

Shun-Fang Wang

List of Publications by Year in descending order

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63
all docs

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docs citations

63
times ranked

196
citing authors

#	ARTICLE	IF	CITATIONS
1	Protein Sub-Nuclear Localization Based on Effective Fusion Representations and Dimension Reduction Algorithm LDA. International Journal of Molecular Sciences, 2015, 16, 30343-30361.	4.1	34
2	Accurate classification of membrane protein types based on sequence and evolutionary information using deep learning. BMC Bioinformatics, 2019, 20, 700.	2.6	27
3	ACEP: improving antimicrobial peptides recognition through automatic feature fusion and amino acid embedding. BMC Genomics, 2020, 21, 597.	2.8	27
4	G-DipC: An Improved Feature Representation Method for Short Sequences to Predict the Type of Cargo in Cell-Penetrating Peptides. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 739-747.	3.0	17
5	Sample size determination for matched-pair equivalence trials using rate ratio. Biostatistics, 2007, 8, 625-631.	1.5	13
6	iEnhancer-RD: Identification of enhancers and their strength using RPKK features and deep neural networks. Analytical Biochemistry, 2021, 630, 114318.	2.4	13
7	An Improved Process for Generating Uniform PSSMs and Its Application in Protein Subcellular Localization via Various Global Dimension Reduction Techniques. IEEE Access, 2019, 7, 42384-42395.	4.2	12
8	Protein subnuclear localization based on a new effective representation and intelligent kernel linear discriminant analysis by dichotomous greedy genetic algorithm. PLoS ONE, 2018, 13, e0195636.	2.5	11
9	Efficient utilization on PSSM combining with recurrent neural network for membrane protein types prediction. Computational Biology and Chemistry, 2019, 81, 9-15.	2.3	11
10	Asymptotic Properties of the Maximum Quasi-Likelihood Estimator in Quasi-Likelihood Nonlinear Models. Communications in Statistics - Theory and Methods, 2008, 37, 2358-2368.	1.0	8
11	DeepFusion-RBP: Using Deep Learning to Fuse Multiple Features to Identify RNA-binding Protein Sequences. Current Bioinformatics, 2021, 16, 1089-1100.	1.5	8
12	Protein Subcellular Localization with Gaussian Kernel Discriminant Analysis and Its Kernel Parameter Selection. International Journal of Molecular Sciences, 2017, 18, 2718.	4.1	7
13	A New Feature Extraction Method Based on the Information Fusion of Entropy Matrix and Covariance Matrix and Its Application in Face Recognition. Entropy, 2015, 17, 4664-4683.	2.2	6
14	Protein sub-cellular localization based on noise-intensity-weighted linear discriminant analysis and an improved k-nearest-neighbor classifier. , 2016, , .		6
15	IMAL: An Improved Meta-learning Approach for Few-shot Classification of Plant Diseases. , 2021, , .		6
16	A protein succinylation sites prediction method based on the hybrid architecture of LSTM network and CNN. Journal of Bioinformatics and Computational Biology, 2022, 20, 2250003.	0.8	6
17	Prediction of protein structural classes by different feature expressions based on 2-D wavelet denoising and fusion. BMC Bioinformatics, 2019, 20, 701.	2.6	5
18	SE-BLTCNN: A channel attention adapted deep learning model based on PSSM for membrane protein classification. Computational Biology and Chemistry, 2022, 98, 107680.	2.3	5

