Ling-Yun Wu

List of Publications by Year
in descending order

71 papers	3,377 citations	172457 29 h-index	149698 56 g-index
74 all docs	74 docs citations	74 times ranked	3265 citing authors

#	Article	IF	Citations
1	Operations Research in the Blockchain Technology. Journal of the Operations Research Society of China, 2022, 10, 401-422.	1.4	2
2	Importance-Penalized Joint Graphical Lasso (IPJGL): differential network inference via GGMs. Bioinformatics, 2022, 38, 770-777.	4.1	2
3	Identifying phenotype-associated subpopulations by integrating bulk and single-cell sequencing data. Nature Biotechnology, 2022, 40, 527-538.	17.5	128
4	Multiple Order Local Information model for link prediction in complex networks. Physica A: Statistical Mechanics and Its Applications, 2022, 600, 127522.	2.6	10
5	Identification of Common Driver Gene Modules and Associations between Cancers through Integrated Network Analysis. Global Challenges, 2021, 5, 2100006.	3.6	2
6	Framework and algorithms for identifying honest blocks in blockchain. PLoS ONE, 2020, 15, e0227531.	2.5	5
7	Framework and algorithms for identifying honest blocks in blockchain. , 2020, 15, e0227531.		0
8	Framework and algorithms for identifying honest blocks in blockchain. , 2020, 15, e0227531.		0
9	Framework and algorithms for identifying honest blocks in blockchain. , 2020, 15, e0227531.		0
10	Framework and algorithms for identifying honest blocks in blockchain. , 2020, 15, e0227531.		0
11	Discovering cooperative biomarkers for heterogeneous complex disease diagnoses. Briefings in Bioinformatics, 2019, 20, 89-101.	6.5	12
12	CEA: Combination-based gene set functional enrichment analysis. Scientific Reports, 2018, 8, 13085.	3.3	4
13	Structure alignment-based classification of RNA-binding pockets reveals regional RNA recognition motifs on protein surfaces. BMC Bioinformatics, 2017, 18, 27.	2.6	7
14	Gly-PseAAC: Identifying protein lysine glycation through sequences. Gene, 2017, 602, 1-7.	2.2	37
15	NetGen: a novel network-based probabilistic generative model for gene set functional enrichment analysis. BMC Systems Biology, 2017, 11, 75.	3.0	3
16	iSulf-Cys: Prediction of S-sulfenylation Sites in Proteins with Physicochemical Properties of Amino Acids. PLoS ONE, 2016, 11, e0154237.	2.5	35
17	Mal-Lys: prediction of lysine malonylation sites in proteins integrated sequence-based features with mRMR feature selection. Scientific Reports, 2016, 6, 38318.	3.3	46
18	iSuc-PseAAC: predicting lysine succinylation in proteins by incorporating peptide position-specific propensity. Scientific Reports, 2015, 5, 10184.	3.3	75

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19	Phogly–PseAAC: Prediction of lysine phosphoglycerylation in proteins incorporating with position-specific propensity. Journal of Theoretical Biology, 2015, 379, 10-15.	1.7	20
20	Cancer stem cells display extremely large evolvability: alternating plastic and rigid networks as a potential Mechanism. Seminars in Cancer Biology, 2015, 30, 42-51.	9.6	48
21	iNitro-Tyr: Prediction of Nitrotyrosine Sites in Proteins with General Pseudo Amino Acid Composition. PLoS ONE, 2014, 9, e105018.	2.5	178
22	Prediction of posttranslational modification sites from amino acid sequences with kernel methods. Journal of Theoretical Biology, 2014, 344, 78-87.	1.7	42
23	Discovery of co-occurring driver pathways in cancer. BMC Bioinformatics, 2014, 15, 271.	2.6	99
24	Corbi: a new R package for biological network alignment and querying. BMC Systems Biology, 2013, 7, S6.	3.0	14
25	Structure and dynamics of core/periphery networks. Journal of Complex Networks, 2013, 1, 93-123.	1.8	296
26	iSNO-PseAAC: Predict Cysteine S-Nitrosylation Sites in Proteins by Incorporating Position Specific Amino Acid Propensity into Pseudo Amino Acid Composition. PLoS ONE, 2013, 8, e55844.	2.5	333
27	GOMA: functional enrichment analysis tool based on GO modules. Chinese Journal of Cancer, 2013, 32, 195-204.	4.9	15
28	iSNO-AAPair: incorporating amino acid pairwise coupling into PseAAC for predicting cysteine *S*-nitrosylation sites in proteins. PeerJ, 2013, 1, e171.	2.0	259
29	CNetA: Network alignment by combining biological and topological features. , 2012, , .		6
30	Potts model based on a Markov process computation solves the community structure problem effectively. Physical Review E, 2012, 86, 016109.	2.1	50
31	Community structure detection based on Potts model and network's spectral characterization. Europhysics Letters, 2012, 97, 48005.	2.0	47
32	Efficient methods for identifying mutated driver pathways in cancer. Bioinformatics, 2012, 28, 2940-2947.	4.1	155
33	Revealing metabolite biomarkers for acupuncture treatment by linear programming based feature selection. BMC Systems Biology, 2012, 6, S15.	3.0	29
34	Analyzing time-course gene expression data using profile-state hidden Markov model. , 2011, , .		4
35	Detecting coherent local patterns from time series gene expression data by a temporal biclustering method. , 2011, , .		2
36	NOA: a novel Network Ontology Analysis method. Nucleic Acids Research, 2011, 39, e87-e87.	14.5	101

