Yu Xue

List of Publications by Year
in descending order

202 papers	18,859 citations	23567 58 h-index	13379 130 g-index
204 all docs	204 docs citations	204 times ranked	32730 citing authors

#	Article	IF	Citations
1	Partial Connection Based on Channel Attention for Differentiable Neural Architecture Search. IEEE Transactions on Industrial Informatics, 2023, 19, 6804-6813.	11.3	16
2	Structure and weights search for classification with feature selection based on brain storm optimization algorithm. Applied Intelligence, 2022, 52, 5857-5866.	5.3	4
3	CPLM 4.0: an updated database with rich annotations for protein lysine modifications. Nucleic Acids Research, 2022, 50, D451-D459.	14.5	20
4	Multi-Objective Feature Selection With Missing Data in Classification. IEEE Transactions on Emerging Topics in Computational Intelligence, 2022, 6, 355-364.	4.9	79
5	Database Resources of the National Genomics Data Center, China National Center for Bioinformation in 2022. Nucleic Acids Research, 2022, 50, D27-D38.	14.5	364
6	GPS-Uber: a hybrid-learning framework for prediction of general and E3-specific lysine ubiquitination sites. Briefings in Bioinformatics, 2022, 23, .	6.5	10
7	A self-adaptive gradient descent search algorithm for fully-connected neural networks. Neurocomputing, 2022, 478, 70-80.	5.9	35
8	An improved brain storm optimization algorithm with new solution generation strategies for classification. Engineering Applications of Artificial Intelligence, 2022, 110, 104677.	8.1	10
9	HemI 2.0: an online service for heatmap illustration. Nucleic Acids Research, 2022, 50, W405-W411.	14.5	24
10	iPCD: A Comprehensive Data Resource of Regulatory Proteins in Programmed Cell Death. Cells, 2022, 11, 2018.	4.1	0
11	GPS-Palm: a deep learning-based graphic presentation system for the prediction of S-palmitoylation sites in proteins. Briefings in Bioinformatics, 2021, 22, 1836-1847.	6.5	64
12	An integrative multi-omics approach uncovers the regulatory role of CDK7 and CDK4 in autophagy activation induced by silica nanoparticles. Autophagy, 2021, 17, 1426-1447.	9.1	33
13	DatabaseÂResources of the National Genomics Data Center, China National Center for Bioinformation in 2021. Nucleic Acids Research, 2021, 49, D18-D28.	14.5	168
14	Bioinformatics Technologies in Autophagy Research. Advances in Experimental Medicine and Biology, 2021, 1208, 387-453.	1.6	3
15	Classification Based on Brain Storm Optimization With Feature Selection. IEEE Access, 2021, 9, 16582-16590.	4.2	6
16	Multi-omic profiling of plasma reveals molecular alterations in children with COVID-19. Theranostics, 2021, 11, 8008-8026.	10.0	27
17	Fuzzy Multilevel Image Thresholding Based on Improved Coyote Optimization Algorithm. IEEE Access, 2021, 9, 33595-33607.	4.2	49
18	Intrusion Detection System Based on an Updated ANN Model. Lecture Notes in Computer Science, 2021, , 472-479.	1.3	0

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19	Phosphorylation of SNX27 by MAPK11/14 links cellular stressâ€"signaling pathways with endocytic recycling. Journal of Cell Biology, 2021, 220, .	5.2	30
20	Stable Flexible Piezoresistive Sensors with Viscoelastic Ni Nanowiresâ€PDMS Composites and Ni Foam Electrodes. Zeitschrift Fur Anorganische Und Allgemeine Chemie, 2021, 647, 1031-1037.	1.2	1
21	Atg9-centered multi-omics integration reveals new autophagy regulators in<i>Saccharomyces cerevisiae</i>. Autophagy, 2021, 17, 4453-4476.	9.1	6
22	Multi-Objective Memetic Algorithms with Tree-Based Genetic Programming and Local Search for Symbolic Regression. Neural Processing Letters, 2021, 53, 2197-2219.	3.2	4