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19	Prediction of oxidoreductase subfamily classes based on RFE-SND-CC-PSSM and machine learning methods. <i>Journal of Bioinformatics and Computational Biology</i> , 2019, 17, 1950029.	0.8	4
20	Predicting antifreeze proteins with weighted generalized dipeptide composition and multi-regression feature selection ensemble. <i>BMC Bioinformatics</i> , 2021, 22, 340.	2.6	4
21	Analysis of the risk difference of marginal and conditional probabilities in an incomplete correlated table. <i>Computational Statistics and Data Analysis</i> , 2006, 50, 1597-1614.	1.2	3
22	Consistency and asymptotic normality of the maximum quasi-likelihood estimator in quasi-likelihood nonlinear models with random regressors. <i>Acta Mathematicae Applicatae Sinica</i> , 2010, 26, 241-250.	0.7	3
23	Improved PCA facial recognition with bootstrap and data standardization in small sample case. , 2011, , .		3
24	Protein sub-nuclear location by fusing AAC and PSSM features based on sequence information. , 2015, , .		3
25	An ensemble classifier based on stacked generalization for predicting membrane protein types. , 2017, , .		3
26	Gene prediction of aging-related diseases based on DNN and Mashup. <i>BMC Bioinformatics</i> , 2021, 22, 597.	2.6	3
27	Homogeneity Test of Risk Differences of Marginal and Conditional Probabilities in Several Incomplete Correlated 2×2 Tables. <i>Communications in Statistics - Theory and Methods</i> , 2007, 36, 2877-2890.	1.0	2
28	Statistical inference of risk difference in $k \times k$ correlated 2×2 tables with structural zero. <i>Pharmaceutical Statistics</i> , 2009, 8, 317-332.	1.3	2
29	Recognition of partially occluded face by error detection with logarithmic operator and KPCA. , 2016, , .		2
30	A New Method of Two-Dimensional Direct LDA and Its Application in Face Recognition. , 2016, , .		2
31	Face recognition based on weighted multi-resolution kernel entropy component analysis. , 2017, , .		2
32	DNA protein binding motif prediction based on fusion of expectation pooling and LSTM. , 2021, , .		2
33	Convergence Rate of Strong Consistency of the Maximum Likelihood Estimator in Exponential Family Nonlinear Models. <i>Communications in Statistics - Theory and Methods</i> , 2007, 36, 103-115.	1.0	1
34	Statistical inference of risk ratio in a correlated 2×2 table with structural zero. <i>Computational Statistics</i> , 2013, 28, 1599-1615.	1.5	1
35	Improved median linear discriminant analysis for face recognition. , 2013, , .		1
36	A face recognition method based on combinational mirror-like odd and even images features. , 2013, , .		1

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37	Improved 2DLDA Algorithm and Its Application in Face Recognition. , 2014, , .		1
38	Research of increasing virtual face samples for small sample problems and its applications in face recognition. , 2014, , .		1
39	Weighted feature dimensions according to Fisher's linear discriminant rate and its application on protein sub-cellular localization. , 2015, , .		1
40	The effective feature representations by integrating PseAAC and PSSM for protein sub-nuclear location. , 2015, , .		1
41	Face recognition based on error detection under partial occlusion. , 2015, , .		1
42	Kernel principal component analysis based on semi-supervised dimensionality reduction and its application on protein subnuclear localization. , 2017, , .		1
43	Using kernel SVM for predicting membrane protein types by fusing PseAAC and DipC. , 2017, , .		1
44	Prediction for Membrane Protein Types Based on Effective Fusion Representation and MIC-GA Feature Selection. IEEE Access, 2018, 6, 75669-75681.	4.2	1
45	The effectiveness of ensemble learning based on four different classifiers for predicting membrane protein types. , 2018, , .		1
46	Stratified studies about risk ratios in 2â€ƒfâ€ƒÃ— 2 tables with structural zero. Statistica Neerlandica, 2012, 66, 183-202.	1.6	0
47	A kernel principal component analysis algorithm based on sample selection according to pseudo-eigenvalue contribution. , 2014, , .		0
48	Face recognition analysis for noise images based on combinational mirror-like odd and even features. , 2014, , .		0
49	Research on prediction of protein sub-cellular location based on KLDA with combined kernel function. , 2015, , .		0
50	Applied biological data mining based on improved K-means clustering algorithm and KNN classifier in protein sub-cellular localization. , 2016, , .		0
51	Optimizing effective fusion representation by particle swarm optimization algorithm for protein sub-nuclear location. , 2017, , .		0
52	Protein subnuclear location based on KLDA with fused kernel and effective fusion representation. , 2017, , .		0
53	Predicting Membrane Protein Subcellular Localization from Gene Ontology Terms Based on a Deep Learning Model. , 2018, , .		0
54	Using Support Tensor Mechine for Predicting Cell Penetrating Peptides by Fusing DipC and TipC. , 2018, , .		0

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55	Membrane Protein Type Prediction for High-Dimensional Imbalanced Datasets. , 2018, , .		0
56	An Improved Face Recognition Fusion Algorithm Based on the Features extracted from Gabor, PCA and KPCA. , 2018, , .		0
57	RNA-binding protein sequence prediction method based on ensemble learning and data over-sampling. , 2021, , .		0
58	Confidence intervals for the common odds ratio based on the inverse sinh transformation. Journal of Biopharmaceutical Statistics, 2021, 31, 583-602.	0.8	0
59	Notice of Removal: An Improved Face Recognition Fusion Algorithm Based on the Features Extracted from Gabor, PCA and KPCA. , 2017, , .		0
60	Multi-feature fusion and dimensional reduction based on the two-step deep ontology and the conjoint triad for the identification of cancerlectins. , 2020, , .		0
61	Assembled graph neural network using graph transformer with edges for protein model quality assessment. Journal of Molecular Graphics and Modelling, 2021, 110, 108053.	2.4	0
62	Prediction of Anuran Antimicrobial Peptides Using AdaBoost and Improved PSSM Profiles. , 2020, , .		0