Jiangning Song

List of Publications by Year
in descending order

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212 papers	8,168 citations	53939 47 h-index	75989 78 g-index
225 all docs	225 docs citations	225 times ranked	7355 citing authors

#	Article	IF	Citations
1	iFeature: a Python package and web server for features extraction and selection from protein and peptide sequences. Bioinformatics, 2018, 34, 2499-2502.	1.8	481
2	ACPred-FL: a sequence-based predictor using effective feature representation to improve the prediction of anti-cancer peptides. Bioinformatics, 2018, 34, 4007-4016.	1.8	326
3	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.	3.2	294
4	PROSPER: An Integrated Feature-Based Tool for Predicting Protease Substrate Cleavage Sites. PLoS ONE, 2012, 7, e50300.	1.1	265
5	APIS: accurate prediction of hot spots in protein interfaces by combining protrusion index with solvent accessibility. BMC Bioinformatics, 2010, 11, 174.	1.2	178
6	GlycoMine: a machine learning-based approach for predicting N-, C- and O-linked glycosylation in the human proteome. Bioinformatics, 2015, 31, 1411-1419.	1.8	167
7	iProt-Sub: a comprehensive package for accurately mapping and predicting protease-specific substrates and cleavage sites. Briefings in Bioinformatics, 2019, 20, 638-658.	3.2	166
8	Quokka: a comprehensive tool for rapid and accurate prediction of kinase family-specific phosphorylation sites in the human proteome. Bioinformatics, 2018, 34, 4223-4231.	1.8	151
9	Cascleave: towards more accurate prediction of caspase substrate cleavage sites. Bioinformatics, 2010, 26, 752-760.	1.8	148
10	POSSUM: a bioinformatics toolkit for generating numerical sequence feature descriptors based on PSSM profiles. Bioinformatics, 2017, 33, 2756-2758.	1.8	145
11	A subset of HLA-I peptides are not genomically templated: Evidence for cis- and trans-spliced peptide ligands. Science Immunology, 2018, 3, .	5.6	142
12	PROSPERous: high-throughput prediction of substrate cleavage sites for 90 proteases with improved accuracy. Bioinformatics, 2018, 34, 684-687.	1.8	131
13	A comprehensive review and performance evaluation of bioinformatics tools for HLA class I peptide-binding prediction. Briefings in Bioinformatics, 2020, 21, 1119-1135.	3.2	127
14	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.	0.8	124
15	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.	6.5	124
16	Production of Octenyl Succinic Anhydride-Modified Waxy Corn Starch and Its Characterization. Journal of Agricultural and Food Chemistry, 2008, 56, 11499-11506.	2.4	114
17	MULTiPly: a novel multi-layer predictor for discovering general and specific types of promoters. Bioinformatics, 2019, 35, 2957-2965.	1.8	109
18	Bastion6: a bioinformatics approach for accurate prediction of type VI secreted effectors. Bioinformatics, 2018, 34, 2546-2555.	1.8	108

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19	DeepCleave: a deep learning predictor for caspase and matrix metalloprotease substrates and cleavage sites. Bioinformatics, 2020, 36, 1057-1065.	1.8	102
20	Large-scale comparative assessment of computational predictors for lysine post-translational modification sites. Briefings in Bioinformatics, 2019, 20, 2267-2290.	3.2	99
21	Comprehensive review and assessment of computational methods for predicting RNA post-transcriptional modification sites from RNA sequences. Briefings in Bioinformatics, 2020, 21, 1676-1696.	3.2	98
22	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.	1.1	97
23	An Interpretable Prediction Model for Identifying N7-Methylguanosine Sites Based on XGBoost and SHAP. Molecular Therapy - Nucleic Acids, 2020, 22, 362-372.	2.3	93
24	Resolvins E1 and D1 inhibit interstitial fibrosis in the obstructed kidney via inhibition of local fibroblast proliferation. Journal of Pathology, 2012, 228, 506-519.	2.1	85
25	DeepTorrent: a deep learning-based approach for predicting DNA N4-methylcytosine sites. Briefings in Bioinformatics, 2021, 22, .	3.2	84
26	Prediction of cis/trans isomerization in proteins using PSI-BLAST profiles and secondary structure information. BMC Bioinformatics, 2006, 7, 124.	1.2	83
27	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.	3.2	82
28	Towards more accurate prediction of ubiquitination sites: a comprehensive review of current methods, tools and features. Briefings in Bioinformatics, 2015, 16, 640-657.	3.2	76
29	PhosphoPredict: A bioinformatics tool for prediction of human kinase-specific phosphorylation substrates and sites by integrating heterogeneous feature selection. Scientific Reports, 2017, 7, 6862.	1.6	72
30	Accurate in silico identification of species-specific acetylation sites by integrating protein sequence-derived and functional features. Scientific Reports, 2014, 4, 5765.	1.6	71
31	Procleave: Predicting Protease-specific Substrate Cleavage Sites by Combining Sequence and Structural Information. Genomics, Proteomics and Bioinformatics, 2020, 18, 52-64.	3.0	71
32	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.	3.2	70
33	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.	1.6	69
34	Bastion3: a two-layer ensemble predictor of type III secreted effectors. Bioinformatics, 2019, 35, 2017-2028.	1.8	69
35	Predicting disulfide connectivity from protein sequence using multiple sequence feature vectors and secondary structure. Bioinformatics, 2007, 23, 3147-3154.	1.8	65
36	Systematic analysis and prediction of type IV secreted effector proteins by machine learning approaches. Briefings in Bioinformatics, 2019, 20, 931-951.	3.2	65