23	Model-based analysis uncovers mutations altering autophagy selectivity in human cancer. Nature Communications, 2021, 12, 3258.	12.8	24
24	iCAL: a new pipeline to investigate autophagy selectivity and cancer. Autophagy, 2021, 17, 1799-1801.	9.1	3
25	Metformin activates chaperone-mediated autophagy and improves disease pathologies in an Alzheimer disease mouse model. Protein and Cell, 2021, 12, 769-787.	11.0	63
26	A Multi-Objective Evolutionary Approach Based on Graph-in-Graph for Neural Architecture Search of Convolutional Neural Networks. International Journal of Neural Systems, 2021, 31, 2150035.	5.2	82
27	Insulin signaling regulates longevity through protein phosphorylation in Caenorhabditis elegans. Nature Communications, 2021, 12, 4568.	12.8	38
28	Spatial and Temporal Characteristics of Rainfall Anomalies in 1961â€"2010 in the Yangtze River Basin, China. Atmosphere, 2021, 12, 960.	2.3	7
29	Post-mortem tissue proteomics reveals the pathogenesis of multi-organ injuries of COVID-19. National Science Review, 2021, 8, nwab143.	9.5	14
30	A Self-Adaptive Mutation Neural Architecture Search Algorithm Based on Blocks. IEEE Computational Intelligence Magazine, 2021, 16, 67-78.	3.2	93
31	Adaptive crossover operator based multi-objective binary genetic algorithm for feature selection in classification. Knowledge-Based Systems, 2021, 227, 107218.	7.1	81
32	EPSD: a well-annotated data resource of protein phosphorylation sites in eukaryotes. Briefings in Bioinformatics, 2021, 22, 298-307.	6.5	49
33	Self-Adaptive Particle Swarm Optimization-Based Echo State Network for Time Series Prediction. International Journal of Neural Systems, 2021, 31, 2150057.	5.2	19
34	Database Resources of the National Genomics Data Center in 2020. Nucleic Acids Research, 2020, 48, D24-D33.	14.5	165
35	DeepPhagy: a deep learning framework for quantitatively measuring autophagy activity in <i>Saccharomyces cerevisiae</i>. Autophagy, 2020, 16, 626-640.	9.1	18
36	Self-adaptive parameter and strategy based particle swarm optimization for large-scale feature selection problems with multiple classifiers. Applied Soft Computing Journal, 2020, 88, 106031.	7.2	105

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37	Plasma Proteomics Identify Biomarkers and Pathogenesis of COVID-19. Immunity, 2020, 53, 1108-1122.e5.	14.3	228
38	HybridSucc: A Hybrid-learning Architecture for General and Species-specific Succinylation Site Prediction. Genomics, Proteomics and Bioinformatics, 2020, 18, 194-207.	6.9	28
39	DrLLPS: a data resource of liquid–liquid phase separation in eukaryotes. Nucleic Acids Research, 2020, 48, D288-D295.	14.5	112
40	An adaptive GP-based memetic algorithm for symbolic regression. Applied Intelligence, 2020, 50, 3961-3975.	5.3	6
41	Open resource of clinical data from patients with pneumonia for the prediction of COVID-19 outcomes via deep learning. Nature Biomedical Engineering, 2020, 4, 1197-1207.	22.5	122
42	PTMsnp: A Web Server for the Identification of Driver Mutations That Affect Protein Post-translational Modification. Frontiers in Cell and Developmental Biology, 2020, 8, 593661.	3.7	7
43	Bi-objective memetic GP with dispersion-keeping Pareto evaluation for real-world regression. Information Sciences, 2020, 539, 16-35.	6.9	4
44	Integrated omics in Drosophila uncover a circadian kinome. Nature Communications, 2020, 11, 2710.	12.8	23
45	dbPSP 2.0, an updated database of protein phosphorylation sites in prokaryotes. Scientific Data, 2020, 7, 164.	5.3	20
