Yu-Yen Ou

List of Publications by Citations

54 papers	1,066 citations	19 h-index	32 g-index
59 ext. papers	1,372 ext. citations	4.3 avg, IF	5.06 L-index

#	Paper	IF	Citations
54	Data classification with radial basis function networks based on a novel kernel density estimation algorithm. *IEEE Transactions on Neural Networks*, **2005**, 16, 225-36		115
53	Protein disorder prediction by condensed PSSM considering propensity for order or disorder. *BMC Bioinformatics*, **2006**, 7, 319	3.6	78
52	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	3.1	76
51	TMBETADISC-RBF: Discrimination of beta-barrel membrane proteins using RBF networks and PSSM profiles. *Computational Biology and Chemistry*, **2008**, 32, 227-31	3.6	67
50	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	3.5	65
49	Prediction of transporter targets using efficient RBF networks with PSSM profiles and biochemical properties. *Bioinformatics*, **2011**, 27, 2062-7	7.2	61
48	Incorporating distant sequence features and radial basis function networks to identify ubiquitin conjugation sites. *PLoS ONE*, **2011**, 6, e17331	3.7	58
47	Classification of transporters using efficient radial basis function networks with position-specific scoring matrices and biochemical properties. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 1789-97	4.2	49
46	Classifying the molecular functions of Rab GTPases in membrane trafficking using deep convolutional neural networks. *Analytical Biochemistry*, **2018**, 555, 33-41	3.1	46
45	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	3.1	43
44	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	3.6	41
43	Prediction of membrane spanning segments and topology in beta-barrel membrane proteins at better accuracy. *Journal of Computational Chemistry*, **2010**, 31, 217-23	3.5	36
42	Bioinformatics approaches for functional annotation of membrane proteins. *Briefings in Bioinformatics*, **2014**, 15, 155-68	13.4	29
41	Incorporating significant amino acid pairs to identify O-linked glycosylation sites on transmembrane proteins and non-transmembrane proteins. *BMC Bioinformatics*, **2010**, 11, 536	3.6	29
40	A transformer architecture based on BERT and 2D convolutional neural network to identify DNA enhancers from sequence information. *Briefings in Bioinformatics*, **2021**, 22,	13.4	28
39	DeepETC: A deep convolutional neural network architecture for investigating and classifying electron transport chain's complexes. *Neurocomputing*, **2020**, 375, 71-79	5.4	27
38	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	2.8	26

37	Advantages and Constraints of a Hybrid Model K-12 E-Learning Assistant Chatbot. *IEEE Access*, **2020**, 8, 77788-77801	3.5	26
36	DeepEfflux: a 2D convolutional neural network model for identifying families of efflux proteins in transporters. *Bioinformatics*, **2018**, 34, 3111-3117	7.2	24
35	Incorporating efficient radial basis function networks and significant amino acid pairs for predicting GTP binding sites in transport proteins. *BMC Bioinformatics*, **2016**, 17, 501	3.6	18
34	Using word embedding technique to efficiently represent protein sequences for identifying substrate specificities of transporters. *Analytical Biochemistry*, **2019**, 577, 73-81	3.1	15
33	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	2.8	10
32	Incorporating post translational modification information for enhancing the predictive performance of membrane transport proteins. *Computational Biology and Chemistry*, **2018**, 77, 251-260	3.6	10
31	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, 1634-43	4.2	9
30	FAD-BERT: Improved prediction of FAD binding sites using pre-training of deep bidirectional transformers. *Computers in Biology and Medicine*, **2021**, 131, 104258	7	8
29	Using two-dimensional convolutional neural networks for identifying GTP binding sites in Rab proteins. *Journal of Bioinformatics and Computational Biology*, **2019**, 17, 1950005	1	7
28	DeepIon: Deep learning approach for classifying ion transporters and ion channels from membrane proteins. *Journal of Computational Chemistry*, **2019**, 40, 1521-1529	3.5	7
27	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	3.7	7
26	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*, **2020**, PP,	3	7
25	GT-Finder: Classify the family of glucose transporters with pre-trained BERT language models. *Computers in Biology and Medicine*, **2021**, 131, 104259	7	5
24	Prediction of protein secondary structures with a novel kernel density estimation based classifier. *BMC Research Notes*, **2008**, 1, 51	2.3	4
23	TNFPred: identifying tumor necrosis factors using hybrid features based on word embeddings. *BMC Medical Genomics*, **2020**, 13, 155	3.7	3
22	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	3
21	Predicting Protein Metal Binding Sites with RBF Networks based on PSSM Profiles and Additional Properties. *Current Bioinformatics*, **2012**, 7, 180-186	4.7	2
20	A novel radial basis function network classifier with centers set by hierarchical clustering		2

#	Title	Metric	Citations
19	Expediting model selection for Support Vector Machines based on data reduction		2
18	Expediting Model Selection for Support Vector Machines Based on an Advanced Data Reduction Algorithm. *Lecture Notes in Computer Science*, **2006**, 1017-1021	0.9	2
17	Using Efficient RBF Networks to Classify Transport Proteins Based on PSSM Profiles and Biochemical Properties. *Lecture Notes in Computer Science*, **2009**, 869-876	0.9	2
16	Topology Prediction of Helical and Barrel Transmembrane Proteins Using RBF Networks. *Lecture Notes in Computer Science*, **2010**, 642-649	0.9	2
15	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	2
14	Addressing data imbalance problems in ligand-binding site prediction using a variational autoencoder and a convolutional neural network. *Briefings in Bioinformatics*, **2021**, 22,	13.4	2
13	DeepSIRT: A deep neural network for identification of sirtuin targets and their subcellular localizations. *Computational Biology and Chemistry*, **2021**, 93, 107514	3.6	2
12	ActTRANS: Functional classification in active transport proteins based on transfer learning and contextual representations. *Computational Biology and Chemistry*, **2021**, 93, 107537	3.6	2
11	Using Language Representation Learning Approach to Efficiently Identify Protein Complex Categories in Electron Transport Chain. *Molecular Informatics*, **2020**, 39, e2000033	3.8	1
10	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	4.6	1
9	Using Efficient RBF Network to Identify Interface Residues Based on PSSM Profiles and Biochemical Properties. *Lecture Notes in Computer Science*, **2007**, 132-141	0.9	1
8	TNFPred: Identifying tumor necrosis factors using hybrid features based on word embeddings		1
7	Enhancing Protein Disorder Detection by Refined Secondary Structure Prediction **2007**, 395-409		1
6	Using Deep Learning with Position Specific Scoring Matrices to Identify Efflux Proteins in Membrane and Transport Proteins **2016**,		1
5	mCNN-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*, **2021**,	13.4	1
4	A Self-Relevant CNN-SVM Model for Problem Classification in K-12 Question-Driven Learning. *IEEE Access*, **2020**, 8, 225822-225830	3.5	0
3	Identification of efflux proteins based on contextual representations with deep bidirectional transformer encoders. *Analytical Biochemistry*, **2021**, 633, 114416	3.1	
2	Structural and Functional Discrimination of Membrane Proteins **2011**, 1-32		

1   Expediting Model Selection for Support Vector Machines Based on an Advanced Data Reduction
    Algorithm **2006**, 1017-1021