

Yu Xue

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6735552/publications.pdf>

Version: 2024-02-01

202
papers

18,859
citations

23500

58
h-index

13727

129
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). <i>Autophagy</i> , 2016, 12, 1-222.	4.3	4,701
2	HemI: A Toolkit for Illustrating Heatmaps. <i>PLoS ONE</i> , 2014, 9, e111988.	1.1	963
3	IBS: an illustrator for the presentation and visualization of biological sequences. <i>Bioinformatics</i> , 2015, 31, 3359-3361.	1.8	817
4	GPS 2.0, a Tool to Predict Kinase-specific Phosphorylation Sites in Hierarchy. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1598-1608.	2.5	587
5	CSS-Palm 2.0: an updated software for palmitoylation sites prediction. <i>Protein Engineering, Design and Selection</i> , 2008, 21, 639-644.	1.0	511
6	DOG 1.0: illustrator of protein domain structures. <i>Cell Research</i> , 2009, 19, 271-273.	5.7	505
7	GPS-SUMO: a tool for the prediction of sumoylation sites and SUMO-interaction motifs. <i>Nucleic Acids Research</i> , 2014, 42, W325-W330.	6.5	417
8	Database Resources of the National Genomics Data Center, China National Center for Bioinformation in 2022. <i>Nucleic Acids Research</i> , 2022, 50, D27-D38.	6.5	364
9	AnimalTFDB 2.0: a resource for expression, prediction and functional study of animal transcription factors. <i>Nucleic Acids Research</i> , 2015, 43, D76-D81.	6.5	287
10	Inhibiting PD-L1 palmitoylation enhances T-cell immune responses against tumours. <i>Nature Biomedical Engineering</i> , 2019, 3, 306-317.	11.6	279
11	A self-adaptive artificial bee colony algorithm based on global best for global optimization. <i>Soft Computing</i> , 2018, 22, 2935-2952.	2.1	274
12	Self-Adaptive Particle Swarm Optimization for Large-Scale Feature Selection in Classification. <i>ACM Transactions on Knowledge Discovery From Data</i> , 2019, 13, 1-27.	2.5	253
13	Plasma Proteomics Identify Biomarkers and Pathogenesis of COVID-19. <i>Immunity</i> , 2020, 53, 1108-1122.e5.	6.6	228
14	Systematic study of protein sumoylation: Development of a site-specific predictor of SUMOsp 2.0. <i>Proteomics</i> , 2009, 9, 3409-3412.	1.3	227
15	GPS-SNO: Computational Prediction of Protein S-Nitrosylation Sites with a Modified GPS Algorithm. <i>PLoS ONE</i> , 2010, 5, e11290.	1.1	223
16	GPS 2.1: enhanced prediction of kinase-specific phosphorylation sites with an algorithm of motif length selection. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 255-260.	1.0	217
17	GPS: a comprehensive www server for phosphorylation sites prediction. <i>Nucleic Acids Research</i> , 2005, 33, W184-W187.	6.5	215
18	Text classification based on deep belief network and softmax regression. <i>Neural Computing and Applications</i> , 2018, 29, 61-70.	3.2	199