46	Preference-driven Pareto front exploitation for bloat control in genetic programming. Applied Soft Computing Journal, 2020, 92, 106254.	7.2	8
47	Mechanism of cargo recognition by retromer-linked SNX-BAR proteins. PLoS Biology, 2020, 18, e3000631.	5.6	51
48	GPS 5.0: An Update on the Prediction of Kinase-specific Phosphorylation Sites in Proteins. Genomics, Proteomics and Bioinformatics, 2020, 18, 72-80.	6.9	197
49	Inhibiting MARSs reduces hyperhomocysteinemia–associated neural tube and congenital heart defects. EMBO Molecular Medicine, 2020, 12, e9469.	6.9	21
50	GPS-PBS: A Deep Learning Framework to Predict Phosphorylation Sites that Specifically Interact with Phosphoprotein-Binding Domains. Cells, 2020, 9, 1266.	4.1	10
51	A Classification Model Based on Improved Self-Adaptive Fireworks Algorithm. Advances in Computational Intelligence and Robotics Book Series, 2020, , 148-175.	0.4	1
52	A feasible density peaks clustering algorithm with a merging strategy. Soft Computing, 2019, 23, 5171-5183.	3.6	27
53	A novel density peaks clustering with sensitivity of local density and density-adaptive metric. Knowledge and Information Systems, 2019, 59, 285-309.	3.2	31
54	BEMD image fusion based on PCNN and compressed sensing. Soft Computing, 2019, 23, 10045-10054.	3.6	5

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55	Self-Adaptive Particle Swarm Optimization for Large-Scale Feature Selection in Classification. ACM Transactions on Knowledge Discovery From Data, 2019, 13, 1-27.	3.5	253
56	Identification of rare variants in cardiac sodium channel β4-subunit gene SCN4B associated with ventricular tachycardia. Molecular Genetics and Genomics, 2019, 294, 1059-1071.	2.1	5
57	Large-Scale Feedforward Neural Network Optimization by a Self-Adaptive Strategy and Parameter Based Particle Swarm Optimization. IEEE Access, 2019, 7, 52473-52483.	4.2	32
58	Inhibiting PD-L1 palmitoylation enhances T-cell immune responses against tumours. Nature Biomedical Engineering, 2019, 3, 306-317.	22.5	279
59	Database Resources of the BIG Data Center in 2019. Nucleic Acids Research, 2019, 47, D8-D14.	14.5	157
60	iEKPD 2.0: an update with rich annotations for eukaryotic protein kinases, protein phosphatases and proteins containing phosphoprotein-binding domains. Nucleic Acids Research, 2019, 47, D344-D350.	14.5	22
61	Outlier detection based on approximation accuracy entropy. International Journal of Machine Learning and Cybernetics, 2019, 10, 2483-2499.	3.6	18
62	Fast and Accurate Classification of Time Series Data Using Extended ELM: Application in Fault Diagnosis of Air Handling Units. IEEE Transactions on Systems, Man, and Cybernetics: Systems, 2019, 49, 1349-1356.	9.3	77
63	A review on multi-class TWSVM. Artificial Intelligence Review, 2019, 52, 775-801.	15.7	29
64	A hybrid biogeography-based optimization and fuzzy C-means algorithm for image segmentation. Soft Computing, 2019, 23, 2033-2046.	3.6	45
65	Unsupervised feature selection based on self-representation sparse regression and local similarity preserving. International Journal of Machine Learning and Cybernetics, 2019, 10, 757-770.	3.6	15
66	A new validity index adapted to fuzzy clustering algorithm. Multimedia Tools and Applications, 2018, 77, 11339-11361.	3.9	4
67	WocEA: The visualization of functional enrichment results in word clouds. Journal of Genetics and Genomics, 2018, 45, 415-417.	3.9	16
68	iUUCD 2.0: an update with rich annotations for ubiquitin and ubiquitin-like conjugations. Nucleic Acids Research, 2018, 46, D447-D453.	14.5	57
