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	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). Autophagy, 2016, 12, 1-222.	9.1	4,701
2	HemI: A Toolkit for Illustrating Heatmaps. PLoS ONE, 2014, 9, e111988.	2.5	963
3	IBS: an illustrator for the presentation and visualization of biological sequences. Bioinformatics, 2015, 31, 3359-3361.	4.1	817
4	GPS 2.0, a Tool to Predict Kinase-specific Phosphorylation Sites in Hierarchy. Molecular and Cellular Proteomics, 2008, 7, 1598-1608.	3.8	587
5	CSS-Palm 2.0: an updated software for palmitoylation sites prediction. Protein Engineering, Design and Selection, 2008, 21, 639-644.	2.1	511
6	DOG 1.0: illustrator of protein domain structures. Cell Research, 2009, 19, 271-273.	12.0	505
7	GPS-SUMO: a tool for the prediction of sumoylation sites and SUMO-interaction motifs. Nucleic Acids Research, 2014, 42, W325-W330.	14.5	417
8	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
9	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
10	Inhibiting PD-L1 palmitoylation enhances T-cell immune responses against tumours. Nature Biomedical Engineering, 2019, 3, 306-317.	22.5	279
11	A self-adaptive artificial bee colony algorithm based on global best for global optimization. Soft Computing, 2018, 22, 2935-2952.	3.6	274
12	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
13	Plasma Proteomics Identify Biomarkers and Pathogenesis of COVID-19. Immunity, 2020, 53, 1108-1122.e5.	14.3	228
14	Systematic study of protein sumoylation: Development of a site€specific predictor of SUMOsp 2.0. Proteomics, 2009, 9, 3409-3412.	2.2	227
15	GPS-SNO: Computational Prediction of Protein S-Nitrosylation Sites with a Modified GPS Algorithm. PLoS ONE, 2010, 5, e11290.	2.5	223
16	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
17	GPS: a comprehensive www server for phosphorylation sites prediction. Nucleic Acids Research, 2005, 33, W184-W187.	14.5	215
18	Text classification based on deep belief network and softmax regression. Neural Computing and Applications, 2018, 29, 61-70.	5.6	199

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19	PLMD: An updated data resource of protein lysine modifications. Journal of Genetics and Genomics, 2017, 44, 243-250.	3.9	198
20	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
21	PPSP: prediction of PK-specific phosphorylation site with Bayesian decision theory. BMC Bioinformatics, 2006, 7, 163.	2.6	183
22	SUMOsp: a web server for sumoylation site prediction. Nucleic Acids Research, 2006, 34, W254-W257.	14.5	179
23	DatabaseÂResources of the National Genomics Data Center, China National Center for Bioinformation in 2021. Nucleic Acids Research, 2021, 49, D18-D28.	14.5	168
24	Database Resources of the National Genomics Data Center in 2020. Nucleic Acids Research, 2020, 48, D24-D33.	14.5	165
25	Systematic Analysis of Protein Phosphorylation Networks From Phosphoproteomic Data. Molecular and Cellular Proteomics, 2012, 11, 1070-1083.	3.8	161
26	Database Resources of the BIG Data Center in 2019. Nucleic Acids Research, 2019, 47, D8-D14.	14.5	157
27	CPLM: a database of protein lysine modifications. Nucleic Acids Research, 2014, 42, D531-D536.	14.5	155
28	GPS: a novel group-based phosphorylation predicting and scoring method. Biochemical and Biophysical Research Communications, 2004, 325, 1443-1448.	2.1	149
29	CSS-Palm: palmitoylation site prediction with a clustering and scoring strategy (CSS). Bioinformatics, 2006, 22, 894-896.	4.1	130
30	PTMD: A Database of Human Disease-associated Post-translational Modifications. Genomics, Proteomics and Bioinformatics, 2018, 16, 244-251.	6.9	129
31	Efficient Feature Selection and Classification for Vehicle Detection. IEEE Transactions on Circuits and Systems for Video Technology, 2015, 25, 508-517.	8.3	128
32	MeMo: a web tool for prediction of protein methylation modifications. Nucleic Acids Research, 2006, 34, W249-W253.	14.5	123
33	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
