neural networks. Briefings in Bioinformatics, 2021, 22, .	6.5	44
23	A Deep Learning-Based Method for Identification of Bacteriophage-Host Interaction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1801-1810.	3.0	31
24	Large-scale comparative review and assessment of computational methods for anti-cancer peptide identification. Briefings in Bioinformatics, 2021, 22, .	6.5	40
25	Systematic evaluation of machine learning methods for identifying humanâ€“pathogen proteinâ€“protein interactions. Briefings in Bioinformatics, 2021, 22, .	6.5	23
26	Computational prediction and interpretation of both general and specific types of promoters in Escherichia coli by exploiting a stacked ensemble-learning framework. Briefings in Bioinformatics, 2021, 22, 2126-2140.	6.5	58
27	DeepTorrent: a deep learning-based approach for predicting DNA N4-methylcytosine sites. Briefings in Bioinformatics, 2021, 22, .	6.5	84
28	DeepVF: a deep learning-based hybrid framework for identifying virulence factors using the stacking strategy. Briefings in Bioinformatics, 2021, 22, .	6.5	40
29	BastionHub: a universal platform for integrating and analyzing substrates secreted by Gram-negative bacteria. Nucleic Acids Research, 2021, 49, D651-D659.	14.5	34
30	Anthem: a user customised tool for fast and accurate prediction of binding between peptides and HLA class I molecules. Briefings in Bioinformatics, 2021, 22, .	6.5	37
31	iLearnPlus:a comprehensive and automated machine-learning platform for nucleic acid and protein sequence analysis, prediction and visualization. Nucleic Acids Research, 2021, 49, e60-e60.	14.5	124
32	Why can deep convolutional neural networks improve protein fold recognition? A visual explanation by interpretation. Briefings in Bioinformatics, 2021, 22, .	6.5	10
33	ReCGBM: a gradient boosting-based method for predicting human dicer cleavage sites. BMC Bioinformatics, 2021, 22, 63.	2.6	2
34	Comprehensive assessment of machine learning-based methods for predicting antimicrobial peptides. Briefings in Bioinformatics, 2021, 22, .	6.5	55
35	Predicting Proteolysis in Complex Proteomes Using Deep Learning. International Journal of Molecular Sciences, 2021, 22, 3071.	4.1	18
36	PCprophet: a framework for protein complex prediction and differential analysis using proteomic data. Nature Methods, 2021, 18, 520-527.	19.0	32

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37	SAResNet: self-attention residual network for predicting DNA-protein binding. Briefings in Bioinformatics, 2021, 22, .	6.5	22
38	Assessing the performance of computational predictors for estimating protein stability changes upon missense mutations. Briefings in Bioinformatics, 2021, 22, .	6.5	30
39	nhKcr: a new bioinformatics tool for predicting crotonylation sites on human nonhistone proteins based on deep learning. Briefings in Bioinformatics, 2021, 22, .	6.5	29
40	Targeted delivery of LM22A-4 by cubosomes protects retinal ganglion cells in an experimental glaucoma model. Acta Biomaterialia, 2021, 126, 433-444.	8.3	12
41	HEAL: an automated deep learning framework for cancer histopathology image analysis. Bioinformatics, 2021, 37, 4291-4295.	4.1	18
42	OCTID: a one-class learning-based Python package for tumor image detection. Bioinformatics, 2021, 37, 3986-3988.	4.1	8
43	Editorial: Computational Resources for Understanding Biomacromolecular Covalent Modifications. Frontiers in Cell and Developmental Biology, 2021, 9, 728127.	3.7	0
44	XRRpred: accurate predictor of crystal structure quality from protein sequence. Bioinformatics, 2021, 37, 4366-4374.	4.1	3
45	Improving protein fold recognition using triplet network and ensemble deep learning. Briefings in Bioinformatics, 2021, 22, .	6.5	12
46	PScL-HDeep: image-based prediction of protein subcellular location in human tissue using ensemble learning of handcrafted and deep learned features with two-layer feature selection. Briefings in Bioinformatics, 2021, 22, .	6.5	27
47	Porpoise: a new approach for accurate prediction of RNA pseudouridine sites. Briefings in Bioinformatics, 2021, 22, .	6.5	39
48	Leveraging the attention mechanism to improve the identification of DNA N6-methyladenine sites. Briefings in Bioinformatics, 2021, 22, .	6.5	29
