

Ling-Yun Wu

List of Publications by Year in descending order

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71
papers

3,377
citations

172457

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149698

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74
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74
docs citations

74
times ranked

3265
citing authors

#	ARTICLE	IF	CITATIONS
1	iSNO-PseAAC: Predict Cysteine S-Nitrosylation Sites in Proteins by Incorporating Position Specific Amino Acid Propensity into Pseudo Amino Acid Composition. <i>PLoS ONE</i> , 2013, 8, e55844.	2.5	333
2	Structure and dynamics of core/periphery networks. <i>Journal of Complex Networks</i> , 2013, 1, 93-123.	1.8	296
3	Semi-supervised drug-protein interaction prediction from heterogeneous biological spaces. <i>BMC Systems Biology</i> , 2010, 4, S6.	3.0	290
4	iSNO-AAPair: incorporating amino acid pairwise coupling into PseAAC for predicting cysteine<i>S</i>-nitrosylation sites in proteins. <i>PeerJ</i> , 2013, 1, e171.	2.0	259
5	iNitro-Tyr: Prediction of Nitrotyrosine Sites in Proteins with General Pseudo Amino Acid Composition. <i>PLoS ONE</i> , 2014, 9, e105018.	2.5	178
6	Efficient methods for identifying mutated driver pathways in cancer. <i>Bioinformatics</i> , 2012, 28, 2940-2947.	4.1	155
7	Prediction of proteinâ€™RNA binding sites by a random forest method with combined features. <i>Bioinformatics</i> , 2010, 26, 1616-1622.	4.1	133
8	Haplotype reconstruction from SNP fragments by minimum error correction. <i>Bioinformatics</i> , 2005, 21, 2456-2462.	4.1	130
9	Identifying phenotype-associated subpopulations by integrating bulk and single-cell sequencing data. <i>Nature Biotechnology</i> , 2022, 40, 527-538.	17.5	128
10	Capacitated facility location problem with general setup cost. <i>Computers and Operations Research</i> , 2006, 33, 1226-1241.	4.0	105
11	NOA: a novel Network Ontology Analysis method. <i>Nucleic Acids Research</i> , 2011, 39, e87-e87.	14.5	101
12	Discovery of co-occurring driver pathways in cancer. <i>BMC Bioinformatics</i> , 2014, 15, 271.	2.6	99
13	Prediction of palmitoylation sites using the composition of k-spaced amino acid pairs. <i>Protein Engineering, Design and Selection</i> , 2009, 22, 707-712.	2.1	89
14	iSuc-PseAAC: predicting lysine succinylation in proteins by incorporating peptide position-specific propensity. <i>Scientific Reports</i> , 2015, 5, 10184.	3.3	75
15	Predicting DNA- and RNA-binding proteins from sequences with kernel methods. <i>Journal of Theoretical Biology</i> , 2009, 258, 289-293.	1.7	67
16	Lysine acetylation sites prediction using an ensemble of support vector machine classifiers. <i>Journal of Theoretical Biology</i> , 2010, 264, 130-135.	1.7	66
17	Haplotype assembly from aligned weighted SNP fragments. <i>Computational Biology and Chemistry</i> , 2005, 29, 281-287.	2.3	59
18	Potts model based on a Markov process computation solves the community structure problem effectively. <i>Physical Review E</i> , 2012, 86, 016109.	2.1	50

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19	Cancer stem cells display extremely large evolvability: alternating plastic and rigid networks as a potential Mechanism. <i>Seminars in Cancer Biology</i> , 2015, 30, 42-51.	9.6	48
20	Models and Algorithms for Haplotyping Problem. <i>Current Bioinformatics</i> , 2006, 1, 105-114.	1.5	47
21	Community structure detection based on Potts model and network's spectral characterization. <i>Europhysics Letters</i> , 2012, 97, 48005.	2.0	47
22	Mal-Lys: prediction of lysine malonylation sites in proteins integrated sequence-based features with mRMR feature selection. <i>Scientific Reports</i> , 2016, 6, 38318.	3.3	46
23	Analysis on multi-domain cooperation for predicting protein-protein interactions. <i>BMC Bioinformatics</i> , 2007, 8, 391.	2.6	45
24	Prediction of posttranslational modification sites from amino acid sequences with kernel methods. <i>Journal of Theoretical Biology</i> , 2014, 344, 78-87.	1.7	42
25	Inferring protein interactions from experimental data by association probabilistic method. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 62, 833-837.	2.6	38
26	Bridging protein local structures and protein functions. <i>Amino Acids</i> , 2008, 35, 627-650.	2.7	37
27	Gly-PseAAC: Identifying protein lysine glycation through sequences. <i>Gene</i> , 2017, 602, 1-7.	2.2	37
28	Revealing divergent evolution, identifying circular permutations and detecting active-sites by protein structure comparison. <i>BMC Structural Biology</i> , 2006, 6, 18.	2.3	36
29	iSulf-Cys: Prediction of S-sulfenylation Sites in Proteins with Physicochemical Properties of Amino Acids. <i>PLoS ONE</i> , 2016, 11, e0154237.	2.5	35
30	Revealing metabolite biomarkers for acupuncture treatment by linear programming based feature selection. <i>BMC Systems Biology</i> , 2012, 6, S15.	3.0	29
31	Reconstruction of DNA sequencing by hybridization. <i>Bioinformatics</i> , 2003, 19, 14-21.	4.1	21
32	Phoglyâ€PseAAC: Prediction of lysine phosphoglycerylation in proteins incorporating with position-specific propensity. <i>Journal of Theoretical Biology</i> , 2015, 379, 10-15.	1.7	20
33	Predicting gene ontology functions from protein's regional surface structures. <i>BMC Bioinformatics</i> , 2007, 8, 475.	2.6	19
34	GOMA: functional enrichment analysis tool based on GO modules. <i>Chinese Journal of Cancer</i> , 2013, 32, 195-204.	4.9	15
35	EXPLORING PROTEIN'S OPTIMAL HP CONFIGURATIONS BY SELF-ORGANIZING MAPPING. <i>Journal of Bioinformatics and Computational Biology</i> , 2005, 03, 385-400.	0.8	14
36	Evaluating Protein Similarity from Coarse Structures. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 583-593.	3.0	14

