Application of SVM to predict membrane protein types

Citation Report

#	Article	IF	Citations
1	Classification of Nuclear Receptors Based on Amino Acid Composition and Dipeptide Composition. Journal of Biological Chemistry, 2004, 279, 23262-23266.	1.6	244
2	Biological applications of support vector machines. Briefings in Bioinformatics, 2004, 5, 328-338.	3.2	171
3	Cooperativity of the oxidization of cysteines in globular proteins. Journal of Theoretical Biology, 2004, 231, 85-95.	0.8	6
4	Multiclass protein fold recognition using multiobjective evolutionary algorithms. , 0, , .		13
5	Using Fourier Spectrum Analysis and Pseudo Amino Acid Composition for Prediction of Membrane Protein Types. Protein Journal, 2005, 24, 385-389.	0.7	72
6	Pattern Recognition Methods for Protein Functional Site Prediction. Current Protein and Peptide Science, 2005, 6, 479-491.	0.7	13
7	GPCRsclass: a web tool for the classification of amine type of G-protein-coupled receptors. Nucleic Acids Research, 2005, 33, W143-W147.	6.5	59
8	Using GO-PseAA predictor to identify membrane proteins and their types. Biochemical and Biophysical Research Communications, 2005, 327, 845-847.	1.0	56
9	Using optimized evidence-theoretic K-nearest neighbor classifier and pseudo-amino acid composition to predict membrane protein types. Biochemical and Biophysical Research Communications, 2005, 334, 288-292.	1.0	178
10	Prediction of Membrane Proteins in Mycobacterium tuberculosis Using a Support Vector Machine Algorithm. Journal of Computational Biology, 2006, 13, 126-129.	0.8	4
11	Operon prediction based on SVM. Computational Biology and Chemistry, 2006, 30, 233-240.	1.1	25
12	Using LogitBoost classifier to predict protein structural classes. Journal of Theoretical Biology, 2006, 238, 172-176.	0.8	182
13	Predicting membrane protein type by functional domain composition and pseudo-amino acid composition. Journal of Theoretical Biology, 2006, 238, 395-400.	0.8	111
14	Predicting rRNA-, RNA-, and DNA-binding proteins from primary structure with support vector machines. Journal of Theoretical Biology, 2006, 240, 175-184.	0.8	111
15	Application of Support Vector Machine to Predict 5-year Survival Status of Patients with Nasopharyngeal Carcinoma after Treatment. Chinese-German Journal of Clinical Oncology, 2006, 5, 8-12.	0.1	1
16	Fuzzy KNN for predicting membrane protein types from pseudo-amino acid composition. Journal of Theoretical Biology, 2006, 240, 9-13.	0.8	172
17	Classification of Cell Membrane Proteins. , 2007, , .		11
18	Methodology development for predicting subcellular localization and other attributes of proteins. Expert Review of Proteomics, 2007, 4, 453-463.	1.3	36

#	Article	IF	Citations
19	Predicting the protein SUMO modification sites based on Properties Sequential Forward Selection (PSFS). Biochemical and Biophysical Research Communications, 2007, 358, 136-139.	1.0	29
20	Time Series Prediction Based on Support Vector Machines Experts and Genetic Algorithm. , 2007, , .		1
21	ECS: An automatic enzyme classifier based on functional domain composition. Computational Biology and Chemistry, 2007, 31, 226-232.	1.1	46
22	Prediction of apoptosis protein subcellular location using improved hybrid approach and pseudo-amino acid composition. Journal of Theoretical Biology, 2007, 248, 377-381.	0.8	188
23	Prediction of membrane protein types from sequences and position-specific scoring matrices. Journal of Theoretical Biology, 2007, 247, 259-265.	0.8	63
24	Prediction of protein structure class by coupling improved genetic algorithm and support vector machine. Amino Acids, 2008, 35, 581-590.	1.2	47