49	Temperature-mortality association during and before the COVID-19 pandemic in Italy: A nationwide time-stratified case-crossover study. Urban Climate, 2021, 39, 100948.	5.7	5
50	Accurate multistage prediction of protein crystallization propensity using deep-cascade forest with sequence-based features. Briefings in Bioinformatics, 2021, 22, .	6.5	11
51	MutTMPredictor: Robust and accurate cascade XGBoost classifier for prediction of mutations in transmembrane proteins. Computational and Structural Biotechnology Journal, 2021, 19, 6400-6416.	4.1	16
52	BigFiRSt: A Software Program Using Big Data Technique for Mining Simple Sequence Repeats From Large-Scale Sequencing Data. Frontiers in Big Data, 2021, 4, 727216.	2.9	2
53	PeNGaRoo, a combined gradient boosting and ensemble learning framework for predicting non-classical secreted proteins. Bioinformatics, 2020, 36, 704-712.	4.1	36
54	A comprehensive review and performance evaluation of bioinformatics tools for HLA class I peptide-binding prediction. Briefings in Bioinformatics, 2020, 21, 1119-1135.	6.5	127

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55	iLearn: an integrated platform and meta-learner for feature engineering, machine-learning analysis and modeling of DNA, RNA and protein sequence data. Briefings in Bioinformatics, 2020, 21, 1047-1057.	6.5	294
56	DeepCleave: a deep learning predictor for caspase and matrix metalloprotease substrates and cleavage sites. Bioinformatics, 2020, 36, 1057-1065.	4.1	102
57	Comprehensive review and assessment of computational methods for predicting RNA post-transcriptional modification sites from RNA sequences. Briefings in Bioinformatics, 2020, 21, 1676-1696.	6.5	98
58	An Interpretable Prediction Model for Identifying N7-Methylguanosine Sites Based on XGBoost and SHAP. Molecular Therapy - Nucleic Acids, 2020, 22, 362-372.	5.1	93
59	Phytantriol-Based Cubosome Formulation as an Antimicrobial against Lipopolysaccharide-Deficient Gram-Negative Bacteria. ACS Applied Materials & Interfaces, 2020, 12, 44485-44498.	8.0	12
60	Immunopeptidomic Analysis Reveals That Deamidated HLA-bound Peptides Arise Predominantly from Deglycosylated Precursors. Molecular and Cellular Proteomics, 2020, 19, 1236-1247.	3.8	25
61	Pippin: A random forest-based method for identifying presynaptic and postsynaptic neurotoxins. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050008.	0.8	1
62	PASSION: an ensemble neural network approach for identifying the binding sites of RBPs on circRNAs. Bioinformatics, 2020, 36, 4276-4282.	4.1	58
63	Procleave: Predicting Protease-specific Substrate Cleavage Sites by Combining Sequence and Structural Information. Genomics, Proteomics and Bioinformatics, 2020, 18, 52-64.	6.9	71
64	The YEATS Domain Histone Crotonylation Readers Control Virulence-Related Biology of a Major Human Pathogen. Cell Reports, 2020, 31, 107528.	6.4	19
65	PROSPECT: A web server for predicting protein histidine phosphorylation sites. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050018.	0.8	25
66	Inspector: a lysine succinylation predictor based on edited nearest-neighbor undersampling and adaptive synthetic oversampling. Analytical Biochemistry, 2020, 593, 113592.	2.4	40
67	A framework towards data analytics on hostâ€“pathogen proteinâ€“protein interactions. Journal of Ambient Intelligence and Humanized Computing, 2020, 11, 4667-4679.	4.9	7
68	Regulating polymyxin resistance in Gram-negative bacteria: roles of two-component systems PhoPQ and PmrAB. Future Microbiology, 2020, 15, 445-459.	2.0	51
69	Pan-transcriptomic analysis identified common differentially expressed genes ofAcinetobacter baumanniiin response to polymyxin treatments. Molecular Omics, 2020, 16, 327-338.	2.8	7
70	PRISMOID: a comprehensive 3D structure database for post-translational modifications and mutations with functional impact. Briefings in Bioinformatics, 2020, 21, 1069-1079.	6.5	38
71	An Overview of Bioinformatics Methods for Analyzing Autism Spectrum Disorders. Current Pharmaceutical Design, 2020, 25, 4552-4559.	1.9	4
72	PhosTransfer: A Deep Transfer Learning Framework for Kinase-Specific Phosphorylation Site Prediction in Hierarchy. Lecture Notes in Computer Science, 2020, , 384-395.	1.3	3