#	ARTICLE	IF	CITATIONS
19	PLMD: An updated data resource of protein lysine modifications. <i>Journal of Genetics and Genomics</i> , 2017, 44, 243-250.	1.7	198
20	GPS 5.0: An Update on the Prediction of Kinase-specific Phosphorylation Sites in Proteins. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 72-80.	3.0	197
21	PPSP: prediction of PK-specific phosphorylation site with Bayesian decision theory. <i>BMC Bioinformatics</i> , 2006, 7, 163.	1.2	183
22	SUMOSp: a web server for sumoylation site prediction. <i>Nucleic Acids Research</i> , 2006, 34, W254-W257.	6.5	179
23	Database Resources of the National Genomics Data Center, China National Center for Bioinformation in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D18-D28.	6.5	168
24	Database Resources of the National Genomics Data Center in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D24-D33.	6.5	165
25	Systematic Analysis of Protein Phosphorylation Networks From Phosphoproteomic Data. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1070-1083.	2.5	161
26	Database Resources of the BIG Data Center in 2019. <i>Nucleic Acids Research</i> , 2019, 47, D8-D14.	6.5	157
27	CPLM: a database of protein lysine modifications. <i>Nucleic Acids Research</i> , 2014, 42, D531-D536.	6.5	155
28	GPS: a novel group-based phosphorylation predicting and scoring method. <i>Biochemical and Biophysical Research Communications</i> , 2004, 325, 1443-1448.	1.0	149
29	CSS-Palm: palmitoylation site prediction with a clustering and scoring strategy (CSS). <i>Bioinformatics</i> , 2006, 22, 894-896.	1.8	130
30	PTMD: A Database of Human Disease-associated Post-translational Modifications. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 244-251.	3.0	129
31	Efficient Feature Selection and Classification for Vehicle Detection. <i>IEEE Transactions on Circuits and Systems for Video Technology</i> , 2015, 25, 508-517.	5.6	128
32	MeMo: a web tool for prediction of protein methylation modifications. <i>Nucleic Acids Research</i> , 2006, 34, W249-W253.	6.5	123
33	Open resource of clinical data from patients with pneumonia for the prediction of COVID-19 outcomes via deep learning. <i>Nature Biomedical Engineering</i> , 2020, 4, 1197-1207.	11.6	122
34	GPS-Lipid: a robust tool for the prediction of multiple lipid modification sites. <i>Scientific Reports</i> , 2016, 6, 28249.	1.6	120
35	DrLLPS: a data resource of liquid-liquid phase separation in eukaryotes. <i>Nucleic Acids Research</i> , 2020, 48, D288-D295.	6.5	112
36	Prediction of N ^ɳ -acetylation on internal lysines implemented in Bayesian Discriminant Method. <i>Biochemical and Biophysical Research Communications</i> , 2006, 350, 818-824.	1.0	106

#	ARTICLE	IF	CITATIONS
37	Self-adaptive parameter and strategy based particle swarm optimization for large-scale feature selection problems with multiple classifiers. <i>Applied Soft Computing Journal</i> , 2020, 88, 106031.	4.1	105
38	Bat algorithm with triangle-flipping strategy for numerical optimization. <i>International Journal of Machine Learning and Cybernetics</i> , 2018, 9, 199-215.	2.3	101
39	UUUCD: a family-based database of ubiquitin and ubiquitin-like conjugation. <i>Nucleic Acids Research</i> , 2013, 41, D445-D451.	6.5	99
40	GPS-YNO2: computational prediction of tyrosine nitration sites in proteins. <i>Molecular BioSystems</i> , 2011, 7, 1197.	2.9	94
41	GPS-CCD: A Novel Computational Program for the Prediction of Calpain Cleavage Sites. <i>PLoS ONE</i> , 2011, 6, e19001.	1.1	94
42	A Self-Adaptive Mutation Neural Architecture Search Algorithm Based on Blocks. <i>IEEE Computational Intelligence Magazine</i> , 2021, 16, 67-78.	3.4	93
43	Pyruvate Kinase M2 Activates mTORC1 by Phosphorylating AKT1S1. <i>Scientific Reports</i> , 2016, 6, 21524.	1.6	92
44	Gene selection for tumor classification using neighborhood rough sets and entropy measures. <i>Journal of Biomedical Informatics</i> , 2017, 67, 59-68.	2.5	90
45	NBA-Palm: prediction of palmitoylation site implemented in Naïve Bayes algorithm. <i>BMC Bioinformatics</i> , 2006, 7, 458.	1.2	88
46	GPS-PAIL: prediction of lysine acetyltransferase-specific modification sites from protein sequences. <i>Scientific Reports</i> , 2016, 6, 39787.	1.6	88
47	A Multi-Objective Evolutionary Approach Based on Graph-in-Graph for Neural Architecture Search of Convolutional Neural Networks. <i>International Journal of Neural Systems</i> , 2021, 31, 2150035.	3.2	82
48	DeepNitro: Prediction of Protein Nitration and Nitrosylation Sites by Deep Learning. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 294-306.	3.0	81
49	Adaptive crossover operator based multi-objective binary genetic algorithm for feature selection in classification. <i>Knowledge-Based Systems</i> , 2021, 227, 107218.	4.0	81
50	Multi-Objective Feature Selection With Missing Data in Classification. <i>IEEE Transactions on Emerging Topics in Computational Intelligence</i> , 2022, 6, 355-364.	3.4	79
51	dbPAF: an integrative database of protein phosphorylation in animals and fungi. <i>Scientific Reports</i> , 2016, 6, 23534.	1.6	78
52	Fast and Accurate Classification of Time Series Data Using Extended ELM: Application in Fault Diagnosis of Air Handling Units. <i>IEEE Transactions on Systems, Man, and Cybernetics: Systems</i> , 2019, 49, 1349-1356.	5.9	77
53	PhosSNP for Systematic Analysis of Genetic Polymorphisms That Influence Protein Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 623-634.	2.5	72
54	Measures of uncertainty for neighborhood rough sets. <i>Knowledge-Based Systems</i> , 2017, 120, 226-235.	4.0	71