69	Text classification based on deep belief network and softmax regression. Neural Computing and Applications, 2018, 29, 61-70.	5.6	199
70	Self-adaptive kernel K-means algorithm based on the shuffled frog leaping algorithm. Soft Computing, 2018, 22, 861-872.	3.6	14
71	Efficient business process consolidation: combining topic features with structure matching. Soft Computing, 2018, 22, 645-657.	3.6	20
72	DPCG: an efficient density peaks clustering algorithm based on grid. International Journal of Machine Learning and Cybernetics, 2018, 9, 743-754.	3.6	50

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73	A novel cluster validity index for fuzzy C-means algorithm. Soft Computing, 2018, 22, 1921-1931.	3.6	17
74	Recognizing the human attention state using cardiac pulse from the noncontact and automatic-based measurements. Soft Computing, 2018, 22, 3937-3949.	3.6	5
75	Memetic algorithm based on extension step and statistical filtering for large-scale capacitated arc routing problems. Natural Computing, 2018, 17, 375-391.	3.0	4
76	A robust density peaks clustering algorithm using fuzzy neighborhood. International Journal of Machine Learning and Cybernetics, 2018, 9, 1131-1140.	3.6	49
77	An improved fingerprint orientation field extraction method based on quality grading scheme. International Journal of Machine Learning and Cybernetics, 2018, 9, 1249-1260.	3.6	5
78	Density peaks clustering using geodesic distances. International Journal of Machine Learning and Cybernetics, 2018, 9, 1335-1349.	3.6	44
79	A self-adaptive artificial bee colony algorithm based on global best for global optimization. Soft Computing, 2018, 22, 2935-2952.	3.6	274
80	Multipurpose watermarking for vector map protection and authentication. Multimedia Tools and Applications, 2018, 77, 7239-7259.	3.9	27
81	Knowledge based differential evolution for cloud computing service composition. Journal of Ambient Intelligence and Humanized Computing, 2018, 9, 565-574.	4.9	23
82	Self-adaptive bat algorithm for large scale cloud manufacturing service composition. Peer-to-Peer Networking and Applications, 2018, 11, 1115-1128.	3.9	22
83	THANATOS: an integrative data resource of proteins and post-translational modifications in the regulation of autophagy. Autophagy, 2018, 14, 296-310.	9.1	41
84	Bat algorithm with triangle-flipping strategy for numerical optimization. International Journal of Machine Learning and Cybernetics, 2018, 9, 199-215.	3.6	101
85	Improved artificial bee colony algorithm with differential evolution for the numerical optimisation problems. International Journal of Computational Science and Engineering, 2018, 16, 73.	0.5	9
86	PTMD: A Database of Human Disease-associated Post-translational Modifications. Genomics, Proteomics and Bioinformatics, 2018, 16, 244-251.	6.9	129
87	Bioinformatics Commons: The Cornerstone of Life and Health Sciences. Genomics, Proteomics and Bioinformatics, 2018, 16, 223-225.	6.9	2
88	DeepNitro: Prediction of Protein Nitration and Nitrosylation Sites by Deep Learning. Genomics, Proteomics and Bioinformatics, 2018, 16, 294-306.	6.9	81
89	An Evolutionary Computation Based Feature Selection Method for Intrusion Detection. Security and Communication Networks, 2018, 2018, 1-10.	1.5	30
90	Predicting lysine‐malonylation sites of proteins using sequence and predicted structural features. Journal of Computational Chemistry, 2018, 39, 1757-1763.	3.3	30

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91	A Self-Adaptive Fireworks Algorithm for Classification Problems. IEEE Access, 2018, 6, 44406-44416.	4.2	20
