Tzong-Yi Lee

List of Publications by Year
in descending order

102 papers	6,320 citations	87888 38 h-index	76900 74 g-index
108 all docs	108 docs citations	108 times ranked	8547 citing authors

#	Article	IF	Citations
1	miRTarBase 2020: updates to the experimentally validated microRNA–target interaction database. Nucleic Acids Research, 2020, 48, D148-D154.	14.5	762
2	PlantPAN 2.0: an update of plant promoter analysis navigator for reconstructing transcriptional regulatory networks in plants. Nucleic Acids Research, 2016, 44, D1154-D1160.	14.5	336
3	KinasePhos 2.0: a web server for identifying protein kinase-specific phosphorylation sites based on sequences and coupling patterns. Nucleic Acids Research, 2007, 35, W588-W594.	14.5	320
4	PlantPAN3.0: a new and updated resource for reconstructing transcriptional regulatory networks from ChIP-seq experiments in plants. Nucleic Acids Research, 2019, 47, D1155-D1163.	14.5	315
5	miRTarBase update 2022: an informative resource for experimentally validated miRNA–target interactions. Nucleic Acids Research, 2022, 50, D222-D230.	14.5	294
6	KinasePhos: a web tool for identifying protein kinase-specific phosphorylation sites. Nucleic Acids Research, 2005, 33, W226-W229.	14.5	292
7	PlantPAN: Plant promoter analysis navigator, for identifying combinatorial cis-regulatory elements with distance constraint in plant gene groups. BMC Genomics, 2008, 9, 561.	2.8	252
8	dbPTM: an information repository of protein post-translational modification. Nucleic Acids Research, 2006, 34, D622-D627.	14.5	217
9	dbPTM 3.0: an informative resource for investigating substrate site specificity and functional association of protein post-translational modifications. Nucleic Acids Research, 2013, 41, D295-D305.	14.5	179
10	dbPTM in 2019: exploring disease association and cross-talk of post-translational modifications. Nucleic Acids Research, 2019, 47, D298-D308.	14.5	179
11	dbPTM 2016: 10-year anniversary of a resource for post-translational modification of proteins. Nucleic Acids Research, 2016, 44, D435-D446.	14.5	154
12	Identifying transcriptional start sites of human microRNAs based on high-throughput sequencing data. Nucleic Acids Research, 2011, 39, 9345-9356.	14.5	149
13	Exploiting maximal dependence decomposition to identify conserved motifs from a group of aligned signal sequences. Bioinformatics, 2011, 27, 1780-1787.	4.1	100
14	Incorporating structural characteristics for identification of protein methylation sites. Journal of Computational Chemistry, 2009, 30, 1532-1543.	3.3	96
15	dbAMP: an integrated resource for exploring antimicrobial peptides with functional activities and physicochemical properties on transcriptome and proteome data. Nucleic Acids Research, 2019, 47, D285-D297.	14.5	93
16	Global characterization of macrophage polarization mechanisms and identification of M2-type polarization inhibitors. Cell Reports, 2021, 37, 109955.	6.4	89
17	Incorporating support vector machine for identifying protein tyrosine sulfation sites. Journal of Computational Chemistry, 2009, 30, 2526-2537.	3.3	84
18	Characterization and identification of antimicrobial peptides with different functional activities. Briefings in Bioinformatics, 2020, 21, 1098-1114.	6.5	83