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37	Computational Identification of Protein Pupylation Sites by Using Profile-Based Composition of k-Spaced Amino Acid Pairs. PLoS ONE, 2015, 10, e0129635.	1.1	65
38	Bioinformatics approaches for improved recombinant protein production in Escherichia coli: protein solubility prediction. Briefings in Bioinformatics, 2014, 15, 953-962.	3.2	64
39	Cascleave 2.0, a new approach for predicting caspase and granzyme cleavage targets. Bioinformatics, 2014, 30, 71-80.	1.8	63
40	Comparative analysis and prediction of quorum-sensing peptides using feature representation learning and machine learning algorithms. Briefings in Bioinformatics, 2018, , .	3.2	60
41	Positive-unlabelled learning of glycosylation sites in the human proteome. BMC Bioinformatics, 2019, 20, 112.	1.2	60
42	PASSION: an ensemble neural network approach for identifying the binding sites of RBPs on circRNAs. Bioinformatics, 2020, 36, 4276-4282.	1.8	58
43	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.	3.2	58
44	Comprehensive assessment of machine learning-based methods for predicting antimicrobial peptides. Briefings in Bioinformatics, 2021, 22, .	3.2	55
45	HSEpred: predict half-sphere exposure from protein sequences. Bioinformatics, 2008, 24, 1489-1497.	1.8	53
46	Predicting residue-wise contact orders in proteins by support vector regression. BMC Bioinformatics, 2006, 7, 425.	1.2	51
47	Comprehensive assessment and performance improvement of effector protein predictors for bacterial secretion systems III, IV and VI. Briefings in Bioinformatics, 2018, 19, bbw100.	3.2	51
48	Regulating polymyxin resistance in Gram-negative bacteria: roles of two-component systems PhoPQ and PmrAB. Future Microbiology, 2020, 15, 445-459.	1.0	51
49	Global metabolic analyses identify key differences in metabolite levels between polymyxin-susceptible and polymyxin-resistant Acinetobacter baumannii. Scientific Reports, 2016, 6, 22287.	1.6	49
50	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.	0.6	44
51	Genome-scale metabolic modeling of responses to polymyxins inPseudomonas aeruginosa. GigaScience, 2018, 7, .	3.3	44
52	Computational identification of eukaryotic promoters based on cascaded deep capsule neural networks. Briefings in Bioinformatics, 2021, 22, .	3.2	44
53	FunSAV: Predicting the Functional Effect of Single Amino Acid Variants Using a Two-Stage Random Forest Model. PLoS ONE, 2012, 7, e43847.	1.1	43
54	Large-scale comparative review and assessment of computational methods for anti-cancer peptide identification. Briefings in Bioinformatics, 2021, 22, .	3.2	40