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73	ColistinDose, a Mobile App for Determining Intravenous Dosage Regimens of Colistimethate in Critically Ill Adult Patients: Clinician-Centered Design and Development Study. JMIR MHealth and UHealth, 2020, 8, e20525.	3.7	4
74	Prediction of secondary structure population and intrinsic disorder of proteins using multitask deep learning. AMIA ... Annual Symposium proceedings, 2020, 2020, 1325-1334.	0.2	0
75	Toward more accurate prediction of caspase cleavage sites: a comprehensive review of current methods, tools and features. Briefings in Bioinformatics, 2019, 20, 1669-1684.	6.5	13
76	Computational analysis and prediction of lysine malonylation sites by exploiting informative features in an integrative machine-learning framework. Briefings in Bioinformatics, 2019, 20, 2185-2199.	6.5	82
77	Synergistic Combination of Polymyxin B and Enrofloxacin Induced Metabolic Perturbations in Extensive Drug-Resistant Pseudomonas aeruginosa. Frontiers in Pharmacology, 2019, 10, 1146.	3.5	17
78	MULTiPly: a novel multi-layer predictor for discovering general and specific types of promoters. Bioinformatics, 2019, 35, 2957-2965.	4.1	109
79	The flagellotropic bacteriophage YSD1 targets Salmonella Typhi with a Chiâ€like protein tailÂfibre. Molecular Microbiology, 2019, 112, 1831-1846.	2.5	24
80	Response to Comment on â€œA subset of HLA-I peptides are not genomically templated: Evidence for cis- and trans-spliced peptide ligandsâ€. Science Immunology, 2019, 4, .	11.9	25
81	Characterization of the Src-regulated kinome identifies SGK1 as a key mediator of Src-induced transformation. Nature Communications, 2019, 10, 296.	12.8	23
82	Deep learning with evolutionary and genomic profiles for identifying cancer subtypes. Journal of Bioinformatics and Computational Biology, 2019, 17, 1940005.	0.8	12
83	Characterization of the ERG-regulated Kinome in Prostate Cancer Identifies TNIK as a Potential Therapeutic Target. Neoplasia, 2019, 21, 389-400.	5.3	20
84	Positive-unlabelled learning of glycosylation sites in the human proteome. BMC Bioinformatics, 2019, 20, 112.	2.6	60
85	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	15
86	SIMLIN: a bioinformatics tool for prediction of S-sulphenylation in theÂhuman proteome based on multi-stage ensemble-learning models. BMC Bioinformatics, 2019, 20, 602.	2.6	10
87	Twenty years of bioinformatics research for protease-specific substrate and cleavage site prediction: a comprehensive revisit and benchmarking of existing methods. Briefings in Bioinformatics, 2019, 20, 2150-2166.	6.5	70
88	Bastion3: a two-layer ensemble predictor of type III secreted effectors. Bioinformatics, 2019, 35, 2017-2028.	4.1	69
89	Large-scale comparative assessment of computational predictors for lysine post-translational modification sites. Briefings in Bioinformatics, 2019, 20, 2267-2290.	6.5	99
90	iProt-Sub: a comprehensive package for accurately mapping and predicting protease-specific substrates and cleavage sites. Briefings in Bioinformatics, 2019, 20, 638-658.	6.5	166

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91	Systematic analysis and prediction of type IV secreted effector proteins by machine learning approaches. Briefings in Bioinformatics, 2019, 20, 931-951.	6.5	65
92	Comprehensive assessment and performance improvement of effector protein predictors for bacterial secretion systems III, IV and VI. Briefings in Bioinformatics, 2018, 19, bbw100.	6.5	51
93	iFeature: a Python package and web server for features extraction and selection from protein and peptide sequences. Bioinformatics, 2018, 34, 2499-2502.	4.1	481
94	Structural Principles Analysis of Host-Pathogen Protein-Protein Interactions: A Structural Bioinformatics Survey. IEEE Access, 2018, 6, 11760-11771.	4.2	12
95	PREvaIL, an integrative approach for inferring catalytic residues using sequence, structural, and network features in a machine-learning framework. Journal of Theoretical Biology, 2018, 443, 125-137.	1.7	124
96	Comparative analysis of phosphoethanolamine transferases involved in polymyxin resistance across 10 clinically relevant Gram-negative bacteria. International Journal of Antimicrobial Agents, 2018, 51, 586-593.	2.5	18
97	Computing Minimum Reaction Modifications in a Boolean Metabolic Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1853-1862.	3.0	2
