

Tzong-Yi Lee

List of Publications by Year in descending order

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Version: 2024-02-01

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	KinasePhos 3.0: Redesign and Expansion of the Prediction on Kinase-specific Phosphorylation Sites. <i>Genomics, Proteomics and Bioinformatics</i> , 2023, 21, 228-241.	6.9	10
2	dbPTM in 2022: an updated database for exploring regulatory networks and functional associations of protein post-translational modifications. <i>Nucleic Acids Research</i> , 2022, 50, D471-D479.	14.5	59
3	CircNet 2.0: an updated database for exploring circular RNA regulatory networks in cancers. <i>Nucleic Acids Research</i> , 2022, 50, D93-D101.	14.5	27
4	miRTarBase update 2022: an informative resource for experimentally validated miRNA-target interactions. <i>Nucleic Acids Research</i> , 2022, 50, D222-D230.	14.5	294
5	dbAMP 2.0: updated resource for antimicrobial peptides with an enhanced scanning method for genomic and proteomic data. <i>Nucleic Acids Research</i> , 2022, 50, D460-D470.	14.5	49
6	Heat-Killed <i>Lactocaseibacillus paracasei</i> GMNL-653 Exerts Antiosteoporotic Effects by Restoring the Gut Microbiota Dysbiosis in Ovariectomized Mice. <i>Frontiers in Nutrition</i> , 2022, 9, 804210.	3.7	7
7	Large-Scale Samples Based Rapid Detection of Ciprofloxacin Resistance in <i>Klebsiella pneumoniae</i> Using Machine Learning Methods. <i>Frontiers in Microbiology</i> , 2022, 13, 827451.	3.5	4
8	Rapid Antibiotic Resistance Serial Prediction in <i>Staphylococcus aureus</i> Based on Large-Scale MALDI-TOF Data by Applying XGBoost in Multi-Label Learning. <i>Frontiers in Microbiology</i> , 2022, 13, 853775.	3.5	6
9	Revealing the Immune Heterogeneity between Systemic Lupus Erythematosus and Rheumatoid Arthritis Based on Multi-Omics Data Analysis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5166.	4.1	18
10	A large-scale investigation and identification of methicillin-resistant <i>Staphylococcus aureus</i> based on peaks binning of matrix-assisted laser desorption ionization-time of flight MS spectra. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	24
11	UbiNet 2.0: a verified, classified, annotated and updated database of E3 ubiquitin ligase-substrate interactions. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	3.0	27
12	Identifying anti-coronavirus peptides by incorporating different negative datasets and imbalanced learning strategies. <i>Briefings in Bioinformatics</i> , 2021, 22, 1085-1095.	6.5	32
13	Incorporating support vector machine with sequential minimal optimization to identify anticancer peptides. <i>BMC Bioinformatics</i> , 2021, 22, 286.	2.6	13
14	Biomarker Identification through Multiomics Data Analysis of Prostate Cancer Prognostication Using a Deep Learning Model and Similarity Network Fusion. <i>Cancers</i> , 2021, 13, 2528.	3.7	29
15	Roles of KLF4 and AMPK in the inhibition of glycolysis by pulsatile shear stress in endothelial cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	27
16	AVPIDen: a new scheme for identification and functional prediction of antiviral peptides based on machine learning approaches. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	35
17	Identification of Differentially Expressed Genes in Different Glioblastoma Regions and Their Association with Cancer Stem Cell Development and Temozolomide Response. <i>Journal of Personalized Medicine</i> , 2021, 11, 1047.	2.5	10
18	A representation and deep learning model for annotating ubiquitylation sentences stating E3 ligase-substrate interaction. <i>BMC Bioinformatics</i> , 2021, 22, 507.	2.6	4