25	Predicting Protein Subcellular Location Using Chous Pseudo Amino Acid Composition and Improved Hybrid Approach. Protein and Peptide Letters, 2008, 15, 612-616.	0.4	198
26	Classifying RNA-Binding Proteins Based on Electrostatic Properties. PLoS Computational Biology, 2008, 4, e1000146.	1.5	65
27	Predicting Membrane Protein Types with Bagging Learner. Protein and Peptide Letters, 2008, 15, 590-594.	0.4	27
28	Automated Prediction of Protein Attributes and Its Impact on Biomedicine and Drug Discovery. , 0, , 97-143.		6
29	Prediction of Presynaptic and Postsynaptic Neurotoxins Using Hybrid Approach and Pseudo Amino Acid Composition. , 2009, , .		0
30	Interaction Models of a Series of Oxadiazole-Substituted α-Isopropoxy Phenylpropanoic Acids Against PPARα and PPARγ: Molecular Modeling and Comparative Molecular Similarity Indices Analysis Studies. Protein and Peptide Letters, 2009, 16, 150-162.	0.4	12
31	Prediction of integral membrane protein type by collocated hydrophobic amino acid pairs. Journal of Computational Chemistry, 2009, 30, 163-172.	1.5	66
32	Prediction of Small Molecules Metabolic Pathways Based on Functional Group Composition. Protein and Peptide Letters, 2009, 16, 969-976.	0.4	25
33	Gene Ontology-Based Protein Function Prediction by Using Sequence Composition Information. Protein and Peptide Letters, 2010, 17, 789-795.	0.4	3
34	Using the Concept of Chous Pseudo Amino Acid Composition to Predict Enzyme Family Classes: An Approach with Support Vector Machine Based on Discrete Wavelet Transform. Protein and Peptide Letters, 2010, 17, 715-722.	0.4	124
35	Predicting mouse transmembrane protein types based on the increment of diversity combined with the support vector machine. , 2010, , .		0
36	Prediction of Subcellular Location of Apoptosis Proteins Using Pseudo Amino Acid Composition: An Approach from Auto Covariance Transformation. Protein and Peptide Letters, 2010, 17, 1263-1269.	0.4	59

#	ARTICLE	IF	CITATIONS
38	Prediction of melatonin excretion patterns in the rat exposed to ELF magnetic fields based on support vector machine and linear discriminant analysis. Micron, 2010, 41, 882-885.	1.1	4
39	Predict potential drug targets from the ion channel proteins based on SVM. Journal of Theoretical Biology, 2010, 262, 750-756.	0.8	32
40	Prediction of the parallel/antiparallel orientation of beta-strands using amino acid pairing preferences and support vector machines. Journal of Theoretical Biology, 2010, 263, 360-368.	0.8	24
41	Protein classification using texture descriptors extracted from the protein backbone image. Journal of Theoretical Biology, 2010, 264, 1024-1032.	0.8	24
42	SecretP: Identifying bacterial secreted proteins by fusing new features into Chou's pseudo-amino acid composition. Journal of Theoretical Biology, 2010, 267, 1-6.	0.8	126
43	The computational model to predict accurately inhibitory activity for inhibitors towardsCYP3A4. Computers in Biology and Medicine, 2010, 40, 845-852.	3.9	10
44	SVM model for amino acid composition based classification of HIV-1 groups. , 2010, , .		2
45	SecretP: A new method for predicting mammalian secreted proteins. Peptides, 2010, 31, 574-578.	1.2	33
46	SMpred: A Support Vector Machine Approach to Identify Structural Motifs in Protein Structure Without Using Evolutionary Information. Journal of Biomolecular Structure and Dynamics, 2010, 28, 405-414.	2.0	5
47	SVM Model for Amino Acid Composition Based Prediction of MMPs and ADAMs. , 2010, , .		0
48	An Improved Profile-Level Domain Linker Propensity Index for Protein Domain Boundary Prediction.. Protein and Peptide Letters, 2011, 18, 7-16.	0.4	14