#	ARTICLE	IF	CITATIONS
55	Discrete gbest-guided artificial bee colony algorithm for cloud service composition. Applied Intelligence, 2015, 42, 661-678.	3.3	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.	3.9	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.	3.2	64
58	A Pythagorean-Type Fuzzy Deep Denoising Autoencoder for Industrial Accident Early Warning. IEEE Transactions on Fuzzy Systems, 2017, 25, 1561-1575.	6.5	63
59	Metformin activates chaperone-mediated autophagy and improves disease pathologies in an Alzheimer disease mouse model. Protein and Cell, 2021, 12, 769-787.	4.8	63
60	OUP accepted manuscript. Nucleic Acids Research, 2017, 45, D264-D270.	6.5	62
61	CPLA 1.0: an integrated database of protein lysine acetylation. Nucleic Acids Research, 2011, 39, D1029-D1034.	6.5	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.	2.5	58
63	iLUCD 2.0: an update with rich annotations for ubiquitin and ubiquitin-like conjugations. Nucleic Acids Research, 2018, 46, D447-D453.	6.5	57
64	CPSS: a computational platform for the analysis of small RNA deep sequencing data. Bioinformatics, 2012, 28, 1925-1927.	1.8	55
65	A Summary of Computational Resources for Protein Phosphorylation. Current Protein and Peptide Science, 2010, 11, 485-496.	0.7	53
66	EKPD: a hierarchical database of eukaryotic protein kinases and protein phosphatases. Nucleic Acids Research, 2014, 42, D496-D502.	6.5	52
67	Mechanism of cargo recognition by retromer-linked SNX-BAR proteins. PLoS Biology, 2020, 18, e3000631.	2.6	51
68	DPCG: an efficient density peaks clustering algorithm based on grid. International Journal of Machine Learning and Cybernetics, 2018, 9, 743-754.	2.3	50
69	A robust density peaks clustering algorithm using fuzzy neighborhood. International Journal of Machine Learning and Cybernetics, 2018, 9, 1131-1140.	2.3	49
70	Fuzzy Multilevel Image Thresholding Based on Improved Coyote Optimization Algorithm. IEEE Access, 2021, 9, 33595-33607.	2.6	49
71	EPSPD: a well-annotated data resource of protein phosphorylation sites in eukaryotes. Briefings in Bioinformatics, 2021, 22, 298-307.	3.2	49
72	Phosphoproteome-based kinase activity profiling reveals the critical role of MAP2K2 and PLK1 in neuronal autophagy. Autophagy, 2017, 13, 1969-1980.	4.3	48