92	Pan-Cancer Analysis Reveals the Functional Importance of Protein Lysine Modification in Cancer Development. Frontiers in Genetics, 2018, 9, 254.	2.3	39
93	NSCTâ€PCNN image fusion based on image gradient motivation. IET Computer Vision, 2018, 12, 377-383.	2.0	24
94	An evolutionary classification method based on fireworks algorithm. International Journal of Bio-Inspired Computation, 2018, 11, 149.	0.9	10
95	Locally adaptive multiple kernel k-means algorithm based on shared nearest neighbors. Soft Computing, 2018, 22, 4573-4583.	3.6	12
96	OUP accepted manuscript. Nucleic Acids Research, 2017, 45, D397-D403.	14.5	42
97	OUP accepted manuscript. Nucleic Acids Research, 2017, 45, D264-D270.	14.5	62
98	Computational prediction of methylation types of covalently modified lysine and arginine residues in proteins. Briefings in Bioinformatics, 2017, 18, bbw041.	6.5	47
99	Research on denoising sparse autoencoder. International Journal of Machine Learning and Cybernetics, 2017, 8, 1719-1729.	3.6	44
100	Prior knowledge guided differential evolution. Soft Computing, 2017, 21, 6841-6858.	3.6	15
101	A Review on Feature Binding Theory and Its Functions Observed in Perceptual Process. Cognitive Computation, 2017, 9, 194-206.	5.2	9
102	Research on Coverage Probability in Ultra-Dense 5G Heterogeneous Cellular Networks Based on Poisson Clustered Process. Wireless Personal Communications, 2017, 95, 2915-2930.	2.7	3
103	Measures of uncertainty for neighborhood rough sets. Knowledge-Based Systems, 2017, 120, 226-235.	7.1	71
104	Gene selection for tumor classification using neighborhood rough sets and entropy measures. Journal of Biomedical Informatics, 2017, 67, 59-68.	4.3	90
105	PLMD: An updated data resource of protein lysine modifications. Journal of Genetics and Genomics, 2017, 44, 243-250.	3.9	198
106	Bioinformaticians wrestling with the big biomedical data. Journal of Genetics and Genomics, 2017, 44, 223-225.	3.9	2
107	Fingerprint image super resolution using sparse representation with ridge pattern prior by classification coupled dictionaries. IET Biometrics, 2017, 6, 342-350.	2.5	15
108	Phosphoproteome-based kinase activity profiling reveals the critical role of MAP2K2 and PLK1 in neuronal autophagy. Autophagy, 2017, 13, 1969-1980.	9.1	48

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109	A Pythagorean-Type Fuzzy Deep Denoising Autoencoder for Industrial Accident Early Warning. IEEE Transactions on Fuzzy Systems, 2017, 25, 1561-1575.	9.8	63
110	Phosphoproteome Analysis Reveals Phosphorylation Underpinnings in the Brains of Nurse and Forager Honeybees (Apis mellifera). Scientific Reports, 2017, 7, 1973.	3.3	11
111	A novel knowledge-guided evolutionary scheduling strategy for energy-efficient connected coverage optimization in WSNs. Peer-to-Peer Networking and Applications, 2017, 10, 547-558.	3.9	6
112	Combining Gabor filtering and classification dictionaries learning for fingerprint enhancement. IET Biometrics, 2017, 6, 438-447.	2.5	13
113	Dependence structure of Gabor wavelets for face recognition. , 2017, , .		1
114	A classification method based on self-adaptive artificial bee colony. , 2017, , .		1
115	Cloud Model-Based Artificial Immune Network for Complex Optimization Problem. Computational Intelligence and Neuroscience, 2017, 2017, 1-17.	1.7	7
116	Dysbindin as a novel biomarker for pancreatic ductal adenocarcinoma identified by proteomic profiling. International Journal of Cancer, 2016, 139, 1821-1829.	5.1	19
