Yu-Yen Ou

List of Publications by Year
in descending order

57 papers	1,633 citations	331670 21 h-index	302126 39 g-index
59 all docs	59 docs citations	59 times ranked	1161 citing authors

#	Article	IF	Citations
1	Data Classification With Radial Basis Function Networks Based on a Novel Kernel Density Estimation Algorithm. IEEE Transactions on Neural Networks, 2005, 16, 225-236.	4.2	145
2	iEnhancer-5Step: Identifying enhancers using hidden information of DNA sequences via Chou's 5-step rule and word embedding. Analytical Biochemistry, 2019, 571, 53-61.	2.4	109
3	A transformer architecture based on BERT and 2D convolutional neural network to identify DNA enhancers from sequence information. Briefings in Bioinformatics, 2021, 22, .	6.5	95
4	Incorporating deep learning with convolutional neural networks and position specific scoring matrices for identifying electron transport proteins. Journal of Computational Chemistry, 2017, 38, 2000-2006.	3.3	90
5	Protein disorder prediction by condensed PSSM considering propensity for order or disorder. BMC Bioinformatics, 2006, 7, 319.	2.6	86
6	Advantages and Constraints of a Hybrid Model K-12 E-Learning Assistant Chatbot. IEEE Access, 2020, 8, 77788-77801.	4.2	83
7	TMBETADISC-RBF: Discrimination of -barrel membrane proteins using RBF networks and PSSM profiles. Computational Biology and Chemistry, 2008, 32, 227-231.	2.3	76
8	Incorporating Distant Sequence Features and Radial Basis Function Networks to Identify Ubiquitin Conjugation Sites. PLoS ONE, 2011, 6, e17331.	2.5	75
9	Prediction of transporter targets using efficient RBF networks with PSSM profiles and biochemical properties. Bioinformatics, 2011, 27, 2062-2067.	4.1	74
10	Classifying the molecular functions of Rab GTPases in membrane trafficking using deep convolutional neural networks. Analytical Biochemistry, 2018, 555, 33-41.	2.4	65
11	DeepETC: A deep convolutional neural network architecture for investigating and classifying electron transport chain's complexes. Neurocomputing, 2020, 375, 71-79.	5.9	56
12	Classification of transporters using efficient radial basis function networks with position†specific scoring matrices and biochemical properties. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1789-1797.	2.6	55
13	Identifying the molecular functions of electron transport proteins using radial basis function networks and biochemical properties. Journal of Molecular Graphics and Modelling, 2017, 73, 166-178.	2.4	54
14	iMotor-CNN: Identifying molecular functions of cytoskeleton motor proteins using 2D convolutional neural network via Chou's 5-step rule. Analytical Biochemistry, 2019, 575, 17-26.	2.4	52
15	Prediction of FAD binding sites in electron transport proteins according to efficient radial basis function networks and significant amino acid pairs. BMC Bioinformatics, 2016, 17, 298.	2.6	50
16	Bioinformatics approaches for functional annotation of membrane proteins. Briefings in Bioinformatics, 2014, 15, 155-168.	6.5	42
17	Prediction of membrane spanning segments and topology in β†barrel membrane proteins at better accuracy. Journal of Computational Chemistry, 2010, 31, 217-223.	3.3	39
18	DeepEfflux: a 2D convolutional neural network model for identifying families of efflux proteins in transporters. Bioinformatics, 2018, 34, 3111-3117.	4.1	35