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55	Inspector: a lysine succinylation predictor based on edited nearest-neighbor undersampling and adaptive synthetic oversampling. Analytical Biochemistry, 2020, 593, 113592.	1.1	40
56	DeepVF: a deep learning-based hybrid framework for identifying virulence factors using the stacking strategy. Briefings in Bioinformatics, 2021, 22, .	3.2	40
57	Prodepth: Predict Residue Depth by Support Vector Regression Approach from Protein Sequences Only. PLoS ONE, 2009, 4, e7072.	1.1	40
58	Improving the accuracy of predicting disulfide connectivity by feature selection. Journal of Computational Chemistry, 2010, 31, 1478-1485.	1.5	39
59	Predicting Residue-Residue Contacts and Helix-Helix Interactions in Transmembrane Proteins Using an Integrative Feature-Based Random Forest Approach. PLoS ONE, 2011, 6, e26767.	1.1	39
60	Porpoise: a new approach for accurate prediction of RNA pseudouridine sites. Briefings in Bioinformatics, 2021, 22, .	3.2	39
61	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.	1.6	38
62	PRISMOID: a comprehensive 3D structure database for post-translational modifications and mutations with functional impact. Briefings in Bioinformatics, 2020, 21, 1069-1079.	3.2	38
63	Cloning, expression and characterization of a pectate lyase from Paenibacillus sp. 0602 in recombinant Escherichia coli. BMC Biotechnology, 2014, 14, 18.	1.7	37
64	SOHPRED: a new bioinformatics tool for the characterization and prediction of human S-sulfenylation sites. Molecular BioSystems, 2016, 12, 2849-2858.	2.9	37
65	Anthem: a user customised tool for fast and accurate prediction of binding between peptides and HLA class I molecules. Briefings in Bioinformatics, 2021, 22, .	3.2	37
66	TANGLE: Two-Level Support Vector Regression Approach for Protein Backbone Torsion Angle Prediction from Primary Sequences. PLoS ONE, 2012, 7, e30361.	1.1	36
67	PeNGaRoo, a combined gradient boosting and ensemble learning framework for predicting non-classical secreted proteins. Bioinformatics, 2020, 36, 704-712.	1.8	36
68	Mathematical Modelling of the MAP Kinase Pathway Using Proteomic Datasets. PLoS ONE, 2012, 7, e42230.	1.1	35
69	Crysalis: an integrated server for computational analysis and design of protein crystallization. Scientific Reports, 2016, 6, 21383.	1.6	35
70	Characterization and high-level expression of a metagenome-derived alkaline pectate lyase in recombinant Escherichia coli. Process Biochemistry, 2014, 49, 69-76.	1.8	34
71	BastionHub: a universal platform for integrating and analyzing substrates secreted by Gram-negative bacteria. Nucleic Acids Research, 2021, 49, D651-D659.	6.5	34
72	ZincExplorer: an accurate hybrid method to improve the prediction of zinc-binding sites from protein sequences. Molecular BioSystems, 2013, 9, 2213.	2.9	33

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73	PCprophet: a framework for protein complex prediction and differential analysis using proteomic data. Nature Methods, 2021, 18, 520-527.	9.0	32
74	BIOINFORMATIC APPROACHES FOR PREDICTING SUBSTRATES OF PROTEASES. Journal of Bioinformatics and Computational Biology, 2011, 09, 149-178.	0.3	31
75	A Deep Learning-Based Method for Identification of Bacteriophage-Host Interaction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1801-1810.	1.9	31
76	A polytherapy based approach to combat antimicrobial resistance using cubosomes. Nature Communications, 2022, 13, 343.	5.8	31
77	Using contrast patterns between true complexes and random subgraphs in PPI networks to predict unknown protein complexes. Scientific Reports, 2016, 6, 21223.	1.6	30
78	Assessing the performance of computational predictors for estimating protein stability changes upon missense mutations. Briefings in Bioinformatics, 2021, 22, .	3.2	30
79	nhKcr: a new bioinformatics tool for predicting crotonylation sites on human nonhistone proteins based on deep learning. Briefings in Bioinformatics, 2021, 22, .	3.2	29
80	Leveraging the attention mechanism to improve the identification of DNA N6-methyladenine sites. Briefings in Bioinformatics, 2021, 22, .	3.2	29
81	Can simple codon pair usage predict proteinâ€“protein interaction?. Molecular BioSystems, 2012, 8, 1396.	2.9	28
82	Exploring drug combinations in genetic interaction network. BMC Bioinformatics, 2012, 13, S7.	1.2	28
83	The drug cocktail network. BMC Systems Biology, 2012, 6, S5.	3.0	28
84	Anthelmintic closantel enhances bacterial killing of polymyxin B against multidrug-resistant Acinetobacter baumannii. Journal of Antibiotics, 2016, 69, 415-421.	1.0	27
85	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.	1.1	27
86	Taxonomic Landscape of the Dark Proteomes: Wholeâ€Proteome Scale Interplay Between Structural Darkness, Intrinsic Disorder, and Crystallization Propensity. Proteomics, 2018, 18, 1800243.	1.3	27
87	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, .	3.2	27
88	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.	1.1	27
89	Positive-unlabeled learning in bioinformatics and computational biology: a brief review. Briefings in Bioinformatics, 2022, 23, .	3.2	26
90	SPAR: a random forest-based predictor for self-interacting proteins with fine-grained domain information. Amino Acids, 2016, 48, 1655-1665.	1.2	25