34	GPS-Lipid: a robust tool for the prediction of multiple lipid modification sites. Scientific Reports, 2016, 6, 28249.	3.3	120
35	DrLLPS: a data resource of liquidâ€"liquid phase separation in eukaryotes. Nucleic Acids Research, 2020, 48, D288-D295.	14.5	112
36	Prediction of NÎµ-acetylation on internal lysines implemented in Bayesian Discriminant Method. Biochemical and Biophysical Research Communications, 2006, 350, 818-824.	2.1	106

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37	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
38	Bat algorithm with triangle-flipping strategy for numerical optimization. International Journal of Machine Learning and Cybernetics, 2018, 9, 199-215.	3.6	101
39	UUCD: a family-based database of ubiquitin and ubiquitin-like conjugation. Nucleic Acids Research, 2013, 41, D445-D451.	14.5	99
40	GPS-YNO2: computational prediction of tyrosine nitration sites in proteins. Molecular BioSystems, 2011, 7, 1197.	2.9	94
41	GPS-CCD: A Novel Computational Program for the Prediction of Calpain Cleavage Sites. PLoS ONE, 2011, 6, e19001.	2.5	94
42	A Self-Adaptive Mutation Neural Architecture Search Algorithm Based on Blocks. IEEE Computational Intelligence Magazine, 2021, 16, 67-78.	3.2	93
43	Pyruvate Kinase M2 Activates mTORC1 by Phosphorylating AKT1S1. Scientific Reports, 2016, 6, 21524.	3.3	92
44	Gene selection for tumor classification using neighborhood rough sets and entropy measures. Journal of Biomedical Informatics, 2017, 67, 59-68.	4.3	90
45	NBA-Palm: prediction of palmitoylation site implemented in Naïve Bayes algorithm. BMC Bioinformatics, 2006, 7, 458.	2.6	88
46	GPS-PAIL: prediction of lysine acetyltransferase-specific modification sites from protein sequences. Scientific Reports, 2016, 6, 39787.	3.3	88
47	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
48	DeepNitro: Prediction of Protein Nitration and Nitrosylation Sites by Deep Learning. Genomics, Proteomics and Bioinformatics, 2018, 16, 294-306.	6.9	81
49	Adaptive crossover operator based multi-objective binary genetic algorithm for feature selection in classification. Knowledge-Based Systems, 2021, 227, 107218.	7.1	81
50	Multi-Objective Feature Selection With Missing Data in Classification. IEEE Transactions on Emerging Topics in Computational Intelligence, 2022, 6, 355-364.	4.9	79
51	dbPAF: an integrative database of protein phosphorylation in animals and fungi. Scientific Reports, 2016, 6, 23534.	3.3	78
52	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
53	PhosSNP for Systematic Analysis of Genetic Polymorphisms That Influence Protein Phosphorylation. Molecular and Cellular Proteomics, 2010, 9, 623-634.	3.8	72
54	Measures of uncertainty for neighborhood rough sets. Knowledge-Based Systems, 2017, 120, 226-235.	7.1	71

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55	Discrete gbest-guided artificial bee colony algorithm for cloud service composition. Applied Intelligence, 2015, 42, 661-678.	5.3	70
56	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
57	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
58	A Pythagorean-Type Fuzzy Deep Denoising Autoencoder for Industrial Accident Early Warning. IEEE Transactions on Fuzzy Systems, 2017, 25, 1561-1575.	9.8	63
59	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
60	OUP accepted manuscript. Nucleic Acids Research, 2017, 45, D264-D270.	14.5	62
61	CPLA 1.0: an integrated database of protein lysine acetylation. Nucleic Acids Research, 2011, 39, D1029-D1034.	14.5	60
62	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
63	iUUCD 2.0: an update with rich annotations for ubiquitin and ubiquitin-like conjugations. Nucleic Acids Research, 2018, 46, D447-D453.	14.5	57
64	CPSS: a computational platform for the analysis of small RNA deep sequencing data. Bioinformatics, 2012, 28, 1925-1927.	4.1	55
65	A Summary of Computational Resources for Protein Phosphorylation. Current Protein and Peptide Science, 2010, 11, 485-496.	1.4	53