#	ARTICLE	IF	CITATIONS
73	Computational prediction of methylation types of covalently modified lysine and arginine residues in proteins. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw041.	3.2	47
74	A genome-wide analysis of sumoylation-related biological processes and functions in human nucleus. <i>FEBS Letters</i> , 2005, 579, 3369-3375.	1.3	46
75	Mal-Lys: prediction of lysine malonylation sites in proteins integrated sequence-based features with mRMR feature selection. <i>Scientific Reports</i> , 2016, 6, 38318.	1.6	46
76	dbPPT: a comprehensive database of protein phosphorylation in plants. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau121.	1.4	45
77	A hybrid biogeography-based optimization and fuzzy C-means algorithm for image segmentation. <i>Soft Computing</i> , 2019, 23, 2033-2046.	2.1	45
78	Enhanced Purification of Ubiquitinated Proteins by Engineered Tandem Hybrid Ubiquitin-binding Domains (ThUBDs). <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1381-1396.	2.5	44
79	Research on denoising sparse autoencoder. <i>International Journal of Machine Learning and Cybernetics</i> , 2017, 8, 1719-1729.	2.3	44
80	Density peaks clustering using geodesic distances. <i>International Journal of Machine Learning and Cybernetics</i> , 2018, 9, 1335-1349.	2.3	44
81	GPS-ARM: Computational Analysis of the APC/C Recognition Motif by Predicting D-Boxes and KEN-Boxes. <i>PLoS ONE</i> , 2012, 7, e34370.	1.1	44
82	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2017, 45, D397-D403.	6.5	42
83	Information Commons for Rice (IC4R). <i>Nucleic Acids Research</i> , 2016, 44, D1172-D1180.	6.5	41
84	THANATOS: an integrative data resource of proteins and post-translational modifications in the regulation of autophagy. <i>Autophagy</i> , 2018, 14, 296-310.	4.3	41
85	GPS-PUP: computational prediction of pupylation sites in prokaryotic proteins. <i>Molecular BioSystems</i> , 2011, 7, 2737.	2.9	40
86	An efficient energy hole alleviating algorithm for wireless sensor networks. <i>IEEE Transactions on Consumer Electronics</i> , 2014, 60, 347-355.	3.0	40
87	Systematic analysis of the in situ crosstalk of tyrosine modifications reveals no additional natural selection on multiply modified residues. <i>Scientific Reports</i> , 2014, 4, 7331.	1.6	39
88	Pan-Cancer Analysis Reveals the Functional Importance of Protein Lysine Modification in Cancer Development. <i>Frontiers in Genetics</i> , 2018, 9, 254.	1.1	39
89	Systematic Analysis of the Phosphoproteome and Kinase-substrate Networks in the Mouse Testis. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3626-3638.	2.5	38
90	Insulin signaling regulates longevity through protein phosphorylation in <i>Caenorhabditis elegans</i> . <i>Nature Communications</i> , 2021, 12, 4568.	5.8	38

#	ARTICLE	IF	CITATIONS
91	A self-adaptive gradient descent search algorithm for fully-connected neural networks. <i>Neurocomputing</i> , 2022, 478, 70-80.	3.5	35
92	An integrative multi-omics approach uncovers the regulatory role of CDK7 and CDK4 in autophagy activation induced by silica nanoparticles. <i>Autophagy</i> , 2021, 17, 1426-1447.	4.3	33
93	Large-Scale Feedforward Neural Network Optimization by a Self-Adaptive Strategy and Parameter Based Particle Swarm Optimization. <i>IEEE Access</i> , 2019, 7, 52473-52483.	2.6	32
94	A novel density peaks clustering with sensitivity of local density and density-adaptive metric. <i>Knowledge and Information Systems</i> , 2019, 59, 285-309.	2.1	31
95	An Evolutionary Computation Based Feature Selection Method for Intrusion Detection. <i>Security and Communication Networks</i> , 2018, 2018, 1-10.	1.0	30
96	Predicting lysine acetylation sites of proteins using sequence and predicted structural features. <i>Journal of Computational Chemistry</i> , 2018, 39, 1757-1763.	1.5	30
97	Phosphorylation of SNX27 by MAPK11/14 links cellular stress signaling pathways with endocytic recycling. <i>Journal of Cell Biology</i> , 2021, 220, .	2.3	30
98	Proteome-wide prediction of PKA phosphorylation sites in eukaryotic kingdom. <i>Genomics</i> , 2008, 92, 457-463.	1.3	29
99	Systematic analysis of the Plk-mediated phosphoregulation in eukaryotes. <i>Briefings in Bioinformatics</i> , 2013, 14, 344-360.	3.2	29
100	A review on multi-class TWSVM. <i>Artificial Intelligence Review</i> , 2019, 52, 775-801.	9.7	29
101	HybridSucc: A Hybrid-learning Architecture for General and Species-specific Succinylation Site Prediction. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 194-207.	3.0	28
102	The E3 ubiquitin ligase HECTD3 regulates ubiquitination and degradation of Tara. <i>Biochemical and Biophysical Research Communications</i> , 2008, 367, 805-812.	1.0	27
103	MiCroKit 3.0: an integrated database of midbody, centrosome and kinetochore. <i>Nucleic Acids Research</i> , 2010, 38, D155-D160.	6.5	27
104	Systematic characterization of small RNAome during zebrafish early developmental stages. <i>BMC Genomics</i> , 2014, 15, 117.	1.2	27
105	Multipurpose watermarking for vector map protection and authentication. <i>Multimedia Tools and Applications</i> , 2018, 77, 7239-7259.	2.6	27
106	A feasible density peaks clustering algorithm with a merging strategy. <i>Soft Computing</i> , 2019, 23, 5171-5183.	2.1	27
107	Multi-omic profiling of plasma reveals molecular alterations in children with COVID-19. <i>Theranostics</i> , 2021, 11, 8008-8026.	4.6	27
108	Prediction of novel pre-microRNAs with high accuracy through boosting and SVM. <i>Bioinformatics</i> , 2011, 27, 1436-1437.	1.8	26