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91	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.	1.6	25
92	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, .	5.6	25
93	Immunopeptidomic Analysis Reveals That Deamidated HLA-bound Peptides Arise Predominantly from Deglycosylated Precursors. Molecular and Cellular Proteomics, 2020, 19, 1236-1247.	2.5	25
94	PROSPECT: A web server for predicting protein histidine phosphorylation sites. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050018.	0.3	25
95	Conditional random field approach to prediction of protein-protein interactions using domain information. BMC Systems Biology, 2011, 5, S8.	3.0	24
96	An Integrative Computational Framework Based on a Two-Step Random Forest Algorithm Improves Prediction of Zinc-Binding Sites in Proteins. PLoS ONE, 2012, 7, e49716.	1.1	24
97	Towards more accurate prediction of protein folding rates: a review of the existing web-based bioinformatics approaches. Briefings in Bioinformatics, 2015, 16, 314-324.	3.2	24
98	The flagellotropic bacteriophage YSD1 targets Salmonella Typhi with a Chiâ€like protein tailÂfibre. Molecular Microbiology, 2019, 112, 1831-1846.	1.2	24
99	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.	6.5	24
100	Characterization of the Src-regulated kinome identifies SGK1 as a key mediator of Src-induced transformation. Nature Communications, 2019, 10, 296.	5.8	23
101	Systematic evaluation of machine learning methods for identifying humanâ€“pathogen proteinâ€“protein interactions. Briefings in Bioinformatics, 2021, 22, .	3.2	23
102	Critical evaluation ofin silicomethods for prediction of coiled-coil domains in proteins. Briefings in Bioinformatics, 2016, 17, 270-282.	3.2	22
103	Critical evaluation of bioinformatics tools for the prediction of protein crystallization propensity. Briefings in Bioinformatics, 2018, 19, 838-852.	3.2	22
104	SAResNet: self-attention residual network for predicting DNA-protein binding. Briefings in Bioinformatics, 2021, 22, .	3.2	22
105	Cell graph neural networks enable the precise prediction of patient survival in gastric cancer. Npj Precision Oncology, 2022, 6, .	2.3	22
106	COMPUTATIONAL ENZYME DESIGN APPROACHES WITH SIGNIFICANT BIOLOGICAL OUTCOMES: PROGRESS AND CHALLENGES. Computational and Structural Biotechnology Journal, 2012, 2, e201209007.	1.9	21
107	Extracellular Overexpression of Chitosanase from Bacillus sp. TS in Escherichia coli. Applied Biochemistry and Biotechnology, 2015, 175, 3271-3286.	1.4	21
108	PredCSF: An Integrated Feature-Based Approach for Predicting Conotoxin Superfamily. Protein and Peptide Letters, 2011, 18, 261-267.	0.4	20

