

# Shun-Fang Wang

## List of Publications by Year in descending order

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Version: 2024-02-01

62  
papers

273  
citations

1040056

9  
h-index

1058476

14  
g-index

63  
all docs

63  
docs citations

63  
times ranked

196  
citing authors

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 1  | A protein succinylation sites prediction method based on the hybrid architecture of LSTM network and CNN. <i>Journal of Bioinformatics and Computational Biology</i> , 2022, 20, 2250003.                                      | 0.8 | 6         |
| 2  | SE-BLTCNN: A channel attention adapted deep learning model based on PSSM for membrane protein classification. <i>Computational Biology and Chemistry</i> , 2022, 98, 107680.   | 2.3 | 5         |
| 3  | Predicting antifreeze proteins with weighted generalized dipeptide composition and multi-regression feature selection ensemble. <i>BMC Bioinformatics</i> , 2021, 22, 340.   | 2.6 | 4         |
| 4  | DNA protein binding motif prediction based on fusion of expectation pooling and LSTM. , 2021, , .  |     | 2         |
| 5  | RNA-binding protein sequence prediction method based on ensemble learning and data over-sampling. , 2021, , .  |     | 0         |
| 6  | Confidence intervals for the common odds ratio based on the inverse sinh transformation. <i>Journal of Biopharmaceutical Statistics</i> , 2021, 31, 583-602.   | 0.8 | 0         |
| 7  | DeepFusion-RBP: Using Deep Learning to Fuse Multiple Features to Identify RNA-binding Protein Sequences. <i>Current Bioinformatics</i> , 2021, 16, 1089-1100.  | 1.5 | 8         |
| 8  | iEnhancer-RD: Identification of enhancers and their strength using RKPK features and deep neural networks. <i>Analytical Biochemistry</i> , 2021, 630, 114318.   | 2.4 | 13        |
| 9  | Assembled graph neural network using graph transformer with edges for protein model quality assessment. <i>Journal of Molecular Graphics and Modelling</i> , 2021, 110, 108053.  | 2.4 | 0         |
| 10 | IMAL: An Improved Meta-learning Approach for Few-shot Classification of Plant Diseases. , 2021, , .  |     | 6         |
| 11 | Gene prediction of aging-related diseases based on DNN and Mashup. <i>BMC Bioinformatics</i> , 2021, 22, 597.  | 2.6 | 3         |
| 12 | G-DipC: An Improved Feature Representation Method for Short Sequences to Predict the Type of Cargo in Cell-Penetrating Peptides. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 739-747. | 3.0 | 17        |
| 13 | ACEP: improving antimicrobial peptides recognition through automatic feature fusion and amino acid embedding. <i>BMC Genomics</i> , 2020, 21, 597.   | 2.8 | 27        |
| 14 | Multi-feature fusion and dimensional reduction based on the two-step deep ontology and the conjoint triad for the identification of cancerlectins. , 2020, , .   |     | 0         |
| 15 | Prediction of Anuran Antimicrobial Peptides Using AdaBoost and Improved PSSM Profiles. , 2020, , .   |     | 0         |
| 16 | Efficient utilization on PSSM combining with recurrent neural network for membrane protein types prediction. <i>Computational Biology and Chemistry</i> , 2019, 81, 9-15.  | 2.3 | 11        |
| 17 | An Improved Process for Generating Uniform PSSMs and Its Application in Protein Subcellular Localization via Various Global Dimension Reduction Techniques. <i>IEEE Access</i> , 2019, 7, 42384-42395.                         | 4.2 | 12        |
| 18 | Accurate classification of membrane protein types based on sequence and evolutionary information using deep learning. <i>BMC Bioinformatics</i> , 2019, 20, 700.   | 2.6 | 27        |

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|----|--|-----|-----------|
| 19 | 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         |
| 20 | Prediction of oxidoreductase subfamily classes based on RFE-SND-CC-PSSM and machine learning methods. Journal of Bioinformatics and Computational Biology, 2019, 17, 1950029.                      | 0.8 | 4         |
| 21 | Predicting Membrane Protein Subcellular Localization from Gene Ontology Terms Based on a Deep Learning Model. , 2018, , .  |     | 0         |
| 22 | Using Support Tensor Mechine for Predicting Cell Penetrating Peptides by Fusing DipC and TipC. , 2018, , .   |     | 0         |
| 23 | Membrane Protein Type Prediction for High-Dimensional Imbalanced Datasets. , 2018, , .   |     | 0         |
| 24 | Prediction for Membrane Protein Types Based on Effective Fusion Representation and MIC-GA Feature Selection. IEEE Access, 2018, 6, 75669-75681.  | 4.2 | 1         |
| 25 | An Improved Face Recognition Fusion Algorithm Based on the Features extracted from Gabor, PCA and KPCA. , 2018, , .  |     | 0         |
| 26 | The effectiveness of ensemble learning based on four different classifiers for predicting membrane protein types. , 2018, , .  |     | 1         |
| 27 | 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        |
| 28 | Face recognition based on weighted multi-resolution kernel entropy component analysis. , 2017, , .   |     | 2         |
| 29 | Kernel principal component analysis based on semi-supervised dimensionality reduction and its application on protein subnuclear localization. , 2017, , .  |     | 1         |
| 30 | Optimizing effective fusion representation by particle swarm optimization algorithm for protein sub-nuclear location. , 2017, , .  |     | 0         |
| 31 | Protein subnuclear location based on KLDA with fused kernel and effective fusion representation. , 2017, , .   |     | 0         |
| 32 | Using kernel SVM for predicting membrane protein types by fusing PseAAC and DipC. , 2017, , .  |     | 1         |
| 33 | Protein Subcellular Localization with Gaussian Kernel Discriminant Analysis and Its Kernel Parameter Selection. International Journal of Molecular Sciences, 2017, 18, 2718.                       | 4.1 | 7         |
| 34 | An ensemble classifier based on stacked generalization for predicting membrane protein types. , 2017, , .  |     | 3         |
| 35 | Notice of Removal: An Improved Face Recognition Fusion Algorithm Based on the Features Extracted from Gabor, PCA and KPCA. , 2017, , .   |     | 0         |
| 36 | Recognition of partially occluded face by error detection with logarithmic operator and KPCA. , 2016, , .  |     | 2         |