98	ProBAPred: Inferring proteinâ€“protein binding affinity by incorporating protein sequence and structural features. Journal of Bioinformatics and Computational Biology, 2018, 16, 1850011.	0.8	4
99	Characteristic and mechanism of immobilization effect of Staphylococcus aureus on human spermatozoa. Microbial Pathogenesis, 2018, 119, 28-34.	2.9	8
100	Bastion6: a bioinformatics approach for accurate prediction of type VI secreted effectors. Bioinformatics, 2018, 34, 2546-2555.	4.1	108
101	Genome-scale metabolic modeling of responses to polymyxins inPseudomonas aeruginosa. GigaScience, 2018, 7, .	6.4	44
102	Critical evaluation of bioinformatics tools for the prediction of protein crystallization propensity. Briefings in Bioinformatics, 2018, 19, 838-852.	6.5	22
103	PROSPERous: high-throughput prediction of substrate cleavage sites for 90 proteases with improved accuracy. Bioinformatics, 2018, 34, 684-687.	4.1	131
104	Comparative analysis and prediction of quorum-sensing peptides using feature representation learning and machine learning algorithms. Briefings in Bioinformatics, 2018, , .	6.5	60
105	A subset of HLA-I peptides are not genomically templated: Evidence for cis- and trans-spliced peptide ligands. Science Immunology, 2018, 3, .	11.9	142
106	Taxonomic Landscape of the Dark Proteomes: Wholeâ€Proteome Scale Interplay Between Structural Darkness, Intrinsic Disorder, and Crystallization Propensity. Proteomics, 2018, 18, 1800243.	2.2	27
107	PhosContext2vec: a distributed representation of residue-level sequence contexts and its application to general and kinase-specific phosphorylation site prediction. Scientific Reports, 2018, 8, 8240.	3.3	25
108	ACPred-FL: a sequence-based predictor using effective feature representation to improve the prediction of anti-cancer peptides. Bioinformatics, 2018, 34, 4007-4016.	4.1	326

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109	Quokka: a comprehensive tool for rapid and accurate prediction of kinase family-specific phosphorylation sites in the human proteome. Bioinformatics, 2018, 34, 4223-4231.	4.1	151
110	FusC, a member of the M16 protease family acquired by bacteria for iron piracy against plants. PLoS Biology, 2018, 16, e2006026.	5.6	17
111	Structural Capacitance in Protein Evolution and Human Diseases. Journal of Molecular Biology, 2018, 430, 3200-3217.	4.2	3
112	Editorial: Network Mining and Machine Learning Methods of the Analysis of the Large-Scale Data in Biology, Medicine and Pharmacy. Current Bioinformatics, 2018, 13, 2-2.	1.5	1
113	SecretEPDB: a comprehensive web-based resource for secreted effector proteins of the bacterial types III, IV and VI secretion systems. Scientific Reports, 2017, 7, 41031.	3.3	38
114	POSSUM: a bioinformatics toolkit for generating numerical sequence feature descriptors based on PSSM profiles. Bioinformatics, 2017, 33, 2756-2758.	4.1	145
115	Antimicrobial susceptibility and mechanisms of fosfomycin resistance in extended-spectrum Î²-lactamase-producing Escherichia coli strains from urinary tract infections in Wenzhou, China. International Journal of Antimicrobial Agents, 2017, 50, 29-34.	2.5	27
116	HIVed, a knowledgebase for differentially expressed human genes and proteins during HIV infection, replication and latency. Scientific Reports, 2017, 7, 45509.	3.3	5
117	Inference Method for Developing Mathematical Models of Cell Signaling Pathways Using Proteomic Datasets. Methods in Molecular Biology, 2017, 1526, 329-344.	0.9	0
118	Structure-based engineering of a pectate lyase with improved specific activity for ramie degumming. Applied Microbiology and Biotechnology, 2017, 101, 2919-2929.	3.6	18
119	Knowledge-transfer learning for prediction of matrix metalloprotease substrate-cleavage sites. Scientific Reports, 2017, 7, 5755.	3.3	17
120	PhosphoPredict: A bioinformatics tool for prediction of human kinase-specific phosphorylation substrates and sites by integrating heterogeneous feature selection. Scientific Reports, 2017, 7, 6862.	3.3	72
121	Leveraging Stacked Denoising Autoencoder in Prediction of Pathogen-Host Protein-Protein Interactions. , 2017, , .		9
122	Reductive evolution in outer membrane protein biogenesis has not compromised cell surface complexity in Helicobacter pylori. MicrobiologyOpen, 2017, 6, e00513.	3.0	10