49	Gaussian Process: A Promising Approach for the Modeling and Prediction of Peptide Binding Affinity to MHC Proteins. Protein and Peptide Letters, 2011, 18, 670-678.	0.4	46
50	Improved Prediction of Palmitoylation Sites Using PWMs and SVM. Protein and Peptide Letters, 2011, 18, 186-193.	0.4	29
51	Predicting Protein Subcellular Localization by Pseudo Amino Acid Composition with a Segment-Weighted and Features-Combined Approach. Protein and Peptide Letters, 2011, 18, 480-487.	0.4	22
52	Predicting Thermophilic Proteins with Pseudo Amino Acid Composition:Approached from Chaos Game Representation and Principal Component Analysis. Protein and Peptide Letters, 2011, 18, 1244-1250.	0.4	23
53	SemiHS: An Iterative Semi-Supervised Approach for Predicting Proteinprotein Interaction Hot Spots. Protein and Peptide Letters, 2011, 18, 896-905.	0.4	8
54	Predicting ion channels and their types by the dipeptide mode of pseudo amino acid composition. Journal of Theoretical Biology, 2011, 269, 64-69.	0.8	146
55	Prediction of protein submitochondria locations based on data fusion of various features of sequences. Journal of Theoretical Biology, 2011, 269, 208-216.	0.8	53

#	Article	IF	Citations
56	AFP-Pred: A random forest approach for predicting antifreeze proteins from sequence-derived properties. Journal of Theoretical Biology, 2011, 270, 56-62.	0.8	226
57	BLProt: prediction of bioluminescent proteins based on support vector machine and relieff feature selection. BMC Bioinformatics, 2011, 12, 345.	1.2	31
58	Predicting membrane protein types by fusing composite protein sequence features into pseudo amino acid composition. Journal of Theoretical Biology, 2011, 271, 10-17.	0.8	148
59	Some remarks on protein attribute prediction and pseudo amino acid composition. Journal of Theoretical Biology, 2011, 273, 236-247.	0.8	1,236
60	Using the concept of pseudo amino acid composition to predict resistance gene against Xanthomonas oryzae pv. oryzae in rice: An approach from chaos games representation. Journal of Theoretical Biology, 2011, 284, 16-23.	0.8	17
61	Discrimination of Thermostable and Thermophilic Lipases Using Support Vector Machines. Protein and Peptide Letters, 2011, 18, 707-717.	0.4	3
62	Prediction of GPCRs with Pseudo Amino Acid Composition: Employing Composite Features and Grey Incidence Degree Based Classification. Protein and Peptide Letters, 2011, 18, 872-878.	0.4	13
63	Identifying GPCRs and their Types with Chou's Pseudo Amino Acid Composition: An Approach from Multi-scale Energy Representation and Position Specific Scoring Matrix. Protein and Peptide Letters, 2012, 19, 890-903.	0.4	83
64	Predicting Protein-Protein Interactions by Combing Various Sequence- Derived Features into the General Form of Chou's Pseudo Amino Acid Composition. Protein and Peptide Letters, 2012, 19, 492-500.	0.4	49
65	Predicting Protein Solubility by the General Form of Chou's Pseudo Amino Acid Composition: Approached from Chaos Game Representation and Fractal Dimension. Protein and Peptide Letters, 2012, 19, 940-948.	0.4	36
66	Predicting Coupling Specificity of GPCRs Based on the Optimization of the Coupling Regions. Combinatorial Chemistry and High Throughput Screening, 2012, 15, 770-774.	0.6	0
67	Dual-Layer Wavelet SVM for Predicting Protein Structural Class Via the General Form of Chou's Pseudo Amino Acid Composition. Protein and Peptide Letters, 2012, 19, 422-429.	0.4	58
68	Predicting Protein Structural Class by Incorporating Patterns of Over- Represented k-mers into the General form of Chou's PseAAC. Protein and Peptide Letters, 2012, 19, 388-397.	0.4	43