#	ARTICLE	IF	CITATIONS
109	A general user interface for prediction servers of proteins' post-translational modification sites. <i>Nature Protocols</i> , 2006, 1, 1318-1321.	5.5	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. <i>Analytical Chemistry</i> , 2009, 81, 5794-5805.	3.2	25
111	NSCT-PCNN image fusion based on image gradient motivation. <i>IET Computer Vision</i> , 2018, 12, 377-383.	1.3	24
112	Model-based analysis uncovers mutations altering autophagy selectivity in human cancer. <i>Nature Communications</i> , 2021, 12, 3258.	5.8	24
113	Heml 2.0: an online service for heatmap illustration. <i>Nucleic Acids Research</i> , 2022, 50, W405-W411.	6.5	24
114	dbPSP: a curated database for protein phosphorylation sites in prokaryotes. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav031.	1.4	23
115	MiCroKiTS 4.0: a database of midbody, centrosome, kinetochore, telomere and spindle. <i>Nucleic Acids Research</i> , 2015, 43, D328-D334.	6.5	23
116	Knowledge based differential evolution for cloud computing service composition. <i>Journal of Ambient Intelligence and Humanized Computing</i> , 2018, 9, 565-574.	3.3	23
117	Integrated omics in <i>Drosophila</i> uncover a circadian kinome. <i>Nature Communications</i> , 2020, 11, 2710.	5.8	23
118	MBA: a literature mining system for extracting biomedical abbreviations. <i>BMC Bioinformatics</i> , 2009, 10, 14.	1.2	22
119	Phosphoproteomic Analysis of the Highly-Metastatic Hepatocellular Carcinoma Cell Line, MHCC97-H. <i>International Journal of Molecular Sciences</i> , 2015, 16, 4209-4225.	1.8	22
120	Self-adaptive bat algorithm for large scale cloud manufacturing service composition. <i>Peer-to-Peer Networking and Applications</i> , 2018, 11, 1115-1128.	2.6	22
121	iEKPD 2.0: an update with rich annotations for eukaryotic protein kinases, protein phosphatases and proteins containing phosphoprotein-binding domains. <i>Nucleic Acids Research</i> , 2019, 47, D344-D350.	6.5	22
122	Inhibiting MARSs reduces hyperhomocysteinemia-associated neural tube and congenital heart defects. <i>EMBO Molecular Medicine</i> , 2020, 12, e9469.	3.3	21
123	An ensemble algorithm with self-adaptive learning techniques for high-dimensional numerical optimization. <i>Applied Mathematics and Computation</i> , 2014, 231, 329-346.	1.4	20
124	Efficient business process consolidation: combining topic features with structure matching. <i>Soft Computing</i> , 2018, 22, 645-657.	2.1	20
125	A Self-Adaptive Fireworks Algorithm for Classification Problems. <i>IEEE Access</i> , 2018, 6, 44406-44416.	2.6	20
126	dbPSP 2.0, an updated database of protein phosphorylation sites in prokaryotes. <i>Scientific Data</i> , 2020, 7, 164.	2.4	20