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19	SNOSite: Exploiting Maximal Dependence Decomposition to Identify Cysteine S-Nitrosylation with Substrate Site Specificity. PLoS ONE, 2011, 6, e21849.	2.5	77
20	Incorporating Distant Sequence Features and Radial Basis Function Networks to Identify Ubiquitin Conjugation Sites. PLoS ONE, 2011, 6, e17331.	2.5	75
21	dbSNO: a database of cysteine *S*-nitrosylation. Bioinformatics, 2012, 28, 2293-2295.	4.1	71
22	RegPhos: a system to explore the protein kinase–substrate phosphorylation network in humans. Nucleic Acids Research, 2011, 39, D777-D787.	14.5	66
23	dbSNO 2.0: a resource for exploring structural environment, functional and disease association and regulatory network of protein S-nitrosylation. Nucleic Acids Research, 2015, 43, D503-D511.	14.5	65
24	PlantPhos: using maximal dependence decomposition to identify plant phosphorylation sites with substrate site specificity. BMC Bioinformatics, 2011, 12, 261.	2.6	63
25	dbPTM in 2022: an updated database for exploring regulatory networks and functional associations of protein post-translational modifications. Nucleic Acids Research, 2022, 50, D471-D479.	14.5	59
26	Incorporating deep learning and multi-omics autoencoding for analysis of lung adenocarcinoma prognostication. Computational Biology and Chemistry, 2020, 87, 107277.	2.3	57
27	Poly-γ-glutamic Acid Synthesis, Gene Regulation, Phylogenetic Relationships, and Role in Fermentation. International Journal of Molecular Sciences, 2017, 18, 2644.	4.1	55
28	GPMiner: an integrated system for mining combinatorial cis-regulatory elements in mammalian gene group. BMC Genomics, 2012, 13, S3.	2.8	51
29	N-Ace: Using solvent accessibility and physicochemical properties to identify protein N-acetylation sites. Journal of Computational Chemistry, 2010, 31, 2759-2771.	3.3	50
30	dbGSH: a database of *S*-glutathionylation. Bioinformatics, 2014, 30, 2386-2388.	4.1	50
31	Gene expression profiling identifies candidate biomarkers for active and latent tuberculosis. BMC Bioinformatics, 2016, 17, 3.	2.6	50
32	Identification of potential biomarkers related to glioma survival by gene expression profile analysis. BMC Medical Genomics, 2019, 11, 34.	1.5	49
33	dbAMP 2.0: updated resource for antimicrobial peptides with an enhanced scanning method for genomic and proteomic data. Nucleic Acids Research, 2022, 50, D460-D470.	14.5	49
34	A new scheme for strain typing of methicillin-resistant Staphylococcus aureus on the basis of matrix-assisted laser desorption ionization time-of-flight mass spectrometry by using machine learning approach. PLoS ONE, 2018, 13, e0194289.	2.5	48
35	Incorporating hidden Markov models for identifying protein kinase-specific phosphorylation sites. Journal of Computational Chemistry, 2005, 26, 1032-1041.	3.3	47
36	UbiSite: incorporating two-layered machine learning method with substrate motifs to predict ubiquitin-conjugation site on lysines. BMC Systems Biology, 2016, 10, 6.	3.0	46

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37	SOHSite: incorporating evolutionary information and physicochemical properties to identify protein S-sulfenylation sites. BMC Genomics, 2016, 17, 9.	2.8	45
38	Characterization and Identification of Natural Antimicrobial Peptides on Different Organisms. International Journal of Molecular Sciences, 2020, 21, 986.	4.1	45
39	A two-layered machine learning method to identify protein O-GlcNAcylation sites with O-GlcNAc transferase substrate motifs. BMC Bioinformatics, 2015, 16, S10.	2.6	41
40	RegPhos 2.0: an updated resource to explore protein kinase–substrate phosphorylation networks in mammals. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau034.	3.0	38
41	Rapid Detection of Heterogeneous Vancomycin-Intermediate Staphylococcus aureus Based on Matrix-Assisted Laser Desorption Ionization Time-of-Flight: Using a Machine Learning Approach and Unbiased Validation. Frontiers in Microbiology, 2018, 9, 2393.	3.5	37
42	Identifying Protein Phosphorylation Sites with Kinase Substrate Specificity on Human Viruses. PLoS ONE, 2012, 7, e40694.	2.5	36
43	Investigation and identification of protein carbonylation sites based on position-specific amino acid composition and physicochemical features. BMC Bioinformatics, 2017, 18, 66.	2.6	36
44	AVPIden: a new scheme for identification and functional prediction of antiviral peptides based on machine learning approaches. Briefings in Bioinformatics, 2021, 22, .	6.5	35
45	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
46	topPTM: a new module of dbPTM for identifying functional post-translational modifications in transmembrane proteins. Nucleic Acids Research, 2014, 42, D537-D545.	14.5	34
47	Identifying anti-coronavirus peptides by incorporating different negative datasets and imbalanced learning strategies. Briefings in Bioinformatics, 2021, 22, 1085-1095.	6.5	32
48	MDD-Palm: Identification of protein S-palmitoylation sites with substrate motifs based on maximal dependence decomposition. PLoS ONE, 2017, 12, e0179529.	2.5	32
49	MDD–SOH: exploiting maximal dependence decomposition to identify *S*-sulfenylation sites with substrate motifs. Bioinformatics, 2016, 32, 165-172.	4.1	30
50	Characterization and Identification of Lysine Succinylation Sites based on Deep Learning Method. Scientific Reports, 2019, 9, 16175.	3.3	30
51	Biomarker Identification through Multiomics Data Analysis of Prostate Cancer Prognostication Using a Deep Learning Model and Similarity Network Fusion. Cancers, 2021, 13, 2528.	3.7	29
52	Investigation and identification of functional post-translational modification sites associated with drug binding and protein-protein interactions. BMC Systems Biology, 2017, 11, 132.	3.0	28
53	Characterization and identification of protein O-GlcNAcylation sites with substrate specificity. BMC Bioinformatics, 2014, 15, S1.	2.6	27
54	UbiNet 2.0: a verified, classified, annotated and updated database of E3 ubiquitin ligase–substrate interactions. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	3.0	27