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|----|---|-----|-----------|
| 37 | Protein sub-cellular localization based on noise-intensity-weighted linear discriminant analysis and an improved k-nearest-neighbor classifier. , 2016, , .                           |     | 6         |
| 38 | Applied biological data mining based on improved K-means clustering algorithm and KNN classifier in protein sub-cellular localization. , 2016, , .                                    |     | 0         |
| 39 | A New Method of Two-Dimensional Direct LDA and Its Application in Face Recognition. , 2016, , .   |     | 2         |
| 40 | Weighted feature dimensions according to Fisher's linear discriminant rate and its application on protein sub-cellular localization. , 2015, , .                                      |     | 1         |
| 41 | Research on prediction of protein sub-cellular location based on KLDA with combined kernel function. , 2015, , .  |     | 0         |
| 42 | 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         |
| 43 | 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        |
| 44 | Protein sub-nuclear location by fusing AAC and PSSM features based on sequence information. , 2015, , .   |     | 3         |
| 45 | The effective feature representations by integrating PseAAC and PSSM for protein sub-nuclear location. , 2015, , .  |     | 1         |
| 46 | Face recognition based on error detection under partial occlusion. , 2015, , .  |     | 1         |
| 47 | A kernel principal component analysis algorithm based on sample selection according to pseudo-eigenvalue contribution. , 2014, , .  |     | 0         |
| 48 | Improved 2DLDA Algorithm and Its Application in Face Recognition. , 2014, , .   |     | 1         |
| 49 | Face recognition analysis for noise images based on combinational mirror-like odd and even features. , 2014, , .  |     | 0         |
| 50 | Research of increasing virtual face samples for small sample problems and its applications in face recognition. , 2014, , .   |     | 1         |
| 51 | Statistical inference of risk ratio in a correlated $2 \times 2$ table with structural zero. Computational Statistics, 2013, 28, 1599-1615.   | 1.5 | 1         |
| 52 | Improved median linear discriminant analysis for face recognition. , 2013, , .  |     | 1         |
| 53 | A face recognition method based on combinational mirror-like odd and even images features. , 2013, , .  |     | 1         |
| 54 | Stratified studies about risk ratios in $2 \times 2$ tables with structural zero. Statistica Neerlandica, 2012, 66, 183-202.  | 1.6 | 0         |

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|----|--|-----|-----------|
| 55 | Improved PCA facial recognition with bootstrap and data standardization in small sample case. , 2011, , .  |     | 3         |
| 56 | Consistency and asymptotic normality of the maximum quasi-likelihood estimator in quasi-likelihood nonlinear models with random regressors. Acta Mathematicae Applicatae Sinica, 2010, 26, 241-250.          | 0.7 | 3         |
| 57 | Statistical inference of risk difference in $k \times k$ correlated $2 \times 2$ tables with structural zero. Pharmaceutical Statistics, 2009, 8, 317-332.   | 1.3 | 2         |
| 58 | 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         |
| 59 | Homogeneity Test of Risk Differences of Marginal and Conditional Probabilities in Several Incomplete Correlated $2 \times 2$ Tables. Communications in Statistics - Theory and Methods, 2007, 36, 2877-2890. | 1.0 | 2         |
| 60 | Sample size determination for matched-pair equivalence trials using rate ratio. Biostatistics, 2007, 8, 625-631.   | 1.5 | 13        |
| 61 | Convergence Rate of Strong Consistency of the Maximum Likelihood Estimator in Exponential Family Nonlinear Models. Communications in Statistics - Theory and Methods, 2007, 36, 103-115.                     | 1.0 | 1         |
| 62 | Analysis of the risk difference of marginal and conditional probabilities in an incomplete correlated table. Computational Statistics and Data Analysis, 2006, 50, 1597-1614.                                | 1.2 | 3         |