66	EKPD: a hierarchical database of eukaryotic protein kinases and protein phosphatases. Nucleic Acids Research, 2014, 42, D496-D502.	14.5	52
67	Mechanism of cargo recognition by retromer-linked SNX-BAR proteins. PLoS Biology, 2020, 18, e3000631.	5.6	51
68	DPCG: an efficient density peaks clustering algorithm based on grid. International Journal of Machine Learning and Cybernetics, 2018, 9, 743-754.	3.6	50
69	A robust density peaks clustering algorithm using fuzzy neighborhood. International Journal of Machine Learning and Cybernetics, 2018, 9, 1131-1140.	3.6	49
70	Fuzzy Multilevel Image Thresholding Based on Improved Coyote Optimization Algorithm. IEEE Access, 2021, 9, 33595-33607.	4.2	49
71	EPSD: a well-annotated data resource of protein phosphorylation sites in eukaryotes. Briefings in Bioinformatics, 2021, 22, 298-307.	6.5	49
72	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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73	Computational prediction of methylation types of covalently modified lysine and arginine residues in proteins. Briefings in Bioinformatics, 2017, 18, bbw041.	6.5	47
74	A genome-wide analysis of sumoylation-related biological processes and functions in human nucleus. FEBS Letters, 2005, 579, 3369-3375.	2.8	46
75	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
76	dbPPT: a comprehensive database of protein phosphorylation in plants. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau121.	3.0	45
77	A hybrid biogeography-based optimization and fuzzy C-means algorithm for image segmentation. Soft Computing, 2019, 23, 2033-2046.	3.6	45
78	Enhanced Purification of Ubiquitinated Proteins by Engineered Tandem Hybrid Ubiquitin-binding Domains (ThUBDs). Molecular and Cellular Proteomics, 2016, 15, 1381-1396.	3.8	44
79	Research on denoising sparse autoencoder. International Journal of Machine Learning and Cybernetics, 2017, 8, 1719-1729.	3.6	44
80	Density peaks clustering using geodesic distances. International Journal of Machine Learning and Cybernetics, 2018, 9, 1335-1349.	3.6	44
81	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
82	OUP accepted manuscript. Nucleic Acids Research, 2017, 45, D397-D403.	14.5	42
83	Information Commons for Rice (IC4R). Nucleic Acids Research, 2016, 44, D1172-D1180.	14.5	41
84	THANATOS: an integrative data resource of proteins and post-translational modifications in the regulation of autophagy. Autophagy, 2018, 14, 296-310.	9.1	41
85	GPS-PUP: computational prediction of pupylation sites in prokaryotic proteins. Molecular BioSystems, 2011, 7, 2737.	2.9	40
86	An efficient energy hole alleviating algorithm for wireless sensor networks. IEEE Transactions on Consumer Electronics, 2014, 60, 347-355.	3.6	40
87	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
88	Pan-Cancer Analysis Reveals the Functional Importance of Protein Lysine Modification in Cancer Development. Frontiers in Genetics, 2018, 9, 254.	2.3	39
89	Systematic Analysis of the Phosphoproteome and Kinase-substrate Networks in the Mouse Testis. Molecular and Cellular Proteomics, 2014, 13, 3626-3638.	3.8	38
90	Insulin signaling regulates longevity through protein phosphorylation in Caenorhabditis elegans. Nature Communications, 2021, 12, 4568.	12.8	38

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91	A self-adaptive gradient descent search algorithm for fully-connected neural networks. Neurocomputing, 2022, 478, 70-80.	5.9	35
92	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
93	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
94	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
95	An Evolutionary Computation Based Feature Selection Method for Intrusion Detection. Security and Communication Networks, 2018, 2018, 1-10.	1.5	30
96	Predicting lysineâ€malonylation sites of proteins using sequence and predicted structural features. Journal of Computational Chemistry, 2018, 39, 1757-1763.	3.3	30
97	Phosphorylation of SNX27 by MAPK11/14 links cellular stressâ€"signaling pathways with endocytic recycling. Journal of Cell Biology, 2021, 220, .	5.2	30