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109	Increased production of alkaline polygalacturonate lyase in the recombinant Pichia pastoris by controlling cell concentration during continuous culture. Bioresource Technology, 2012, 124, 338-346.	4.8	20
110	Characterization of the ERG-regulated Kinome in Prostate Cancer Identifies TNIK as a Potential Therapeutic Target. Neoplasia, 2019, 21, 389-400.	2.3	20
111	The YEATS Domain Histone Crotonylation Readers Control Virulence-Related Biology of a Major Human Pathogen. Cell Reports, 2020, 31, 107528.	2.9	19
112	Prediction of the disulfide-bonding state of cysteines in proteins based on dipeptide composition. Biochemical and Biophysical Research Communications, 2004, 318, 142-147.	1.0	18
113	Structure-based engineering of a pectate lyase with improved specific activity for ramie degumming. Applied Microbiology and Biotechnology, 2017, 101, 2919-2929.	1.7	18
114	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.	1.1	18
115	Predicting Proteolysis in Complex Proteomes Using Deep Learning. International Journal of Molecular Sciences, 2021, 22, 3071.	1.8	18
116	HEAL: an automated deep learning framework for cancer histopathology image analysis. Bioinformatics, 2021, 37, 4291-4295.	1.8	18
117	Efficient large-scale protein sequence comparison and gene matching to identify orthologs and co-orthologs. Nucleic Acids Research, 2012, 40, e44-e44.	6.5	17
118	Knowledge-transfer learning for prediction of matrix metalloprotease substrate-cleavage sites. Scientific Reports, 2017, 7, 5755.	1.6	17
119	FusC, a member of the M16 protease family acquired by bacteria for iron piracy against plants. PLoS Biology, 2018, 16, e2006026.	2.6	17
120	Synergistic Combination of Polymyxin B and Enrofloxacin Induced Metabolic Perturbations in Extensive Drug-Resistant Pseudomonas aeruginosa. Frontiers in Pharmacology, 2019, 10, 1146.	1.6	17
121	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.	1.9	17
122	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, .	0.7	17
123	Prediction of Protein Folding Rates from Structural Topology and Complex Network Properties. IPSJ Transactions on Bioinformatics, 2010, 3, 40-53.	0.2	16
124	Computational characterization of parallel dimeric and trimeric coiled-coils using effective amino acid indices. Molecular BioSystems, 2015, 11, 354-360.	2.9	16
125	MutTMPredictor: Robust and accurate cascade XGBoost classifier for prediction of mutations in transmembrane proteins. Computational and Structural Biotechnology Journal, 2021, 19, 6400-6416.	1.9	16
126	Process optimization of high-level extracellular production of alkaline pectate lyase in recombinant Escherichia coli BL21 (DE3). Biochemical Engineering Journal, 2015, 93, 38-46.	1.8	15

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127	DephosSite: a machine learning approach for discovering phosphotase-specific dephosphorylation sites. Scientific Reports, 2016, 6, 23510.	1.6	15
128	Periscope: quantitative prediction of soluble protein expression in the periplasm of Escherichia coli. Scientific Reports, 2016, 6, 21844.	1.6	15
129	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	15
130	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.	1.4	14
131	Deep Ensemble Machine Learning Framework for the Estimation of PM2.5 Concentrations. Environmental Health Perspectives, 2022, 130, 37004.	2.8	14
132	The exploration of network motifs as potential drug targets from post-translational regulatory networks. Scientific Reports, 2016, 6, 20558.	1.6	13
133	Toward more accurate prediction of caspase cleavage sites: a comprehensive review of current methods, tools and features. Briefings in Bioinformatics, 2019, 20, 1669-1684.	3.2	13
134	Prediction of disease-associated nsSNPs by integrating multi-scale ResNet models with deep feature fusion. Briefings in Bioinformatics, 2022, 23, .	3.2	13
135	Development of thermodynamic optimum searching (TOS) to improve the prediction accuracy of flux balance analysis. Biotechnology and Bioengineering, 2013, 110, 914-923.	1.7	12
136	Structural Principles Analysis of Host-Pathogen Protein-Protein Interactions: A Structural Bioinformatics Survey. IEEE Access, 2018, 6, 11760-11771.	2.6	12
137	Deep learning with evolutionary and genomic profiles for identifying cancer subtypes. Journal of Bioinformatics and Computational Biology, 2019, 17, 1940005.	0.3	12
138	Phytantriol-Based Cubosome Formulation as an Antimicrobial against Lipopolysaccharide-Deficient Gram-Negative Bacteria. ACS Applied Materials & Interfaces, 2020, 12, 44485-44498.	4.0	12
139	Targeted delivery of LM22A-4 by cubosomes protects retinal ganglion cells in an experimental glaucoma model. Acta Biomaterialia, 2021, 126, 433-444.	4.1	12
140	Improving protein fold recognition using triplet network and ensemble deep learning. Briefings in Bioinformatics, 2021, 22, .	3.2	12
141	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, .	3.2	12
142	Identification of Catalytic Residues Using a Novel Feature that Integrates the Microenvironment and Geometrical Location Properties of Residues. PLoS ONE, 2012, 7, e41370.	1.1	12
143	Accurate multistage prediction of protein crystallization propensity using deep-cascade forest with sequence-based features. Briefings in Bioinformatics, 2021, 22, .	3.2	11
144	Critical assessment of computational tools for prokaryotic and eukaryotic promoter prediction. Briefings in Bioinformatics, 2022, 23, .	3.2	11