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19	Incorporating significant amino acid pairs to identify O-linked glycosylation sites on transmembrane proteins and non-transmembrane proteins. BMC Bioinformatics, 2010, 11, 536.	2.6	34
20	Using word embedding technique to efficiently represent protein sequences for identifying substrate specificities of transporters. Analytical Biochemistry, 2019, 577, 73-81.	2.4	33
21	Incorporating efficient radial basis function networks and significant amino acid pairs for predicting GTP binding sites in transport proteins. BMC Bioinformatics, 2016, 17, 501.	2.6	27
22	FAD-BERT: Improved prediction of FAD binding sites using pre-training of deep bidirectional transformers. Computers in Biology and Medicine, 2021, 131, 104258.	7.0	26
23	Prediction of ATP-binding sites in membrane proteins using a two-dimensional convolutional neural network. Journal of Molecular Graphics and Modelling, 2019, 92, 86-93.	2.4	24
24	GT-Finder: Classify the family of glucose transporters with pre-trained BERT language models. Computers in Biology and Medicine, 2021, 131, 104259.	7.0	21
25	Using two-dimensional convolutional neural networks for identifying GTP binding sites in Rab proteins. Journal of Bioinformatics and Computational Biology, 2019, 17, 1950005.	0.8	20
26	TRP-BERT: Discrimination of transient receptor potential (TRP) channels using contextual representations from deep bidirectional transformer based on BERT. Computers in Biology and Medicine, 2021, 137, 104821.	7.0	13
27	Incorporating post translational modification information for enhancing the predictive performance of membrane transport proteins. Computational Biology and Chemistry, 2018, 77, 251-260.	2.3	12
28	DeepIon: Deep learning approach for classifying ion transporters and ion channels from membrane proteins. Journal of Computational Chemistry, 2019, 40, 1521-1529.	3.3	12
29	Identification of efflux proteins using efficient radial basis function networks with position-specific scoring matrices and biochemical properties. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1634-1643.	2.6	11
30	TNFPred: identifying tumor necrosis factors using hybrid features based on word embeddings. BMC Medical Genomics, 2020, 13, 155.	1.5	10
31	A novel radial basis function network classifier with centers set by hierarchical clustering. , 0, , .		9
32	Use Chou's 5-steps rule with different word embedding types to boost performance of electron transport protein prediction model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	9
33	Prediction of protein secondary structures with a novel kernel density estimation based classifier. BMC Research Notes, 2008, 1, 51.	1.4	8
34	ETMB-RBF: Discrimination of Metal-Binding Sites in Electron Transporters Based on RBF Networks with PSSM Profiles and Significant Amino Acid Pairs. PLoS ONE, 2013, 8, e46572.	2.5	7
35	*m*CNN-ETC: identifying electron transporters and their functional families by using multiple windows scanning techniques in convolutional neural networks with evolutionary information of protein sequences. Briefings in Bioinformatics, 2022, 23, .	6.5	7
36	Addressing data imbalance problems in ligand-binding site prediction using a variational autoencoder and a convolutional neural network. Briefings in Bioinformatics, 2021, 22, .	6.5	6

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37	ActTRANS: Functional classification in active transport proteins based on transfer learning and contextual representations. Computational Biology and Chemistry, 2021, 93, 107537.	2.3	6
38	A novel learning algorithm for data classification with radial basis function networks. , 0, , .		5
39	An Extensive Examination of Discovering 5-Methylcytosine Sites in Genome-Wide DNA Promoters Using Machine Learning Based Approaches. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 87-94.	3.0	5
40	Incorporating a transfer learning technique with amino acid embeddings to efficiently predict N-linked glycosylation sites in ion channels. Computers in Biology and Medicine, 2021, 130, 104212.	7.0	5
41	MFPS_CNN: Multi‐filter Pattern Scanning from Position‐specific Scoring Matrix with Convolutional Neural Network for Efficient Prediction of Ion Transporters. Molecular Informatics, 2022, 41, .	2.5	5
42	Expediting model selection for support vector machines based on data reduction. , 0, , .		4
43	A Self-Relevant CNN-SVM Model for Problem Classification in K-12 Question-Driven Learning. IEEE Access, 2020, 8, 225822-225830.	4.2	4
44	Using Language Representation Learning Approach to Efficiently Identify Protein Complex Categories in Electron Transport Chain. Molecular Informatics, 2020, 39, e2000033.	2.5	4
45	DeepSIRT: A deep neural network for identification of sirtuin targets and their subcellular localizations. Computational Biology and Chemistry, 2021, 93, 107514.	2.3	4
46	Using Efficient RBF Networks to Classify Transport Proteins Based on PSSM Profiles and Biochemical Properties. Lecture Notes in Computer Science, 2009, , 869-876.	1.3	3
47	Using multiple convolutional window scanning of convolutional neural network for an efficient prediction of ATP‐binding sites in transport proteins. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1486-1492.	2.6	3
48	Data classification with a relaxed model of variable kernel density estimation. , 0, , .		2
49	Predicting Protein Metal Binding Sites with RBF Networks based on PSSM Profiles and Additional Properties. Current Bioinformatics, 2012, 7, 180-186.	1.5	2
50	Topology Prediction of Î±-Helical and Î²-Barrel Transmembrane Proteins Using RBF Networks. Lecture Notes in Computer Science, 2010, , 642-649.	1.3	2
51	Using k-mer embeddings learned from a Skip-gram based neural network for building a cross-species DNA N6-methyladenine site prediction model. Plant Molecular Biology, 2021, 107, 533-542.	3.9	2
52	Using Deep Learning with Position Specific Scoring Matrices to Identify Efflux Proteins in Membrane and Transport Proteins. , 2016, , .		1
53	Enhancing Protein Disorder Detection by Refined Secondary Structure Prediction. , 2007, , 395-409.		1
54	Identification of efflux proteins based on contextual representations with deep bidirectional transformer encoders. Analytical Biochemistry, 2021, 633, 114416.	2.4	1

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55	Using Efficient RBF Network to Identify Interface Residues Based on PSSM Profiles and Biochemical Properties. Lecture Notes in Computer Science, 2007, , 132-141.	1.3	1
56	Structural and Functional Discrimination of Membrane Proteins. , 2011, , 1-32.		0
57	Expediting Model Selection for Support Vector Machines Based on an Advanced Data Reduction Algorithm. , 2006, , 1017-1021.		0