117	GPS-PAIL: prediction of lysine acetyltransferase-specific modification sites from protein sequences. Scientific Reports, 2016, 6, 39787.	3.3	88
118	Mal-Lys: prediction of lysine malonylation sites in proteins integrated sequence-based features with mRMR feature selection. Scientific Reports, 2016, 6, 38318.	3.3	46
119	Classification Based on Brain Storm Optimization Algorithm. Communications in Computer and Information Science, 2016, , 371-376.	0.5	5
120	Enhanced Purification of Ubiquitinated Proteins by Engineered Tandem Hybrid Ubiquitin-binding Domains (ThUBDs). Molecular and Cellular Proteomics, 2016, 15, 1381-1396.	3.8	15
121	Genome of Plant Maca (Lepidium meyenii) Illuminates Genomic Basis for High-Altitude Adaptation in the Central Andes. Molecular Plant, 2016, 9, 1066-1077.	8.3	69
122	Weight Uncertainty in Boltzmann Machine. Cognitive Computation, 2016, 8, 1064-1073.	5.2	11
123	Pyruvate Kinase M2 Activates mTORC1 by Phosphorylating AKT1S1. Scientific Reports, 2016, 6, 21524.	3.3	92
124	Precision Medicine: What Challenges Are We Facing?. Genomics, Proteomics and Bioinformatics, 2016, 14, 253-261.	6.9	15
125	GPS-Lipid: a robust tool for the prediction of multiple lipid modification sites. Scientific Reports, 2016, 6, 28249.	3.3	120
126	dbPAF: an integrative database of protein phosphorylation in animals and fungi. Scientific Reports, 2016, 6, 23534.	3.3	78

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127	Multi-objective layout optimization of a satellite module using the Wang-Landau sampling method with local search. Frontiers of Information Technology and Electronic Engineering, 2016, 17, 527-542.	2.6	15
128	Ray Wu, fifth business or father of DNA sequencing?. Protein and Cell, 2016, 7, 467-470.	11.0	4
129	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). Autophagy, 2016, 12, 1-222.	9.1	4,701
130	Correlated expression of retrocopies and parental genes in zebrafish. Molecular Genetics and Genomics, 2016, 291, 723-737.	2.1	7
131	Enhanced Purification of Ubiquitinated Proteins by Engineered Tandem Hybrid Ubiquitin-binding Domains (ThUBDs). Molecular and Cellular Proteomics, 2016, 15, 1381-1396.	3.8	44
132	Information Commons for Rice (IC4R). Nucleic Acids Research, 2016, 44, D1172-D1180.	14.5	41
133	Security system construction of land and resources network based on intrusion detection. , 2015, , .		0
134	dbPSP: a curated database for protein phosphorylation sites in prokaryotes. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav031.	3.0	23
135	Phosphoproteomic Analysis of the Highly-Metastatic Hepatocellular Carcinoma Cell Line, MHCC97-H. International Journal of Molecular Sciences, 2015, 16, 4209-4225.	4.1	22
136	IBS: an illustrator for the presentation and visualization of biological sequences. Bioinformatics, 2015, 31, 3359-3361.	4.1	817
137	Efficient Feature Selection and Classification for Vehicle Detection. IEEE Transactions on Circuits and Systems for Video Technology, 2015, 25, 508-517.	8.3	128
138	Reconfiguring phosphorylation signaling by genetic polymorphisms affects cancer susceptibility. Journal of Molecular Cell Biology, 2015, 7, 187-202.	3.3	17
139	MiCroKiTS 4.0: a database of midbody, centrosome, kinetochore, telomere and spindle. Nucleic Acids Research, 2015, 43, D328-D334.	14.5	23
140	AnimalTFDB 2.0: a resource for expression, prediction and functional study of animal transcription factors. Nucleic Acids Research, 2015, 43, D76-D81.	14.5	287
141	Analysis of phosphorylation sites on autophagy proteins. Protein and Cell, 2015, 6, 698-701.	11.0	5