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55	Roles of KLF4 and AMPK in the inhibition of glycolysis by pulsatile shear stress in endothelial cells. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	27
56	CircNet 2.0: an updated database for exploring circular RNA regulatory networks in cancers. Nucleic Acids Research, 2022, 50, D93-D101.	14.5	27
57	Carboxylator: incorporating solvent-accessible surface area for identifying protein carboxylation sites. Journal of Computer-Aided Molecular Design, 2011, 25, 987-995.	2.9	26
58	Systematic Expression Profiling Analysis Identifies Specific MicroRNA-Gene Interactions that May Differentiate between Active and Latent Tuberculosis Infection. BioMed Research International, 2014, 2014, 1-9.	1.9	26
59	GSHSite: Exploiting an Iteratively Statistical Method to Identify S-Glutathionylation Sites with Substrate Specificity. PLoS ONE, 2015, 10, e0118752.	2.5	26
60	UbiNet: an online resource for exploring the functional associations and regulatory networks of protein ubiquitylation. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw054.	3.0	25
61	Identification and characterization of lysine-methylated sites on histones and non-histone proteins. Computational Biology and Chemistry, 2014, 50, 11-18.	2.3	24
62	A large-scale investigation and identification of methicillin-resistant Staphylococcus aureus based on peaks binning of matrix-assisted laser desorption ionization-time of flight MS spectra. Briefings in Bioinformatics, 2021, 22, .	6.5	24
63	Machine Learning-Based Method for Obesity Risk Evaluation Using Single-Nucleotide Polymorphisms Derived from Next-Generation Sequencing. Journal of Computational Biology, 2018, 25, 1347-1360.	1.6	23
64	Characterization and identification of lysine glutarylation based on intrinsic interdependence between positions in the substrate sites. BMC Bioinformatics, 2019, 19, 384.	2.6	23
65	MDD-carb: a combinatorial model for the identification of protein carbonylation sites with substrate motifs. BMC Systems Biology, 2017, 11, 137.	3.0	22
66	Rapid classification of group B Streptococcus serotypes based on matrix-assisted laser desorption ionization-time of flight mass spectrometry and machine learning techniques. BMC Bioinformatics, 2019, 20, 703.	2.6	22
67	Computational analysis for identification of the extracellular matrix molecules involved in endometrial cancer progression. PLoS ONE, 2020, 15, e0231594.	2.5	21
68	An Intelligent System for Identifying Acetylated Lysine on Histones and Nonhistone Proteins. BioMed Research International, 2014, 2014, 1-11.	1.9	20
69	Incorporating Statistical Test and Machine Intelligence Into Strain Typing of Staphylococcus haemolyticus Based on Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry. Frontiers in Microbiology, 2019, 10, 2120.	3.5	20
70	Decoding the S-Nitrosoproteomic Atlas in Individualized Human Colorectal Cancer Tissues Using a Label-Free Quantitation Strategy. Journal of Proteome Research, 2014, 13, 4942-4958.	3.7	19
71	Characterization and identification of ubiquitin conjugation sites with E3 ligase recognition specificities. BMC Bioinformatics, 2015, 16, S1.	2.6	19
72	Identification of natural antimicrobial peptides from bacteria through metagenomic and metatranscriptomic analysis of high-throughput transcriptome data of Taiwanese oolong teas. BMC Systems Biology, 2017, 11, 131.	3.0	19