98	Proteome-wide prediction of PKA phosphorylation sites in eukaryotic kingdom. Genomics, 2008, 92, 457-463.	2.9	29
99	Systematic analysis of the Plk-mediated phosphoregulation in eukaryotes. Briefings in Bioinformatics, 2013, 14, 344-360.	6.5	29
100	A review on multi-class TWSVM. Artificial Intelligence Review, 2019, 52, 775-801.	15.7	29
101	HybridSucc: A Hybrid-learning Architecture for General and Species-specific Succinylation Site Prediction. Genomics, Proteomics and Bioinformatics, 2020, 18, 194-207.	6.9	28
102	The E3 ubiquitin ligase HECTD3 regulates ubiquitination and degradation of Tara. Biochemical and Biophysical Research Communications, 2008, 367, 805-812.	2.1	27
103	MiCroKit 3.0: an integrated database of midbody, centrosome and kinetochore. Nucleic Acids Research, 2010, 38, D155-D160.	14.5	27
104	Systematic characterization of small RNAome during zebrafish early developmental stages. BMC Genomics, 2014, 15, 117.	2.8	27
105	Multipurpose watermarking for vector map protection and authentication. Multimedia Tools and Applications, 2018, 77, 7239-7259.	3.9	27
106	A feasible density peaks clustering algorithm with a merging strategy. Soft Computing, 2019, 23, 5171-5183.	3.6	27
107	Multi-omic profiling of plasma reveals molecular alterations in children with COVID-19. Theranostics, 2021, 11, 8008-8026.	10.0	27
108	Prediction of novel pre-microRNAs with high accuracy through boosting and SVM. Bioinformatics, 2011, 27, 1436-1437.	4.1	26

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109	A general user interface for prediction servers of proteins' post-translational modification sites. Nature Protocols, 2006, 1, 1318-1321.	12.0	25
110	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
111	NSCTâ€PCNN image fusion based on image gradient motivation. IET Computer Vision, 2018, 12, 377-383.	2.0	24
112	Model-based analysis uncovers mutations altering autophagy selectivity in human cancer. Nature Communications, 2021, 12, 3258.	12.8	24
113	HemI 2.0: an online service for heatmap illustration. Nucleic Acids Research, 2022, 50, W405-W411.	14.5	24
114	dbPSP: a curated database for protein phosphorylation sites in prokaryotes. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav031.	3.0	23
115	MiCroKiTS 4.0: a database of midbody, centrosome, kinetochore, telomere and spindle. Nucleic Acids Research, 2015, 43, D328-D334.	14.5	23
116	Knowledge based differential evolution for cloud computing service composition. Journal of Ambient Intelligence and Humanized Computing, 2018, 9, 565-574.	4.9	23
117	Integrated omics in Drosophila uncover a circadian kinome. Nature Communications, 2020, 11, 2710.	12.8	23
118	MBA: a literature mining system for extracting biomedical abbreviations. BMC Bioinformatics, 2009, 10, 14.	2.6	22
119	Phosphoproteomic Analysis of the Highly-Metastatic Hepatocellular Carcinoma Cell Line, MHCC97-H. International Journal of Molecular Sciences, 2015, 16, 4209-4225.	4.1	22
120	Self-adaptive bat algorithm for large scale cloud manufacturing service composition. Peer-to-Peer Networking and Applications, 2018, 11, 1115-1128.	3.9	22
121	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
122	Inhibiting MARSs reduces hyperhomocysteinemiaâ€associated neural tube and congenital heart defects. EMBO Molecular Medicine, 2020, 12, e9469.	6.9	21
123	An ensemble algorithm with self-adaptive learning techniques for high-dimensional numerical optimization. Applied Mathematics and Computation, 2014, 231, 329-346.	2.2	20
124	Efficient business process consolidation: combining topic features with structure matching. Soft Computing, 2018, 22, 645-657.	3.6	20
125	A Self-Adaptive Fireworks Algorithm for Classification Problems. IEEE Access, 2018, 6, 44406-44416.	4.2	20
126	dbPSP 2.0, an updated database of protein phosphorylation sites in prokaryotes. Scientific Data, 2020, 7, 164.	5.3	20