69	Identification of mycobacterial membrane proteins and their types using over-represented tripeptide compositions. Journal of Proteomics, 2012, 77, 321-328.	1.2	90
70	Identifying protein submitochondrial location by using features of sequence. , 2012, , .		0
71	Identifying Bacterial Virulent Proteins by Fusing a Set of Classifiers Based on Variants of Chou's Pseudo Amino Acid Composition and on Evolutionary Information. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 467-475.	1.9	156
72	Annotating the protein-RNA interaction sites in proteins using evolutionary information and protein backbone structure. Journal of Theoretical Biology, 2012, 312, 55-64.	0.8	5
73	Identification of voltage-gated potassium channel subfamilies from sequence information using support vector machine. Computers in Biology and Medicine, 2012, 42, 504-507.	3.9	39

#	Article	IF	Citations
74	Identification of Amino Acid Propensities That Are Strong Determinants of Linear B-cell Epitope Using Neural Networks. PLoS ONE, 2012, 7, e30617.	1.1	19
75	Interconnection Between the Protein Solubility and Amino Acid and Dipeptide Compositions. Protein and Peptide Letters, 2012, 20, 88-95.	0.4	2
76	Predicting subcellular location of apoptosis proteins with pseudo amino acid composition: approach from amino acid substitution matrix and auto covariance transformation. Amino Acids, 2012, 42, 1619-1625.	1.2	49
77	Prediction of membrane proteins using split amino acid and ensemble classification. Amino Acids, 2012, 42, 2447-2460.	1.2	68
78	Predicting protein submitochondria locations by combining different descriptors into the general form of Chou's pseudo amino acid composition. Amino Acids, 2012, 43, 545-555.	1.2	83
79	Prediction of ketoacyl synthase family using reduced amino acid alphabets. Journal of Industrial Microbiology and Biotechnology, 2012, 39, 579-584.	1.4	31
80	Mem-PHybrid: Hybrid features-based prediction system for classifying membrane protein types. Analytical Biochemistry, 2012, 424, 35-44.	1.1	39
81	MemHyb: Predicting membrane protein types by hybridizing SAAC and PSSM. Journal of Theoretical Biology, 2012, 292, 93-102.	0.8	82
82	A new hybrid fractal algorithm for predicting thermophilic nucleotide sequences. Journal of Theoretical Biology, 2012, 293, 74-81.	0.8	8
83	Predict mycobacterial proteins subcellular locations by incorporating pseudo-average chemical shift into the general form of Chou's pseudo amino acid composition. Journal of Theoretical Biology, 2012, 304, 88-95.	0.8	94
84	In silico identification of Gram-negative bacterial secreted proteins from primary sequence. Computers in Biology and Medicine, 2013, 43, 1177-1181.	3.9	14
85	Predicting membrane protein types by incorporating protein topology, domains, signal peptides, and physicochemical properties into the general form of Chou's pseudo amino acid composition. Journal of Theoretical Biology, 2013, 318, 1-12.	0.8	131
86	Locating apoptosis proteins by incorporating the signal peptide cleavage sites into the general form of Chou's Pseudo amino acid composition. International Journal of Quantum Chemistry, 2013, 113, 1660-1667.	1.0	26
87	Predicting freight with fuzzy granular computing and support vector machine model. , 2013, , .		0
88	Predicting acidic and alkaline enzymes by incorporating the average chemical shift and gene ontology informations into the general form of Chou's PseAAC. Process Biochemistry, 2013, 48, 1048-1053.	1.8	38
89	Applications of evolutionary SVM to prediction of membrane alpha-helices. Expert Systems With Applications, 2013, 40, 3412-3420.	4.4	12