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19	Global characterization of macrophage polarization mechanisms and identification of M2-type polarization inhibitors. <i>Cell Reports</i> , 2021, 37, 109955.	6.4	89
20	Clinically Applicable System for Rapidly Predicting <i>Enterococcus faecium</i> Susceptibility to Vancomycin. <i>Microbiology Spectrum</i> , 2021, 9, e0091321.	3.0	9
21	MDRSA: A Web Based-Tool for Rapid Identification of Multidrug Resistant <i>Staphylococcus aureus</i> Based on Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry. <i>Frontiers in Microbiology</i> , 2021, 12, 766206.	3.5	4
22	Residueâ€“Residue Contact Can Be a Potential Feature for the Prediction of Lysine Crotonylation Sites. <i>Frontiers in Genetics</i> , 2021, 12, 788467.	2.3	1
23	miRTarBase 2020: updates to the experimentally validated microRNAâ€“target interaction database. <i>Nucleic Acids Research</i> , 2020, 48, D148-D154.	14.5	762
24	Large-scale mass spectrometry data combined with demographics analysis rapidly predicts methicillin resistance in <i>Staphylococcus aureus</i> . <i>Briefings in Bioinformatics</i> , 2020, 22, .	6.5	11
25	Incorporating Deep Learning With Word Embedding to Identify Plant Ubiquitylation Sites. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 572195.	3.7	16
26	EXPath 2.0: An Updated Database for Integrating High-Throughput Gene Expression Data with Biological Pathways. <i>Plant and Cell Physiology</i> , 2020, 61, 1818-1827.	3.1	10
27	Characterization and identification of lysine crotonylation sites based on machine learning method on both plant and mammalian. <i>Scientific Reports</i> , 2020, 10, 20447.	3.3	12
28	Characterization and identification of antimicrobial peptides with different functional activities. <i>Briefings in Bioinformatics</i> , 2020, 21, 1098-1114.	6.5	83
29	Incorporating deep learning and multi-omics autoencoding for analysis of lung adenocarcinoma prognostication. <i>Computational Biology and Chemistry</i> , 2020, 87, 107277.	2.3	57
30	sRIS: A Small RNA Illustration System for Plant Next-Generation Sequencing Data Analysis. <i>Plant and Cell Physiology</i> , 2020, 61, 1204-1212.	3.1	4
31	SuccSite: Incorporating Amino Acid Composition and Informative k-spaced Amino Acid Pairs to Identify Protein Succinylation Sites. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 208-219.	6.9	19
32	Incorporating hybrid models into lysine malonylation sites prediction on mammalian and plant proteins. <i>Scientific Reports</i> , 2020, 10, 10541.	3.3	10
33	Characterization and Identification of Natural Antimicrobial Peptides on Different Organisms. <i>International Journal of Molecular Sciences</i> , 2020, 21, 986.	4.1	45
34	Computational analysis for identification of the extracellular matrix molecules involved in endometrial cancer progression. <i>PLoS ONE</i> , 2020, 15, e0231594.	2.5	21
35	Increase <i>Trichomonas vaginalis</i> detection based on urine routine analysis through a machine learning approach. <i>Scientific Reports</i> , 2019, 9, 11074.	3.3	9
36	Characterization and Identification of Lysine Succinylation Sites based on Deep Learning Method. <i>Scientific Reports</i> , 2019, 9, 16175.	3.3	30

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37	Incorporating Statistical Test and Machine Intelligence Into Strain Typing of <i>Staphylococcus haemolyticus</i> Based on Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry. <i>Frontiers in Microbiology</i> , 2019, 10, 2120.	3.5	20
38	Identification of potential biomarkers related to glioma survival by gene expression profile analysis. <i>BMC Medical Genomics</i> , 2019, 11, 34.	1.5	49
39	Characterization and identification of lysine glutarylation based on intrinsic interdependence between positions in the substrate sites. <i>BMC Bioinformatics</i> , 2019, 19, 384.	2.6	23
40	Rapid classification of group B <i>Streptococcus</i> serotypes based on matrix-assisted laser desorption ionization-time of flight mass spectrometry and machine learning techniques. <i>BMC Bioinformatics</i> , 2019, 20, 703.	2.6	22
41	dbPTM in 2019: exploring disease association and cross-talk of post-translational modifications. <i>Nucleic Acids Research</i> , 2019, 47, D298-D308.	14.5	179
42	PlantPAN3.0: a new and updated resource for reconstructing transcriptional regulatory networks from ChIP-seq experiments in plants. <i>Nucleic Acids Research</i> , 2019, 47, D1155-D1163.	14.5	315
43	dbAMP: an integrated resource for exploring antimicrobial peptides with functional activities and physicochemical properties on transcriptome and proteome data. <i>Nucleic Acids Research</i> , 2019, 47, D285-D297.	14.5	93
44	Rapid Detection of Heterogeneous Vancomycin-Intermediate <i>Staphylococcus aureus</i> Based on Matrix-Assisted Laser Desorption Ionization Time-of-Flight: Using a Machine Learning Approach and Unbiased Validation. <i>Frontiers in Microbiology</i> , 2018, 9, 2393.	3.5	37
45	Machine Learning-Based Method for Obesity Risk Evaluation Using Single-Nucleotide Polymorphisms Derived from Next-Generation Sequencing. <i>Journal of Computational Biology</i> , 2018, 25, 1347-1360.	1.6	23
46	Delineation of condition specific Cis- and Trans-acting elements in plant promoters under various Endo- and exogenous stimuli. <i>BMC Genomics</i> , 2018, 19, 85.	2.8	18
47	A new scheme for strain typing of methicillin-resistant <i>Staphylococcus aureus</i> on the basis of matrix-assisted laser desorption ionization time-of-flight mass spectrometry by using machine learning approach. <i>PLoS ONE</i> , 2018, 13, e0194289.	2.5	48
48	Genome-wide discovery of viral microRNAs based on phylogenetic analysis and structural evolution of various human papillomavirus subtypes. <i>Briefings in Bioinformatics</i> , 2018, 19, 1102-1114.	6.5	11
49	State-of-the-Art on Viral microRNAs in HPV Infection and Cancer Development. <i>MicroRNA (Shariqah)</i> , Tj ETQq1 1 0.784314 rgBT /Over 1.2		
50	Investigation and identification of protein carbonylation sites based on position-specific amino acid composition and physicochemical features. <i>BMC Bioinformatics</i> , 2017, 18, 66.	2.6	36
51	Poly- β -glutamic Acid Synthesis, Gene Regulation, Phylogenetic Relationships, and Role in Fermentation. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2644.	4.1	55
52	MDD-carb: a combinatorial model for the identification of protein carbonylation sites with substrate motifs. <i>BMC Systems Biology</i> , 2017, 11, 137.	3.0	22
53	Identification of natural antimicrobial peptides from bacteria through metagenomic and metatranscriptomic analysis of high-throughput transcriptome data of Taiwanese oolong teas. <i>BMC Systems Biology</i> , 2017, 11, 131.	3.0	19
54	Investigation and identification of functional post-translational modification sites associated with drug binding and protein-protein interactions. <i>BMC Systems Biology</i> , 2017, 11, 132.	3.0	28