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127	CPLM 4.0: an updated database with rich annotations for protein lysine modifications. Nucleic Acids Research, 2022, 50, D451-D459.	14.5	20
128	Dysbindin as a novel biomarker for pancreatic ductal adenocarcinoma identified by proteomic profiling. International Journal of Cancer, 2016, 139, 1821-1829.	5.1	19
129	Self-Adaptive Particle Swarm Optimization-Based Echo State Network for Time Series Prediction. International Journal of Neural Systems, 2021, 31, 2150057.	5.2	19
130	Outlier detection based on approximation accuracy entropy. International Journal of Machine Learning and Cybernetics, 2019, 10, 2483-2499.	3.6	18
131	DeepPhagy: a deep learning framework for quantitatively measuring autophagy activity in <i>Saccharomyces cerevisiae</i>. Autophagy, 2020, 16, 626-640.	9.1	18
132	Towards a better understanding of the novel avian-origin H7N9 influenza A virus in China. Scientific Reports, 2013, 3, 2318.	3.3	17
133	Reconfiguring phosphorylation signaling by genetic polymorphisms affects cancer susceptibility. Journal of Molecular Cell Biology, 2015, 7, 187-202.	3.3	17
134	A novel cluster validity index for fuzzy C-means algorithm. Soft Computing, 2018, 22, 1921-1931.	3.6	17
135	Phosphoproteomics-based network medicine. FEBS Journal, 2013, 280, 5696-5704.	4.7	16
136	WocEA: The visualization of functional enrichment results in word clouds. Journal of Genetics and Genomics, 2018, 45, 415-417.	3.9	16
137	Partial Connection Based on Channel Attention for Differentiable Neural Architecture Search. IEEE Transactions on Industrial Informatics, 2023, 19, 6804-6813.	11.3	16
138	Enhanced Purification of Ubiquitinated Proteins by Engineered Tandem Hybrid Ubiquitin-binding Domains (ThUBDs). Molecular and Cellular Proteomics, 2016, 15, 1381-1396.	3.8	15
139	Precision Medicine: What Challenges Are We Facing?. Genomics, Proteomics and Bioinformatics, 2016, 14, 253-261.	6.9	15
140	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
141	Prior knowledge guided differential evolution. Soft Computing, 2017, 21, 6841-6858.	3.6	15
142	Fingerprint image super resolution using sparse representation with ridge pattern prior by classification coupled dictionaries. IET Biometrics, 2017, 6, 342-350.	2.5	15
143	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
144	Self-adaptive kernel K-means algorithm based on the shuffled frog leaping algorithm. Soft Computing, 2018, 22, 861-872.	3.6	14

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145	Post-mortem tissue proteomics reveals the pathogenesis of multi-organ injuries of COVID-19. National Science Review, 2021, 8, nwab143.	9.5	14
146	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
147	Combining Gabor filtering and classification dictionaries learning for fingerprint enhancement. IET Biometrics, 2017, 6, 438-447.	2.5	13
148	Computational Analysis of Phosphoproteomics: Progresses and Perspectives. Current Protein and Peptide Science, 2011, 12, 591-601.	1.4	13
149	A Hybrid Evolutionary Algorithm for Numerical Optimization Problem. Intelligent Automation and Soft Computing, 2015, 21, 473-490.	2.1	12
150	Locally adaptive multiple kernel k-means algorithm based on shared nearest neighbors. Soft Computing, 2018, 22, 4573-4583.	3.6	12
151	Weight Uncertainty in Boltzmann Machine. Cognitive Computation, 2016, 8, 1064-1073.	5.2	11
152	Phosphoproteome Analysis Reveals Phosphorylation Underpinnings in the Brains of Nurse and Forager Honeybees (Apis mellifera). Scientific Reports, 2017, 7, 1973.	3.3	11
153	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
154	An evolutionary classification method based on fireworks algorithm. International Journal of Bio-Inspired Computation, 2018, 11, 149.	0.9	10
155	GPS-PBS: A Deep Learning Framework to Predict Phosphorylation Sites that Specifically Interact with Phosphoprotein-Binding Domains. Cells, 2020, 9, 1266.	4.1	10
156	GPS-Uber: a hybrid-learning framework for prediction of general and E3-specific lysine ubiquitination sites. Briefings in Bioinformatics, 2022, 23, .	6.5	10