90	Discriminating bioluminescent proteins by incorporating average chemical shift and evolutionary information into the general form of Chou's pseudo amino acid composition. Journal of Theoretical Biology, 2013, 334, 45-51.	0.8	60
91	Using the concept of Chou's pseudo amino acid composition to predict protein solubility: An approach with entropies in information theory. Journal of Theoretical Biology, 2013, 332, 211-217.	0.8	39

#	Article	IF	Citations
92	GFO: A data driven approach for optimizing the Gaussian function based similarity metric in computational biology. Neurocomputing, 2013, 99, 307-315.	3.5	12
93	PreDNA: accurate prediction of DNA-binding sites in proteins by integrating sequence and geometric structure information. Bioinformatics, 2013, 29, 678-685.	1.8	41
94	Protein Remote Homology Detection by Combining Chou's Pseudo Amino Acid Composition and Profile‐Based Protein Representation. Molecular Informatics, 2013, 32, 775-782.	1.4	103
95	Prediction of Protein Methylation Sites Using Conditional Random Field. Protein and Peptide Letters, 2013, 20, 71-77.	0.4	19
96	Interconnection Between the Protein Solubility and Amino Acid and Dipeptide Compositions. Protein and Peptide Letters, 2013, 20, 88-95.	0.4	3
97	BinMemPredict: a Web Server and Software for Predicting Membrane Protein Types. Current Proteomics, 2013, 10, 2-9.	0.1	59
98	Statistical approach for lysosomal membrane proteins (LMPs) identification. Systems and Synthetic Biology, 2014, 8, 313-319.	1.0	3
99	A two-stage SVM method to predict membrane protein types by incorporating amino acid classifications and physicochemical properties into a general form of Chou's PseAAC. Journal of Theoretical Biology, 2014, 344, 31-39.	0.8	82
100	Modeling of Membrane Proteins. Springer Series in Bio-/neuroinformatics, 2014, , 357-431.	0.1	0
101	Discriminating lysosomal membrane protein types using dynamic neural network. Journal of Biomolecular Structure and Dynamics, 2014, 32, 1575-1582.	2.0	7
102	Predicting the protein solubility by integrating chaos games representation and entropy in information theory. Expert Systems With Applications, 2014, 41, 1672-1679.	4.4	29
103	Identification of novel biomass‐degrading enzymes from genomic dark matter: Populating genomic sequence space with functional annotation. Biotechnology and Bioengineering, 2014, 111, 1550-1565.	1.7	22
104	Chou×³s pseudo amino acid composition improves sequence-based antifreeze protein prediction. Journal of Theoretical Biology, 2014, 356, 30-35.	0.8	126
105	A Multi-label Classifier for Prediction Membrane Protein Functional Types in Animal. Journal of Membrane Biology, 2014, 247, 1141-1148.	1.0	10
106	TI2BioP â€" Topological Indices to BioPolymers. A Graphicalâ€" Numerical Approach for Bioinformatics. , 2016, , .		0
107	A Prediction Model for Membrane Proteins Using Moments Based Features. BioMed Research International, 2016, 2016, 1-7.	0.9	56
108	Design of a man-machine interaction robot based on visual servo system. , 2016, , .		0
109	iAFP-Ense: An Ensemble Classifier for Identifying Antifreeze Protein by Incorporating Grey Model and PSSM into PseAAC. Journal of Membrane Biology, 2016, 249, 845-854.	1.0	25

#	Article	IF	Citations
110	Non-coding RNA identification based on topology secondary structure and reading frame in organelle genome level. Genomics, 2016, 107, 9-15.	1.3	16
111	Predicting membrane protein types using various decision tree classifiers based on various modes of general PseAAC for imbalanced datasets. Journal of Theoretical Biology, 2017, 435, 208-217.	0.8	29