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37	An efficient network querying method based on conditional random fields. Bioinformatics, 2011, 27, 3173-3178.	4.1	14
38	SANA: an algorithm for sequential and non-sequential protein structure alignment. Amino Acids, 2010, 39, 417-425.	2.7	5
39	An information-flow-based model with dissipation, saturation and direction for active pathway inference. BMC Systems Biology, 2010, 4, 72.	3.0	5
40	Lysine acetylation sites prediction using an ensemble of support vector machine classifiers. Journal of Theoretical Biology, 2010, 264, 130-135.	1.7	66
41	Semi-supervised drug-protein interaction prediction from heterogeneous biological spaces. BMC Systems Biology, 2010, 4, S6.	3.0	290
42	Prediction of protein–RNA binding sites by a random forest method with combined features. Bioinformatics, 2010, 26, 1616-1622.	4.1	133
43	Conditional random pattern algorithm for LOH inference and segmentation. Bioinformatics, 2009, 25, 61-67.	4.1	9
44	Prediction of palmitoylation sites using the composition of k-spaced amino acid pairs. Protein Engineering, Design and Selection, 2009, 22, 707-712.	2.1	89
45	Predicting DNA- and RNA-binding proteins from sequences with kernel methods. Journal of Theoretical Biology, 2009, 258, 289-293.	1.7	67
46	Multiple distinct clones may co-exist in different lineages in myelodysplastic syndromes. Leukemia Research, 2009, 33, 847-853.	0.8	10
47	Self-organizing map approaches for the haplotype assembly problem. Mathematics and Computers in Simulation, 2009, 79, 3026-3037.	4.4	8
48	Evaluating Protein Similarity from Coarse Structures. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 583-593.	3.0	14
49	Bridging protein local structures and protein functions. Amino Acids, 2008, 35, 627-650.	2.7	37
50	A fast haplotype inference method for large population genotype data. Computational Statistics and Data Analysis, 2008, 52, 4891-4902.	1.2	4
51	Protein cavity clustering based on community structure of pocket similarity network. International Journal of Bioinformatics Research and Applications, 2008, 4, 445.	0.2	5
52	Analysis of Protein Surface Patterns by Pocket Similarity Network. Protein and Peptide Letters, 2008, 15, 448-455.	0.9	9
53	Supervised classification of protein structures based on convex hull representation. International Journal of Bioinformatics Research and Applications, 2007, 3, 123.	0.2	4
54	An optimization approach to the reconstruction of positional DNA sequencing by hybridization with errors. European Journal of Operational Research, 2007, 182, 413-427.	5.7	4

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55	Analysis on multi-domain cooperation for predicting protein-protein interactions. BMC Bioinformatics, 2007, 8, 391.	2.6	45
56	Predicting gene ontology functions from protein's regional surface structures. BMC Bioinformatics, 2007, 8, 475.	2.6	19
57	Protein Comparison Based on Both Structure and Sequence Data. , 2007, , 174-177.		0
58	Inferring Protein-Protein Interactions by Combinatorial Models. , 2007, , 183-186.		2
59	Minimum conflict individual haplotyping from SNP fragments and related genotype. Evolutionary Bioinformatics, 2007, 2, 261-70.	1.2	2
60	Models and Algorithms for Haplotyping Problem. Current Bioinformatics, 2006, 1, 105-114.	1.5	47
61	Minimum Conflict Individual Haplotyping from SNP Fragments and Related Genotype. Evolutionary Bioinformatics, 2006, 2, 117693430600200.	1.2	12
62	Revealing divergent evolution, identifying circular permutations and detecting active-sites by protein structure comparison. BMC Structural Biology, 2006, 6, 18.	2.3	36
63	Inferring protein interactions from experimental data by association probabilistic method. Proteins: Structure, Function and Bioinformatics, 2006, 62, 833-837.	2.6	38
64	Capacitated facility location problem with general setup cost. Computers and Operations Research, 2006, 33, 1226-1241.	4.0	105
65	Automatic Classification of Protein Structures Based on Convex Hull Representation by Integrated Neural Network. Lecture Notes in Computer Science, 2006, , 505-514.	1.3	5
66	Haplotype assembly from aligned weighted SNP fragments. Computational Biology and Chemistry, 2005, 29, 281-287.	2.3	59
67	Haplotype reconstruction from SNP fragments by minimum error correction. Bioinformatics, 2005, 21, 2456-2462.	4.1	130
68	EXPLORING PROTEIN'S OPTIMAL HP CONFIGURATIONS BY SELF-ORGANIZING MAPPING. Journal of Bioinformatics and Computational Biology, 2005, 03, 385-400.	0.8	14
69	Comparison of protein structures by multi-objective optimization. Genome Informatics, 2005, 16, 114-24.	0.4	3
70	Reconstruction of DNA sequencing by hybridization. Bioinformatics, 2003, 19, 14-21.	4.1	21
71	Preface: Special Issue on New Developments in Mathematical Programming and Operations Research. Journal of the Operations Research Society of China, 0, , 1.	1.4	0