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145	ASPIRER: a new computational approach for identifying non-classical secreted proteins based on deep learning. Briefings in Bioinformatics, 2022, 23, .	3.2	11
146	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
147	Reductive evolution in outer membrane protein biogenesis has not compromised cell surface complexity in Helicobacter pylori. MicrobiologyOpen, 2017, 6, e00513.	1.2	10
148	SIMLIN: a bioinformatics tool for prediction of S-sulphenylation in theÂhuman proteome based on multi-stage ensemble-learning models. BMC Bioinformatics, 2019, 20, 602.	1.2	10
149	Why can deep convolutional neural networks improve protein fold recognition? A visual explanation by interpretation. Briefings in Bioinformatics, 2021, 22, .	3.2	10
150	Structural Propensities of Human Ubiquitination Sites: Accessibility, Centrality and Local Conformation. PLoS ONE, 2013, 8, e83167.	1.1	10
151	Leveraging Stacked Denoising Autoencoder in Prediction of Pathogen-Host Protein-Protein Interactions. , 2017, , .		9
152	DeepBL: a deep learning-based approach for in silico discovery of beta-lactamases. Briefings in Bioinformatics, 2021, 22, .	3.2	9
153	Co-Occurring Atomic Contacts for the Characterization of Protein Binding Hot Spots. PLoS ONE, 2015, 10, e0144486.	1.1	8
154	Towards Data Analytics of Pathogen-Host Protein-Protein Interaction: A Survey. , 2016, , .		8
155	Characteristic and mechanism of immobilization effect of Staphylococcus aureus on human spermatozoa. Microbial Pathogenesis, 2018, 119, 28-34.	1.3	8
156	OCTID: a one-class learning-based Python package for tumor image detection. Bioinformatics, 2021, 37, 3986-3988.	1.8	8
157	EGM: encapsulated gene-by-gene matching to identify gene orthologs and homologous segments in genomes. Bioinformatics, 2010, 26, 2076-2084.	1.8	7
158	Predicting Serpin/Protease Interactions. Methods in Enzymology, 2011, 501, 237-273.	0.4	7
159	Computing Smallest Intervention Strategies for Multiple Metabolic Networks in a Boolean Model. Journal of Computational Biology, 2015, 22, 85-110.	0.8	7
160	Identification of WD40 repeats by secondary structure-aided profileâ€“profile alignment. Journal of Theoretical Biology, 2016, 398, 122-129.	0.8	7
161	A framework towards data analytics on hostâ€“pathogen proteinâ€“protein interactions. Journal of Ambient Intelligence and Humanized Computing, 2020, 11, 4667-4679.	3.3	7
162	MAResNet: predicting transcription factor binding sites by combining multi-scale bottom-up and top-down attention and residual network. Briefings in Bioinformatics, 2022, 23, .	3.2	7

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163	Pan-transcriptomic analysis identified common differentially expressed genes ofAcinetobacter baumanniiin response to polymyxin treatments. Molecular Omics, 2020, 16, 327-338.	1.4	7
164	Integer Programming-Based Method for Designing Synthetic Metabolic Networks by Minimum Reaction Insertion in a Boolean Model. PLoS ONE, 2014, 9, e92637.	1.1	7
165	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.	0.7	7
166	Recent Advances in Predicting Functional Impact of Single Amino Acid Polymorphisms: A Review of Useful Features, Computational Methods and Available Tools. Current Bioinformatics, 2013, 8, 161-176.	0.7	7
167	Cooperativity of the oxidization of cysteines in globular proteins. Journal of Theoretical Biology, 2004, 231, 85-95.	0.8	6
168	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
169	RBP-TSTL is a two-stage transfer learning framework for genome-scale prediction of RNA-binding proteins. Briefings in Bioinformatics, 2022, 23, .	3.2	6
170	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.	1.9	6
171	PScL-DDCFPred: an ensemble deep learning-based approach for characterizing multiclass subcellular localization of human proteins from bioimage data. Bioinformatics, 2022, 38, 4019-4026.	1.8	6
172	DeepGenGrep: a general deep learning-based predictor for multiple genomic signals and regions. Bioinformatics, 2022, 38, 4053-4061.	1.8	6
173	Discriminative random field approach to prediction of protein residue contacts. , 2011, , .		5
174	Exploring drug combinations in a drug-cocktail network. , 2011, , .		5
175	HIVed, a knowledgebase for differentially expressed human genes and proteins during HIV infection, replication and latency. Scientific Reports, 2017, 7, 45509.	1.6	5
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