112	iSS-PC: Identifying Splicing Sites via Physical-Chemical Properties Using Deep Sparse Auto-Encoder. Scientific Reports, 2017, 7, 8222.	1.6	21
113	A Treatise to Computational Approaches Towards Prediction of Membrane Protein and Its Subtypes. Journal of Membrane Biology, 2017, 250, 55-76.	1.0	63
114	iMem-2LSAAC: A two-level model for discrimination of membrane proteins and their types by extending the notion of SAAC into chou's pseudo amino acid composition. Journal of Theoretical Biology, 2018, 442, 11-21.	0.8	96
115	Prediction of Protein Subcellular Location Using the Information Entropy and the Auto Covariance Transformation. , 2018, , .		0
116	Predicting membrane protein types by incorporating a novel feature set into Chou's general PseAAC. Journal of Theoretical Biology, 2018, 455, 319-328.	0.8	52
117	Computational Prediction and Analysis of Associations between Small Molecules and Binding-Associated S-Nitrosylation Sites. Molecules, 2018, 23, 954.	1.7	5
118	Identification of Human Membrane Protein Types by Incorporating Network Embedding Methods. IEEE Access, 2019, 7, 140794-140805.	2.6	81
119	Employing a novel 2-gram subgroup intra pattern (2GSIP) with stacked auto encoder for membrane protein classification. Molecular Biology Reports, 2019, 46, 2259-2272.	1.0	19
120	CO2 Control System Design Based ON Optimized Regulation Model. Applied Engineering in Agriculture, 2019, 35, 377-388.	0.3	7
121	Identification of hormone-binding proteins using a novel ensemble classifier. Computing (Vienna/New) Tj ETQq1 1 0.784314 rgBT /Ov	3.2	14
122	Prediction of membrane protein types by exploring local discriminative information from evolutionary profiles. Analytical Biochemistry, 2019, 564-565, 123-132.	1.1	21
123	Identification of membrane protein types via multivariate information fusion with Hilbertâ€"Schmidt Independence Criterion. Neurocomputing, 2020, 383, 257-269.	3.5	105
124	KD-KLNMF: Identification of lncRNAs subcellular localization with multiple features and nonnegative matrix factorization. Analytical Biochemistry, 2020, 610, 113995.	1.1	16
125	Classification of membrane protein using Tetra Peptide Pattern. Analytical Biochemistry, 2020, 606, 113845.	1.1	4
126	Prediction of membrane protein types by fusing protein-protein interaction and protein sequence information. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2020, 1868, 140524.	1.1	7
127	Using Chouâ€™s 5-steps rule to identify N6-methyladenine sites by ensemble learning combined with multiple feature extraction methods. Journal of Biomolecular Structure and Dynamics, 2020, , 1-11.	2.0	3

#	Article	IF	Citations
128	iDHS-DASTS: identifying DNase I hypersensitive sites based on LASSO and stacking learning. Molecular Omics, 2021, 17, 130-141.	1.4	6
129	The Remarkable Impacts of Gordon Life Science Institute. Natural Science, 2021, 13, 43-75.	0.2	2
130	Membrane Protein Identification via Multiple Kernel Fuzzy SVM. Lecture Notes in Computer Science, 2021, , 634-646.	1.0	0
131	Prediction of Maize Yield at the City Level in China Using Multi-Source Data. Remote Sensing, 2021, 13, 146.	1.8	14
132	The Development and Application of Support Vector Machine. Journal of Physics: Conference Series, 2021, 1748, 052006.	0.3	12
133	Characterization and Prediction of Presynaptic and Postsynaptic Neurotoxins Based on Reduced Amino Acids and Biological Properties. Current Bioinformatics, 2021, 16, 364-370.	0.7	4
134	The Significant and Profound Impacts of Gordon Life Science Institute. Voice of the Publisher, 2021, 07, 6-31.	0.0	0
135	Bio-kernel Self-organizing Map for HIV Drug Resistance Classification. Lecture Notes in Computer Science, 2005, , 179-186.	1.0	2