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55	MDD-Palm: Identification of protein S-palmitoylation sites with substrate motifs based on maximal dependence decomposition. <i>PLoS ONE</i> , 2017, 12, e0179529.	2.5	32
56	MDD-SOH: exploiting maximal dependence decomposition to identify S-sulfenylation sites with substrate motifs. <i>Bioinformatics</i> , 2016, 32, 165-172.	4.1	30
57	UbiNet: an online resource for exploring the functional associations and regulatory networks of protein ubiquitylation. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw054.	3.0	25
58	Gene expression profiling identifies candidate biomarkers for active and latent tuberculosis. <i>BMC Bioinformatics</i> , 2016, 17, 3.	2.6	50
59	A new scheme to discover functional associations and regulatory networks of E3 ubiquitin ligases. <i>BMC Systems Biology</i> , 2016, 10, 3.	3.0	6
60	PlantPAN 2.0: an update of plant promoter analysis navigator for reconstructing transcriptional regulatory networks in plants. <i>Nucleic Acids Research</i> , 2016, 44, D1154-D1160.	14.5	336
61	SOHSite: incorporating evolutionary information and physicochemical properties to identify protein S-sulfenylation sites. <i>BMC Genomics</i> , 2016, 17, 9.	2.8	45
62	UbiSite: incorporating two-layered machine learning method with substrate motifs to predict ubiquitin-conjugation site on lysines. <i>BMC Systems Biology</i> , 2016, 10, 6.	3.0	46
63	dbPTM 2016: 10-year anniversary of a resource for post-translational modification of proteins. <i>Nucleic Acids Research</i> , 2016, 44, D435-D446.	14.5	154
64	A two-layered machine learning method to identify protein O-GlcNAcylation sites with O-GlcNAc transferase substrate motifs. <i>BMC Bioinformatics</i> , 2015, 16, S10.	2.6	41
65	Characterization and identification of ubiquitin conjugation sites with E3 ligase recognition specificities. <i>BMC Bioinformatics</i> , 2015, 16, S1.	2.6	19
66	dbSNO 2.0: a resource for exploring structural environment, functional and disease association and regulatory network of protein S-nitrosylation. <i>Nucleic Acids Research</i> , 2015, 43, D503-D511.	14.5	65
67	GSHSite: Exploiting an Iteratively Statistical Method to Identify S-Glutathionylation Sites with Substrate Specificity. <i>PLoS ONE</i> , 2015, 10, e0118752.	2.5	26
68	An Intelligent System for Identifying Acetylated Lysine on Histones and Nonhistone Proteins. <i>BioMed Research International</i> , 2014, 2014, 1-11.	1.9	20
69	Novel Bioinformatics Approaches for Analysis of High-Throughput Biological Data. <i>BioMed Research International</i> , 2014, 2014, 1-3.	1.9	5
70	RegPhos 2.0: an updated resource to explore protein kinase substrate phosphorylation networks in mammals. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau034.	3.0	38
71	Systematic Expression Profiling Analysis Identifies Specific MicroRNA-Gene Interactions that May Differentiate between Active and Latent Tuberculosis Infection. <i>BioMed Research International</i> , 2014, 2014, 1-9.	1.9	26
72	Incorporating Amino Acids Composition and Functional Domains for Identifying Bacterial Toxin Proteins. <i>BioMed Research International</i> , 2014, 2014, 1-7.	1.9	3