123	Staged heterogeneity learning to identify conformational B-cell epitopes from antigen sequences. BMC Genomics, 2017, 18, 113.	2.8	5
124	Collaborative data analytics towards prediction on pathogen-host protein-protein interactions. , 2017, , .		2
125	Towards Elucidating the Structural Principles of Host-Pathogen Protein-Protein Interaction Networks: A Bioinformatics Survey. , 2017, , .		2
126	Survey of Predictors of Propensity for Protein Production and Crystallization with Application to Predict Resolution of Crystal Structures. Current Protein and Peptide Science, 2017, 19, 200-210.	1.4	7

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127	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. Current Bioinformatics, 2017, 12, .	1.5	17
128	Integrated Analysis of Multiscale Large-Scale Biological Data for Investigating Human Disease 2016. BioMed Research International, 2016, 2016, 1-2.	1.9	2
129	SOHPRED: a new bioinformatics tool for the characterization and prediction of human S-sulfenylation sites. Molecular BioSystems, 2016, 12, 2849-2858.	2.9	37
130	PolyQ 2.0: an improved version of PolyQ, a database of human polyglutamine proteins. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw021.	3.0	3
131	DephosSite: a machine learning approach for discovering phosphotase-specific dephosphorylation sites. Scientific Reports, 2016, 6, 23510.	3.3	15
132	Crysalis: an integrated server for computational analysis and design of protein crystallization. Scientific Reports, 2016, 6, 21383.	3.3	35
133	Global metabolic analyses identify key differences in metabolite levels between polymyxin-susceptible and polymyxin-resistant Acinetobacter baumannii. Scientific Reports, 2016, 6, 22287.	3.3	49
134	Host-Pathogen Protein Interaction Prediction Based on Local Topology Structures of a Protein Interaction Network. , 2016, , .		2
135	Periscope: quantitative prediction of soluble protein expression in the periplasm of Escherichia coli. Scientific Reports, 2016, 6, 21844.	3.3	15
136	The exploration of network motifs as potential drug targets from post-translational regulatory networks. Scientific Reports, 2016, 6, 20558.	3.3	13
137	Identification of WD40 repeats by secondary structure-aided profileâ€“profile alignment. Journal of Theoretical Biology, 2016, 398, 122-129.	1.7	7
138	SPAR: a random forest-based predictor for self-interacting proteins with fine-grained domain information. Amino Acids, 2016, 48, 1655-1665.	2.7	25
139	Towards Data Analytics of Pathogen-Host Protein-Protein Interaction: A Survey. , 2016, , .		8
140	A neural network learning approach for improving the prediction of residue depth based on sequence-derived features. RSC Advances, 2016, 6, 67729-67738.	3.6	1
141	GlycoMinestruct: a new bioinformatics tool for highly accurate mapping of the human N-linked and O-linked glycoproteomes by incorporating structural features. Scientific Reports, 2016, 6, 34595.	3.3	69
142	Using contrast patterns between true complexes and random subgraphs in PPI networks to predict unknown protein complexes. Scientific Reports, 2016, 6, 21223.	3.3	30
143	KinetochoreDB: a comprehensive online resource for the kinetochore and its related proteins. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw019.	3.0	0
144	A highly Conserved Aspartic Acid Residue of the Chitosanase from Bacillus Sp. TS Is Involved in the Substrate Binding. Applied Biochemistry and Biotechnology, 2016, 180, 1167-1179.	2.9	4

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145	Anthelmintic closantel enhances bacterial killing of polymyxin B against multidrug-resistant Acinetobacter baumannii. Journal of Antibiotics, 2016, 69, 415-421.	2.0	27
146	Critical evaluation ofin silicomethods for prediction of coiled-coil domains in proteins. Briefings in Bioinformatics, 2016, 17, 270-282.	6.5	22
147	Draft Genome Sequence of Lysinibacillus fusiformis Strain SW-B9, a Novel Strain for Biotransformation of Isoeugenol to Vanillin. Genome Announcements, 2015, 3, .	0.8	6
148	Integrated Analysis of Multiscale Large-Scale Biological Data for Investigating Human Disease. BioMed Research International, 2015, 2015, 1-2.	1.9	0
149	Co-Occurring Atomic Contacts for the Characterization of Protein Binding Hot Spots. PLoS ONE, 2015, 10, e0144486.	2.5	8