136	Modeling of Membrane Proteins. Springer Series on Bio- and Neurosystems, 2019, , 371-451.	0.2	5
137	Prediction of Multi-Type Membrane Proteins in Human by an Integrated Approach. PLoS ONE, 2014, 9, e93553.	1.1	15
138	Prediction of Enzyme Subfamily Class via Pseudo Amino Acid Composition by Incorporating the Conjoint Triad Feature. Protein and Peptide Letters, 2010, 17, 1441-1449.	0.4	62
139	SVM Model for Amino Acid Composition Based Prediction of Mycobacterium tuberculosis. Journal of Computer Science and Systems Biology, 2011, 04, .	0.0	4
140	Multi Class Classification Approach for Classification of ADAMs, MMPs and Their Subclasses. International Journal of Engineering and Technology, 2010, 2, 302-307.	0.1	1
141	iMPT-FDNPL: Identification of Membrane Protein Types with Functional Domains and a Natural Language Processing Approach. Computational and Mathematical Methods in Medicine, 2021, 2021, 1-10.	0.7	31
142	Molecular biocoding of insulin â€" amino acid Ser. Journal of Bioengineering & Biomedical Science, 2011, 01, .	0.2	2
144	SOME INTRIGUING HIGH-THROUGHPUT DNA SEQUENCE VARIANTS PREDICTION OVER PROTEIN FUNCTIONALITY. Jurnal Teknologi (Sciences and Engineering), 2016, 78, .	0.3	0
145	iAI-DSAE: A Computational Method for Adenosine to Inosine Editing Site Prediction. Letters in Organic Chemistry, 2019, 16, 347-355.	0.2	1
146	Identifikasi Citra berdasarkan Gigitan Ular menggunakan Metode Active Contour Model dan Support Vector Machine. Jurnal Media Informatika Budidarma, 2019, 3, 299.	0.1	0

#	ARTICLE	IF	CITATIONS
147	Utalk: Sri Lankan Sign Language Converter Mobile App using Image Processing and Machine Learning. , 2020, , .		7
148	Pseudo Amino Acid Feature-based Protein Function Prediction using Support Vector Machine and K-Nearest Neighbors. International Journal of Advanced Computer Science and Applications, 2020, 11, .	0.5	0
149	The Limitations in Current Studies of Organic Fouling and Future Prospects. Membranes, 2021, 11, 922.	1.4	3
151	A lagrangian-based approach for universum twin bounded support vector machine with its applications. Annals of Mathematics and Artificial Intelligence, 2023, 91, 109-131.	0.9	5
152	Identifying Membrane Protein Types Based on Lifelong Learning With Dynamically Scalable Networks. Frontiers in Genetics, 2021, 12, 834488.	1.1	2
153	Membrane Protein Identification via Multi-view Graph Regularized k-Local Hyperplane Distance Nearest Neighbor Model. , 2021, , .		2
154	SVM and ANN Modelling Approach for the Optimization of Membrane Permeability of a Membrane Rotating Biological Contactor for Wastewater Treatment. Membranes, 2022, 12, 821.	1.4	17
155	Multi-View Kernel Sparse Representation for Identification of Membrane Protein Types. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2023, 20, 1234-1245.	1.9	7
156	A Review on Data-Driven Quality Prediction in the Production Process with Machine Learning for Industry 4.0. Processes, 2022, 10, 1966.	1.3	13
157	Multi-objective Optimization of PVA/TiO2/MMT Mixed Matrix Membrane for Food Packaging. Journal of Polymers and the Environment, 0, , .	2.4	2
158	Inverse free reduced universum twin support vector machine for imbalanced data classification. Neural Networks, 2023, 157, 125-135.	3.3	20
159	Separating Two Polyhedra Utilizing Alternative Theorems andÂPenalty Function. Lecture Notes in Computer Science, 2022, , 27-39.	1.0	0
160	Protein Dihedral Angle Prediction: The State of the Art. ChemistrySelect, 2023, 8, .	0.7	1
162	Using Numerous Biographical andÂEnrolling Observations toÂPredict Student Performance. Algorithms for Intelligent Systems, 2023, , 649-660.	0.5	0