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73	topPTM: a new module of dbPTM for identifying functional post-translational modifications in transmembrane proteins. <i>Nucleic Acids Research</i> , 2014, 42, D537-D545.	14.5	34
74	dbGSH: a database of <i>S</i> -glutathionylation. <i>Bioinformatics</i> , 2014, 30, 2386-2388.	4.1	50
75	Decoding the S-Nitrosoproteomic Atlas in Individualized Human Colorectal Cancer Tissues Using a Label-Free Quantitation Strategy. <i>Journal of Proteome Research</i> , 2014, 13, 4942-4958.	3.7	19
76	Systematic pipeline for the analysis of microRNA-gene interactions in active and latent TB infection. , 2014, , .		0
77	Identification and characterization of lysine-methylated sites on histones and non-histone proteins. <i>Computational Biology and Chemistry</i> , 2014, 50, 11-18.	2.3	24
78	Characterization and identification of protein O-GlcNAcylation sites with substrate specificity. <i>BMC Bioinformatics</i> , 2014, 15, S1.	2.6	27
79	ViralPhos: incorporating a recursively statistical method to predict phosphorylation sites on virus proteins. <i>BMC Bioinformatics</i> , 2013, 14, S10.	2.6	14
80	dbPTM 3.0: an informative resource for investigating substrate site specificity and functional association of protein post-translational modifications. <i>Nucleic Acids Research</i> , 2013, 41, D295-D305.	14.5	179
81	dbSNO: a database of cysteine <i>S</i> -nitrosylation. <i>Bioinformatics</i> , 2012, 28, 2293-2295.	4.1	71
82	Identifying Protein Phosphorylation Sites with Kinase Substrate Specificity on Human Viruses. <i>PLoS ONE</i> , 2012, 7, e40694.	2.5	36
83	GPMiner: an integrated system for mining combinatorial cis-regulatory elements in mammalian gene group. <i>BMC Genomics</i> , 2012, 13, S3.	2.8	51
84	RegPhos: a system to explore the protein kinaseâ€™ substrate phosphorylation network in humans. <i>Nucleic Acids Research</i> , 2011, 39, D777-D787.	14.5	66
85	PlantPhos: using maximal dependence decomposition to identify plant phosphorylation sites with substrate site specificity. <i>BMC Bioinformatics</i> , 2011, 12, 261.	2.6	63
86	Incorporating Evolutionary Information and Functional Domains for Identifying RNA Splicing Factors in Humans. <i>PLoS ONE</i> , 2011, 6, e27567.	2.5	16
87	Carboxylator: incorporating solvent-accessible surface area for identifying protein carboxylation sites. <i>Journal of Computer-Aided Molecular Design</i> , 2011, 25, 987-995.	2.9	26
88	Investigation and identification of protein γ -glutamyl carboxylation sites. <i>BMC Bioinformatics</i> , 2011, 12, S10.	2.6	8
89	Exploiting maximal dependence decomposition to identify conserved motifs from a group of aligned signal sequences. <i>Bioinformatics</i> , 2011, 27, 1780-1787.	4.1	100
90	Identifying transcriptional start sites of human microRNAs based on high-throughput sequencing data. <i>Nucleic Acids Research</i> , 2011, 39, 9345-9356.	14.5	149

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91	Incorporating Distant Sequence Features and Radial Basis Function Networks to Identify Ubiquitin Conjugation Sites. PLoS ONE, 2011, 6, e17331.	2.5	75
92	SNOSite: Exploiting Maximal Dependence Decomposition to Identify Cysteine S-Nitrosylation with Substrate Site Specificity. PLoS ONE, 2011, 6, e21849.	2.5	77
93	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
94	NACE: Using solvent accessibility and physicochemical properties to identify protein N-acetylation sites. Journal of Computational Chemistry, 2010, 31, 2759-2771.	3.3	50
95	Incorporating structural characteristics for identification of protein methylation sites. Journal of Computational Chemistry, 2009, 30, 1532-1543.	3.3	96
96	Incorporating support vector machine for identifying protein tyrosine sulfation sites. Journal of Computational Chemistry, 2009, 30, 2526-2537.	3.3	84
97	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
98	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
99	dbPTM: an information repository of protein post-translational modification. Nucleic Acids Research, 2006, 34, D622-D627.	14.5	217
100	An agent-based system to discover protein-protein interactions, identify protein complexes and proteins with multiple peptide mass fingerprints. Journal of Computational Chemistry, 2006, 27, 1020-1032.	3.3	3
101	Incorporating hidden Markov models for identifying protein kinase-specific phosphorylation sites. Journal of Computational Chemistry, 2005, 26, 1032-1041.	3.3	47
102	KinasePhos: a web tool for identifying protein kinase-specific phosphorylation sites. Nucleic Acids Research, 2005, 33, W226-W229.	14.5	292