150	Extracellular Overexpression of Chitosanase from Bacillus sp. TS in Escherichia coli. Applied Biochemistry and Biotechnology, 2015, 175, 3271-3286.	2.9	21
151	GlycoMine: a machine learning-based approach for predicting N-, C- and O-linked glycosylation in the human proteome. Bioinformatics, 2015, 31, 1411-1419.	4.1	167
152	Computing Smallest Intervention Strategies for Multiple Metabolic Networks in a Boolean Model. Journal of Computational Biology, 2015, 22, 85-110.	1.6	7
153	Significantly improving the yield of recombinant proteins in Bacillus subtilis by a novel powerful mutagenesis tool (ARTP): Alkaline Î±-amylase as a case study. Protein Expression and Purification, 2015, 114, 82-88.	1.3	44
154	Towards more accurate prediction of ubiquitination sites: a comprehensive review of current methods, tools and features. Briefings in Bioinformatics, 2015, 16, 640-657.	6.5	76
155	Computational characterization of parallel dimeric and trimeric coiled-coils using effective amino acid indices. Molecular BioSystems, 2015, 11, 354-360.	2.9	16
156	Towards more accurate prediction of protein folding rates: a review of the existing web-based bioinformatics approaches. Briefings in Bioinformatics, 2015, 16, 314-324.	6.5	24
157	Process optimization of high-level extracellular production of alkaline pectate lyase in recombinant Escherichia coli BL21 (DE3). Biochemical Engineering Journal, 2015, 93, 38-46.	3.6	15
158	Computational Identification of Protein Pupylation Sites by Using Profile-Based Composition of k-Spaced Amino Acid Pairs. PLoS ONE, 2015, 10, e0129635.	2.5	65
159	Cascleave 2.0, a new approach for predicting caspase and granzyme cleavage targets. Bioinformatics, 2014, 30, 71-80.	4.1	63
160	Cloning, expression and characterization of a pectate lyase from Paenibacillus sp. 0602 in recombinant Escherichia coli. BMC Biotechnology, 2014, 14, 18.	3.3	37
161	Metabolic Changes in Klebsiella oxytoca in Response to Low Oxidoreduction Potential, as Revealed by Comparative Proteomic Profiling Integrated with Flux Balance Analysis. Applied and Environmental Microbiology, 2014, 80, 2833-2841.	3.1	14
162	Bioinformatics approaches for improved recombinant protein production in Escherichia coli: protein solubility prediction. Briefings in Bioinformatics, 2014, 15, 953-962.	6.5	64

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163	Characterization and high-level expression of a metagenome-derived alkaline pectate lyase in recombinant Escherichia coli. Process Biochemistry, 2014, 49, 69-76.	3.7	34
164	Accurate in silico identification of species-specific acetylation sites by integrating protein sequence-derived and functional features. Scientific Reports, 2014, 4, 5765.	3.3	71
165	Integer Programming-Based Method for Designing Synthetic Metabolic Networks by Minimum Reaction Insertion in a Boolean Model. PLoS ONE, 2014, 9, e92637.	2.5	7
166	PredPPCrys: Accurate Prediction of Sequence Cloning, Protein Production, Purification and Crystallization Propensity from Protein Sequences Using Multi-Step Heterogeneous Feature Fusion and Selection. PLoS ONE, 2014, 9, e105902.	2.5	27
167	hCKSAAP_UbSite: Improved prediction of human ubiquitination sites by exploiting amino acid pattern and properties. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 1461-1467.	2.3	97
168	Prediction of protein-RNA residue-base contacts using two-dimensional conditional random field with the lasso. BMC Systems Biology, 2013, 7, S15.	3.0	10
169	ZincExplorer: an accurate hybrid method to improve the prediction of zinc-binding sites from protein sequences. Molecular BioSystems, 2013, 9, 2213.	2.9	33
170	Development of thermodynamic optimum searching (TOS) to improve the prediction accuracy of flux balance analysis. Biotechnology and Bioengineering, 2013, 110, 914-923.	3.3	12
171	Structural Propensities of Human Ubiquitination Sites: Accessibility, Centrality and Local Conformation. PLoS ONE, 2013, 8, e83167.	2.5	10
172	Identifying Coevolution Between Amino Acid Residues in Protein Families: Advances in the Improvement and Evaluation of Correlated Mutation Algorithms. Current Bioinformatics, 2013, 8, 148-160.	1.5	3
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