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37	An efficient network querying method based on conditional random fields. <i>Bioinformatics</i> , 2011, 27, 3173-3178.	4.1	14
38	Corbi: a new R package for biological network alignment and querying. <i>BMC Systems Biology</i> , 2013, 7, S6.	3.0	14
39	Minimum Conflict Individual Haplotyping from SNP Fragments and Related Genotype. <i>Evolutionary Bioinformatics</i> , 2006, 2, 117693430600200.	1.2	12
40	Discovering cooperative biomarkers for heterogeneous complex disease diagnoses. <i>Briefings in Bioinformatics</i> , 2019, 20, 89-101.	6.5	12
41	Multiple distinct clones may co-exist in different lineages in myelodysplastic syndromes. <i>Leukemia Research</i> , 2009, 33, 847-853.	0.8	10
42	Multiple Order Local Information model for link prediction in complex networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2022, 600, 127522.	2.6	10
43	Analysis of Protein Surface Patterns by Pocket Similarity Network. <i>Protein and Peptide Letters</i> , 2008, 15, 448-455.	0.9	9
44	Conditional random pattern algorithm for LOH inference and segmentation. <i>Bioinformatics</i> , 2009, 25, 61-67.	4.1	9
45	Self-organizing map approaches for the haplotype assembly problem. <i>Mathematics and Computers in Simulation</i> , 2009, 79, 3026-3037.	4.4	8
46	Structure alignment-based classification of RNA-binding pockets reveals regional RNA recognition motifs on protein surfaces. <i>BMC Bioinformatics</i> , 2017, 18, 27.	2.6	7
47	CNetA: Network alignment by combining biological and topological features. , 2012, , .		6
48	Protein cavity clustering based on community structure of pocket similarity network. <i>International Journal of Bioinformatics Research and Applications</i> , 2008, 4, 445.	0.2	5
49	SANA: an algorithm for sequential and non-sequential protein structure alignment. <i>Amino Acids</i> , 2010, 39, 417-425.	2.7	5
50	An information-flow-based model with dissipation, saturation and direction for active pathway inference. <i>BMC Systems Biology</i> , 2010, 4, 72.	3.0	5
51	Framework and algorithms for identifying honest blocks in blockchain. <i>PLoS ONE</i> , 2020, 15, e0227531.	2.5	5
52	Automatic Classification of Protein Structures Based on Convex Hull Representation by Integrated Neural Network. <i>Lecture Notes in Computer Science</i> , 2006, , 505-514.	1.3	5
53	Supervised classification of protein structures based on convex hull representation. <i>International Journal of Bioinformatics Research and Applications</i> , 2007, 3, 123.	0.2	4
54	An optimization approach to the reconstruction of positional DNA sequencing by hybridization with errors. <i>European Journal of Operational Research</i> , 2007, 182, 413-427.	5.7	4

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55	A fast haplotype inference method for large population genotype data. Computational Statistics and Data Analysis, 2008, 52, 4891-4902.	1.2	4
56	Analyzing time-course gene expression data using profile-state hidden Markov model. , 2011, , .		4
57	CEA: Combination-based gene set functional enrichment analysis. Scientific Reports, 2018, 8, 13085.	3.3	4
58	NetGen: a novel network-based probabilistic generative model for gene set functional enrichment analysis. BMC Systems Biology, 2017, 11, 75.	3.0	3
59	Comparison of protein structures by multi-objective optimization. Genome Informatics, 2005, 16, 114-24.	0.4	3
60	Detecting coherent local patterns from time series gene expression data by a temporal biclustering method. , 2011, , .		2
61	Identification of Common Driver Gene Modules and Associations between Cancers through Integrated Network Analysis. Global Challenges, 2021, 5, 2100006.	3.6	2
62	Operations Research in the Blockchain Technology. Journal of the Operations Research Society of China, 2022, 10, 401-422.	1.4	2
63	Importance-Penalized Joint Graphical Lasso (IPJGL): differential network inference via GGMs. Bioinformatics, 2022, 38, 770-777.	4.1	2
64	Inferring Protein-Protein Interactions by Combinatorial Models. , 2007, , 183-186.		2
65	Minimum conflict individual haplotyping from SNP fragments and related genotype. Evolutionary Bioinformatics, 2007, 2, 261-70.	1.2	2
66	Protein Comparison Based on Both Structure and Sequence Data. , 2007, , 174-177.		0
67	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
68	Framework and algorithms for identifying honest blocks in blockchain. , 2020, 15, e0227531.		0
69	Framework and algorithms for identifying honest blocks in blockchain. , 2020, 15, e0227531.		0
70	Framework and algorithms for identifying honest blocks in blockchain. , 2020, 15, e0227531.		0
71	Framework and algorithms for identifying honest blocks in blockchain. , 2020, 15, e0227531.		0