142	Discrete gbest-guided artificial bee colony algorithm for cloud service composition. Applied Intelligence, 2015, 42, 661-678.	5.3	70
143	A Hybrid Evolutionary Algorithm for Numerical Optimization Problem. Intelligent Automation and Soft Computing, 2015, 21, 473-490.	2.1	12
144	Computational Identification of Protein Kinases and Kinase-Specific Substrates in Plants. Methods in Molecular Biology, 2015, 1306, 195-205.	0.9	1

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145	A Sensitivity-Based Improving Learning Algorithm for Madaline Rule II. Mathematical Problems in Engineering, 2014, 2014, 1-8.	1.1	0
146	dbPPT: a comprehensive database of protein phosphorylation in plants. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau121.	3.0	45
147	Systematic Analysis of the Phosphoproteome and Kinase-substrate Networks in the Mouse Testis. Molecular and Cellular Proteomics, 2014, 13, 3626-3638.	3.8	38
148	Wang-Landau sampling in face-centered-cubic hydrophobic-hydrophilic lattice model proteins. Physical Review E, 2014, 90, 042715.	2.1	7
149	An efficient energy hole alleviating algorithm for wireless sensor networks. IEEE Transactions on Consumer Electronics, 2014, 60, 347-355.	3.6	40
150	GPS-SUMO: a tool for the prediction of sumoylation sites and SUMO-interaction motifs. Nucleic Acids Research, 2014, 42, W325-W330.	14.5	417
151	HemI: A Toolkit for Illustrating Heatmaps. PLoS ONE, 2014, 9, e111988.	2.5	963
152	An ensemble algorithm with self-adaptive learning techniques for high-dimensional numerical optimization. Applied Mathematics and Computation, 2014, 231, 329-346.	2.2	20
153	Systematic characterization of small RNAome during zebrafish early developmental stages. BMC Genomics, 2014, 15, 117.	2.8	27
154	EKPD: a hierarchical database of eukaryotic protein kinases and protein phosphatases. Nucleic Acids Research, 2014, 42, D496-D502.	14.5	52
155	CPLM: a database of protein lysine modifications. Nucleic Acids Research, 2014, 42, D531-D536.	14.5	155
156	Computationally characterizing and comprehensive analysis of zinc-binding sites in proteins. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 171-180.	2.3	10
157	Self-adaptive learning based discrete differential evolution algorithm for solving CJWTA problem. Journal of Systems Engineering and Electronics, 2014, 25, 59-68.	2.2	13
158	Systematic analysis of the in situ crosstalk of tyrosine modifications reveals no additional natural selection on multiply modified residues. Scientific Reports, 2014, 4, 7331.	3.3	39
159	Towards a better understanding of the novel avian-origin H7N9 influenza A virus in China. Scientific Reports, 2013, 3, 2318.	3.3	17
160	Systematic analysis of the Plk-mediated phosphoregulation in eukaryotes. Briefings in Bioinformatics, 2013, 14, 344-360.	6.5	29
161	Stable Isotope Metabolic Labeling-based Quantitative Phosphoproteomic Analysis of Arabidopsis Mutants Reveals Ethylene-regulated Time-dependent Phosphoproteins and Putative Substrates of Constitutive Triple Response 1 Kinase. Molecular and Cellular Proteomics, 2013, 12, 3559-3582.	3.8	58
162	UUCD: a family-based database of ubiquitin and ubiquitin-like conjugation. Nucleic Acids Research, 2013, 41, D445-D451.	14.5	99

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163	Phosphoproteomics–based network medicine. FEBS Journal, 2013, 280, 5696-5704.	4.7	16
164	CPSS: a computational platform for the analysis of small RNA deep sequencing data. Bioinformatics, 2012, 28, 1925-1927.	4.1	55