#	ARTICLE	IF	CITATIONS
127	CPLM 4.0: an updated database with rich annotations for protein lysine modifications. <i>Nucleic Acids Research</i> , 2022, 50, D451-D459.	6.5	20
128	Dysbindin as a novel biomarker for pancreatic ductal adenocarcinoma identified by proteomic profiling. <i>International Journal of Cancer</i> , 2016, 139, 1821-1829.	2.3	19
129	Self-Adaptive Particle Swarm Optimization-Based Echo State Network for Time Series Prediction. <i>International Journal of Neural Systems</i> , 2021, 31, 2150057.	3.2	19
130	Outlier detection based on approximation accuracy entropy. <i>International Journal of Machine Learning and Cybernetics</i> , 2019, 10, 2483-2499.	2.3	18
131	DeepPhagy: a deep learning framework for quantitatively measuring autophagy activity in <i>Saccharomyces cerevisiae</i> . <i>Autophagy</i> , 2020, 16, 626-640.	4.3	18
132	Towards a better understanding of the novel avian-origin H7N9 influenza A virus in China. <i>Scientific Reports</i> , 2013, 3, 2318.	1.6	17
133	Reconfiguring phosphorylation signaling by genetic polymorphisms affects cancer susceptibility. <i>Journal of Molecular Cell Biology</i> , 2015, 7, 187-202.	1.5	17
134	A novel cluster validity index for fuzzy C-means algorithm. <i>Soft Computing</i> , 2018, 22, 1921-1931.	2.1	17
135	Phosphoproteomics-based network medicine. <i>FEBS Journal</i> , 2013, 280, 5696-5704.	2.2	16
136	WocEA: The visualization of functional enrichment results in word clouds. <i>Journal of Genetics and Genomics</i> , 2018, 45, 415-417.	1.7	16
137	Partial Connection Based on Channel Attention for Differentiable Neural Architecture Search. <i>IEEE Transactions on Industrial Informatics</i> , 2023, 19, 6804-6813.	7.2	16
138	Enhanced Purification of Ubiquitinated Proteins by Engineered Tandem Hybrid Ubiquitin-binding Domains (ThUBDs). <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1381-1396.	2.5	15
139	Precision Medicine: What Challenges Are We Facing?. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 253-261.	3.0	15
140	Multi-objective layout optimization of a satellite module using the Wang-Landau sampling method with local search. <i>Frontiers of Information Technology and Electronic Engineering</i> , 2016, 17, 527-542.	1.5	15
141	Prior knowledge guided differential evolution. <i>Soft Computing</i> , 2017, 21, 6841-6858.	2.1	15
142	Fingerprint image super resolution using sparse representation with ridge pattern prior by classification coupled dictionaries. <i>IET Biometrics</i> , 2017, 6, 342-350.	1.6	15
143	Unsupervised feature selection based on self-representation sparse regression and local similarity preserving. <i>International Journal of Machine Learning and Cybernetics</i> , 2019, 10, 757-770.	2.3	15
144	Self-adaptive kernel K-means algorithm based on the shuffled frog leaping algorithm. <i>Soft Computing</i> , 2018, 22, 861-872.	2.1	14