157	An improved brain storm optimization algorithm with new solution generation strategies for classification. Engineering Applications of Artificial Intelligence, 2022, 110, 104677.	8.1	10
158	A Review on Feature Binding Theory and Its Functions Observed in Perceptual Process. Cognitive Computation, 2017, 9, 194-206.	5.2	9
159	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
160	GPS-MBA: Computational Analysis of MHC Class II Epitopes in Type 1 Diabetes. PLoS ONE, 2012, 7, e33884.	2.5	9
161	Computational Analyses of TBC Protein Family in Eukaryotes. Protein and Peptide Letters, 2008, 15, 505-509.	0.9	8
162	Preference-driven Pareto front exploitation for bloat control in genetic programming. Applied Soft Computing Journal, 2020, 92, 106254.	7.2	8

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163	Wang-Landau sampling in face-centered-cubic hydrophobic-hydrophilic lattice model proteins. Physical Review E, 2014, 90, 042715.	2.1	7
164	Correlated expression of retrocopies and parental genes in zebrafish. Molecular Genetics and Genomics, 2016, 291, 723-737.	2.1	7
165	Cloud Model-Based Artificial Immune Network for Complex Optimization Problem. Computational Intelligence and Neuroscience, 2017, 2017, 1-17.	1.7	7
166	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
167	Spatial and Temporal Characteristics of Rainfall Anomalies in 1961â€"2010 in the Yangtze River Basin, China. Atmosphere, 2021, 12, 960.	2.3	7
168	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
169	An adaptive GP-based memetic algorithm for symbolic regression. Applied Intelligence, 2020, 50, 3961-3975.	5.3	6
170	Classification Based on Brain Storm Optimization With Feature Selection. IEEE Access, 2021, 9, 16582-16590.	4.2	6
171	Atg9-centered multi-omics integration reveals new autophagy regulators in<i>Saccharomyces cerevisiae</i>. Autophagy, 2021, 17, 4453-4476.	9.1	6
172	Analysis of phosphorylation sites on autophagy proteins. Protein and Cell, 2015, 6, 698-701.	11.0	5
173	Classification Based on Brain Storm Optimization Algorithm. Communications in Computer and Information Science, 2016, , 371-376.	0.5	5
174	Recognizing the human attention state using cardiac pulse from the noncontact and automatic-based measurements. Soft Computing, 2018, 22, 3937-3949.	3.6	5
175	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
176	BEMD image fusion based on PCNN and compressed sensing. Soft Computing, 2019, 23, 10045-10054.	3.6	5
177	Identification of rare variants in cardiac sodium channel Î²4-subunit gene SCN4B associated with ventricular tachycardia. Molecular Genetics and Genomics, 2019, 294, 1059-1071.	2.1	5
178	Ray Wu, fifth business or father of DNA sequencing?. Protein and Cell, 2016, 7, 467-470.	11.0	4
179	A new validity index adapted to fuzzy clustering algorithm. Multimedia Tools and Applications, 2018, 77, 11339-11361.	3.9	4
180	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

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181	Bi-objective memetic GP with dispersion-keeping Pareto evaluation for real-world regression. Information Sciences, 2020, 539, 16-35.	6.9	4
182	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
183	Structure and weights search for classification with feature selection based on brain storm optimization algorithm. Applied Intelligence, 2022, 52, 5857-5866.	5.3	4
184	A novel genome-wide full-length kinesin prediction analysis reveals additional mammalian kinesins. Science Bulletin, 2006, 51, 1836-1847.	1.7	3
185	An efficient site-directed mutagenesis method for ColE1-type ori plasmid. Analytical Biochemistry, 2007, 363, 151-153.	2.4	3
186	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
187	Bioinformatics Technologies in Autophagy Research. Advances in Experimental Medicine and Biology, 2021, 1208, 387-453.	1.6	3
188	iCAL: a new pipeline to investigate autophagy selectivity and cancer. Autophagy, 2021, 17, 1799-1801.	9.1	3
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