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73	SuccSite: Incorporating Amino Acid Composition and Informative k-spaced Amino Acid Pairs to Identify Protein Succinylation Sites. Genomics, Proteomics and Bioinformatics, 2020, 18, 208-219.	6.9	19
74	Delineation of condition specific Cis- and Trans-acting elements in plant promoters under various Endo- and exogenous stimuli. BMC Genomics, 2018, 19, 85.	2.8	18
75	Revealing the Immune Heterogeneity between Systemic Lupus Erythematosus and Rheumatoid Arthritis Based on Multi-Omics Data Analysis. International Journal of Molecular Sciences, 2022, 23, 5166.	4.1	18
76	Incorporating Evolutionary Information and Functional Domains for Identifying RNA Splicing Factors in Humans. PLoS ONE, 2011, 6, e27567.	2.5	16
77	Incorporating Deep Learning With Word Embedding to Identify Plant Ubiquitylation Sites. Frontiers in Cell and Developmental Biology, 2020, 8, 572195.	3.7	16
78	ViralPhos: incorporating a recursively statistical method to predict phosphorylation sites on virus proteins. BMC Bioinformatics, 2013, 14, S10.	2.6	14
79	Incorporating support vector machine with sequential minimal optimization to identify anticancer peptides. BMC Bioinformatics, 2021, 22, 286.	2.6	13
80	Characterization and identification of lysine crotonylation sites based on machine learning method on both plant and mammalian. Scientific Reports, 2020, 10, 20447.	3.3	12
81	Large-scale mass spectrometry data combined with demographics analysis rapidly predicts methicillin resistance in Staphylococcus aureus. Briefings in Bioinformatics, 2020, 22, .	6.5	11
82	Genome-wide discovery of viral microRNAs based on phylogenetic analysis and structural evolution of various human papillomavirus subtypes. Briefings in Bioinformatics, 2018, 19, 1102-1114.	6.5	11
83	EXPath 2.0: An Updated Database for Integrating High-Throughput Gene Expression Data with Biological Pathways. Plant and Cell Physiology, 2020, 61, 1818-1827.	3.1	10
84	Incorporating hybrid models into lysine malonylation sites prediction on mammalian and plant proteins. Scientific Reports, 2020, 10, 10541.	3.3	10
85	Identification of Differentially Expressed Genes in Different Glioblastoma Regions and Their Association with Cancer Stem Cell Development and Temozolomide Response. Journal of Personalized Medicine, 2021, 11, 1047.	2.5	10
86	KinasePhos 3.0: Redesign and Expansion of the Prediction on Kinase-specific Phosphorylation Sites. Genomics, Proteomics and Bioinformatics, 2023, 21, 228-241.	6.9	10
87	Increase Trichomonas vaginalis detection based on urine routine analysis through a machine learning approach. Scientific Reports, 2019, 9, 11074.	3.3	9
88	Clinically Applicable System for Rapidly Predicting Enterococcus faecium Susceptibility to Vancomycin. Microbiology Spectrum, 2021, 9, e0091321.	3.0	9
89	Investigation and identification of protein Î³-glutamyl carboxylation sites. BMC Bioinformatics, 2011, 12, S10.	2.6	8
90	Heat-Killed Lacticaseibacillus paracasei GMNL-653 Exerts Antiosteoporotic Effects by Restoring the Gut Microbiota Dysbiosis in Ovariectomized Mice. Frontiers in Nutrition, 2022, 9, 804210.	3.7	7

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91	A new scheme to discover functional associations and regulatory networks of E3 ubiquitin ligases. BMC Systems Biology, 2016, 10, 3.	3.0	6
92	Rapid Antibiotic Resistance Serial Prediction in Staphylococcus aureus Based on Large-Scale MALDI-TOF Data by Applying XGBoost in Multi-Label Learning. Frontiers in Microbiology, 2022, 13, 853775.	3.5	6
93	Novel Bioinformatics Approaches for Analysis of High-Throughput Biological Data. BioMed Research International, 2014, 2014, 1-3.	1.9	5
94	sRIS: A Small RNA Illustration System for Plant Next-Generation Sequencing Data Analysis. Plant and Cell Physiology, 2020, 61, 1204-1212.	3.1	4
95	A representation and deep learning model for annotating ubiquitylation sentences stating E3 ligaseÂ- substrate interaction. BMC Bioinformatics, 2021, 22, 507.	2.6	4
96	MDRSA: A Web Based-Tool for Rapid Identification of Multidrug Resistant Staphylococcus aureus Based on Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry. Frontiers in Microbiology, 2021, 12, 766206.	3.5	4
97	Large-Scale Samples Based Rapid Detection of Ciprofloxacin Resistance in Klebsiella pneumoniae Using Machine Learning Methods. Frontiers in Microbiology, 2022, 13, 827451.	3.5	4
98	An agent-based system to discover proteinâ€"protein interactions, identify protein complexes and proteins with multiple peptide mass fingerprints. Journal of Computational Chemistry, 2006, 27, 1020-1032.	3.3	3
99	Incorporating Amino Acids Composition and Functional Domains for Identifying Bacterial Toxin Proteins. BioMed Research International, 2014, 2014, 1-7.	1.9	3
100	State-of-the-Art on Viral microRNAs in HPV Infection and Cancer Development. MicroRNA (Shariqah,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.2	3
101	Residueâ€"Residue Contact Can Be a Potential Feature for the Prediction of Lysine Crotonylation Sites. Frontiers in Genetics, 2021, 12, 788467.	2.3	1
102	Systematic pipeline for the analysis of microRNA-gene interactions in active and latent TB infection. , 2014, , .		0