#	ARTICLE	IF	CITATIONS
145	Post-mortem tissue proteomics reveals the pathogenesis of multi-organ injuries of COVID-19. National Science Review, 2021, 8, nwab143.	4.6	14
146	Self-adaptive learning based discrete differential evolution algorithm for solving CJWTA problem. Journal of Systems Engineering and Electronics, 2014, 25, 59-68.	1.1	13
147	Combining Gabor filtering and classification dictionaries learning for fingerprint enhancement. IET Biometrics, 2017, 6, 438-447.	1.6	13
148	Computational Analysis of Phosphoproteomics: Progresses and Perspectives. Current Protein and Peptide Science, 2011, 12, 591-601.	0.7	13
149	A Hybrid Evolutionary Algorithm for Numerical Optimization Problem. Intelligent Automation and Soft Computing, 2015, 21, 473-490.	1.6	12
150	Locally adaptive multiple kernel k-means algorithm based on shared nearest neighbors. Soft Computing, 2018, 22, 4573-4583.	2.1	12
151	Weight Uncertainty in Boltzmann Machine. Cognitive Computation, 2016, 8, 1064-1073.	3.6	11
152	Phosphoproteome Analysis Reveals Phosphorylation Underpinnings in the Brains of Nurse and Forager Honeybees (<i>Apis mellifera</i>). Scientific Reports, 2017, 7, 1973.	1.6	11
153	Computationally characterizing and comprehensive analysis of zinc-binding sites in proteins. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 171-180.	1.1	10
154	An evolutionary classification method based on fireworks algorithm. International Journal of Bio-Inspired Computation, 2018, 11, 149.	0.6	10
155	GPS-PBS: A Deep Learning Framework to Predict Phosphorylation Sites that Specifically Interact with Phosphoprotein-Binding Domains. Cells, 2020, 9, 1266.	1.8	10
156	GPS-Uber: a hybrid-learning framework for prediction of general and E3-specific lysine ubiquitination sites. Briefings in Bioinformatics, 2022, 23, .	3.2	10
157	An improved brain storm optimization algorithm with new solution generation strategies for classification. Engineering Applications of Artificial Intelligence, 2022, 110, 104677.	4.3	10
158	A Review on Feature Binding Theory and Its Functions Observed in Perceptual Process. Cognitive Computation, 2017, 9, 194-206.	3.6	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.	0.4	9
160	GPS-MBA: Computational Analysis of MHC Class II Epitopes in Type 1 Diabetes. PLoS ONE, 2012, 7, e33884.	1.1	9
161	Computational Analyses of TBC Protein Family in Eukaryotes. Protein and Peptide Letters, 2008, 15, 505-509.	0.4	8
162	Preference-driven Pareto front exploitation for bloat control in genetic programming. Applied Soft Computing Journal, 2020, 92, 106254.	4.1	8

#	ARTICLE	IF	CITATIONS
163	Wang-Landau sampling in face-centered-cubic hydrophobic-hydrophilic lattice model proteins. <i>Physical Review E</i> , 2014, 90, 042715.	0.8	7
164	Correlated expression of retrocopies and parental genes in zebrafish. <i>Molecular Genetics and Genomics</i> , 2016, 291, 723-737.	1.0	7
165	Cloud Model-Based Artificial Immune Network for Complex Optimization Problem. <i>Computational Intelligence and Neuroscience</i> , 2017, 2017, 1-17.	1.1	7
166	PTMsnip: A Web Server for the Identification of Driver Mutations That Affect Protein Post-translational Modification. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 593661.	1.8	7
167	Spatial and Temporal Characteristics of Rainfall Anomalies in 1961–2010 in the Yangtze River Basin, China. <i>Atmosphere</i> , 2021, 12, 960.	1.0	7
168	A novel knowledge-guided evolutionary scheduling strategy for energy-efficient connected coverage optimization in WSNs. <i>Peer-to-Peer Networking and Applications</i> , 2017, 10, 547-558.	2.6	6
169	An adaptive GP-based memetic algorithm for symbolic regression. <i>Applied Intelligence</i> , 2020, 50, 3961-3975.	3.3	6
170	Classification Based on Brain Storm Optimization With Feature Selection. <i>IEEE Access</i> , 2021, 9, 16582-16590.	2.6	6
171	Atg9-centered multi-omics integration reveals new autophagy regulators in <i>Saccharomyces cerevisiae</i> . <i>Autophagy</i> , 2021, 17, 4453-4476.	4.3	6
172	Analysis of phosphorylation sites on autophagy proteins. <i>Protein and Cell</i> , 2015, 6, 698-701.	4.8	5
173	Classification Based on Brain Storm Optimization Algorithm. <i>Communications in Computer and Information Science</i> , 2016, , 371-376.	0.4	5
174	Recognizing the human attention state using cardiac pulse from the noncontact and automatic-based measurements. <i>Soft Computing</i> , 2018, 22, 3937-3949.	2.1	5
175	An improved fingerprint orientation field extraction method based on quality grading scheme. <i>International Journal of Machine Learning and Cybernetics</i> , 2018, 9, 1249-1260.	2.3	5
176	BEMD image fusion based on PCNN and compressed sensing. <i>Soft Computing</i> , 2019, 23, 10045-10054.	2.1	5
177	Identification of rare variants in cardiac sodium channel β_4 -subunit gene SCN4B associated with ventricular tachycardia. <i>Molecular Genetics and Genomics</i> , 2019, 294, 1059-1071.	1.0	5
178	Ray Wu, fifth business or father of DNA sequencing?. <i>Protein and Cell</i> , 2016, 7, 467-470.	4.8	4
179	A new validity index adapted to fuzzy clustering algorithm. <i>Multimedia Tools and Applications</i> , 2018, 77, 11339-11361.	2.6	4
180	Memetic algorithm based on extension step and statistical filtering for large-scale capacitated arc routing problems. <i>Natural Computing</i> , 2018, 17, 375-391.	1.8	4