165	Systematic Analysis of Protein Phosphorylation Networks From Phosphoproteomic Data. Molecular and Cellular Proteomics, 2012, 11, 1070-1083.	3.8	161
166	GPS-MBA: Computational Analysis of MHC Class II Epitopes in Type 1 Diabetes. PLoS ONE, 2012, 7, e33884.	2.5	9
167	GPS-ARM: Computational Analysis of the APC/C Recognition Motif by Predicting D-Boxes and KEN-Boxes. PLoS ONE, 2012, 7, e34370.	2.5	44
168	GPS-PUP: computational prediction of pupylation sites in prokaryotic proteins. Molecular BioSystems, 2011, 7, 2737.	2.9	40
169	GPS-YNO2: computational prediction of tyrosine nitration sites in proteins. Molecular BioSystems, 2011, 7, 1197.	2.9	94
170	GPS-CCD: A Novel Computational Program for the Prediction of Calpain Cleavage Sites. PLoS ONE, 2011, 6, e19001.	2.5	94
171	CPLA 1.0: an integrated database of protein lysine acetylation. Nucleic Acids Research, 2011, 39, D1029-D1034.	14.5	60
172	GPS 2.1: enhanced prediction of kinase-specific phosphorylation sites with an algorithm of motif length selection. Protein Engineering, Design and Selection, 2011, 24, 255-260.	2.1	217
173	Prediction of novel pre-microRNAs with high accuracy through boosting and SVM. Bioinformatics, 2011, 27, 1436-1437.	4.1	26
174	Computational Analysis of Phosphoproteomics: Progresses and Perspectives. Current Protein and Peptide Science, 2011, 12, 591-601.	1.4	13
175	GPS-SNO: Computational Prediction of Protein S-Nitrosylation Sites with a Modified GPS Algorithm. PLoS ONE, 2010, 5, e11290.	2.5	223
176	PhosSNP for Systematic Analysis of Genetic Polymorphisms That Influence Protein Phosphorylation. Molecular and Cellular Proteomics, 2010, 9, 623-634.	3.8	72
177	MiCroKit 3.0: an integrated database of midbody, centrosome and kinetochore. Nucleic Acids Research, 2010, 38, D155-D160.	14.5	27
178	A Summary of Computational Resources for Protein Phosphorylation. Current Protein and Peptide Science, 2010, 11, 485-496.	1.4	53
179	MBA: a literature mining system for extracting biomedical abbreviations. BMC Bioinformatics, 2009, 10, 14.	2.6	22
180	Systematic study of protein sumoylation: Development of a site–specific predictor of SUMOsp 2.0. Proteomics, 2009, 9, 3409-3412.	2.2	227

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181	DOG 1.0: illustrator of protein domain structures. Cell Research, 2009, 19, 271-273.	12.0	505
182	Comprehensive and Reliable Phosphorylation Site Mapping of Individual Phosphoproteins by Combination of Multiple Stage Mass Spectrometric Analysis with a Target-Decoy Database Search. Analytical Chemistry, 2009, 81, 5794-5805.	6.5	25
183	Proteome-wide prediction of PKA phosphorylation sites in eukaryotic kingdom. Genomics, 2008, 92, 457-463.	2.9	29
184	The E3 ubiquitin ligase HECTD3 regulates ubiquitination and degradation of Tara. Biochemical and Biophysical Research Communications, 2008, 367, 805-812.	2.1	27
185	GPS 2.0, a Tool to Predict Kinase-specific Phosphorylation Sites in Hierarchy. Molecular and Cellular Proteomics, 2008, 7, 1598-1608.	3.8	587
186	CSS-Palm 2.0: an updated software for palmitoylation sites prediction. Protein Engineering, Design and Selection, 2008, 21, 639-644.	2.1	511
187	Computational Analyses of TBC Protein Family in Eukaryotes. Protein and Peptide Letters, 2008, 15, 505-509.	0.9	8
188	An efficient site-directed mutagenesis method for ColE1-type ori plasmid. Analytical Biochemistry, 2007, 363, 151-153.	2.4	3
189	MeMo: a web tool for prediction of protein methylation modifications. Nucleic Acids Research, 2006, 34, W249-W253.	14.5	123
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