#	ARTICLE	IF	CITATIONS
181	Bi-objective memetic GP with dispersion-keeping Pareto evaluation for real-world regression. Information Sciences, 2020, 539, 16-35.	4.0	4
182	Multi-Objective Memetic Algorithms with Tree-Based Genetic Programming and Local Search for Symbolic Regression. Neural Processing Letters, 2021, 53, 2197-2219.	2.0	4
183	Structure and weights search for classification with feature selection based on brain storm optimization algorithm. Applied Intelligence, 2022, 52, 5857-5866.	3.3	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.	1.1	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.	1.8	3
187	Bioinformatics Technologies in Autophagy Research. Advances in Experimental Medicine and Biology, 2021, 1208, 387-453.	0.8	3
188	iCAL: a new pipeline to investigate autophagy selectivity and cancer. Autophagy, 2021, 17, 1799-1801.	4.3	3
189	Bioinformaticians wrestling with the big biomedical data. Journal of Genetics and Genomics, 2017, 44, 223-225.	1.7	2
190	Bioinformatics Commons: The Cornerstone of Life and Health Sciences. Genomics, Proteomics and Bioinformatics, 2018, 16, 223-225.	3.0	2
191	Research on a collaboration model of green closed-loop supply chains towards intelligent manufacturing. Multimedia Tools and Applications, 0, , 1.	2.6	2
192	Dependence structure of Gabor wavelets for face recognition. , 2017, , .		1
193	A classification method based on self-adaptive artificial bee colony. , 2017, , .		1
194	Stable Flexible Piezoresistive Sensors with Viscoelastic Ni Nanowiresâ€PDMS Composites and Ni Foam Electrodes. Zeitschrift Fur Anorganische Und Allgemeine Chemie, 2021, 647, 1031-1037.	0.6	1
195	Computational Identification of Protein Kinases and Kinase-Specific Substrates in Plants. Methods in Molecular Biology, 2015, 1306, 195-205.	0.4	1
196	A Classification Model Based on Improved Self-Adaptive Fireworks Algorithm. Advances in Computational Intelligence and Robotics Book Series, 2020, , 148-175.	0.4	1
197	A Sensitivity-Based Improving Learning Algorithm for Madaline Rule II. Mathematical Problems in Engineering, 2014, 2014, 1-8.	0.6	0
198	Security system construction of land and resources network based on intrusion detection. , 2015, , .		0

#	ARTICLE	IF	CITATIONS
199	Intrusion Detection System Based on an Updated ANN Model. Lecture Notes in Computer Science, 2021, , 472-479.	1.0	0
200	Bloat-aware GP-based methods with bloat quantification. Applied Intelligence, 0, , 1.	3.3	0
201	Preference-driven multi-objective GP search for regression models with new dominance principle and performance indicators. Applied Intelligence, 0, , 1.	3.3	0
202	iPCD: A Comprehensive Data Resource of Regulatory Proteins in Programmed Cell Death. Cells, 2022, 11, 2018.	1.8	0