

# Ting-Yi Sung

## List of Publications by Year in descending order

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Version: 2024-02-01

88  
papers

2,345  
citations

218381

26  
h-index

233125

45  
g-index

89  
all docs

89  
docs citations

89  
times ranked

3358  
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteogenomics of Non-smoking Lung Cancer in East Asia Delineates Molecular Signatures of Pathogenesis and Progression. <i>Cell</i> , 2020, 182, 226-244.e17.	13.5	178
2	Edge congestion and topological properties of crossed cubes. <i>IEEE Transactions on Parallel and Distributed Systems</i> , 2000, 11, 64-80.	4.0	126
3	IDEAL-Q, an Automated Tool for Label-free Quantitation Analysis Using an Efficient Peptide Alignment Approach and Spectral Data Validation. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 131-144.	2.5	114
4	Predicting RNA-binding sites of proteins using support vector machines and evolutionary information. <i>BMC Bioinformatics</i> , 2008, 9, S6.	1.2	110
5	Multi-Q: A Fully Automated Tool for Multiplexed Protein Quantitation. <i>Journal of Proteome Research</i> , 2006, 5, 2328-2338.	1.8	107
6	Sequential Phosphoproteomic Enrichment through Complementary Metal-Directed Immobilized Metal Ion Affinity Chromatography. <i>Analytical Chemistry</i> , 2014, 86, 685-693.	3.2	100
7	NERBio: using selected word conjunctions, term normalization, and global patterns to improve biomedical named entity recognition. <i>BMC Bioinformatics</i> , 2006, 7, S11.	1.2	98
8	Various criteria in the evaluation of biomedical named entity recognition. <i>BMC Bioinformatics</i> , 2006, 7, 92.	1.2	80
9	MAGIC: An Automated N-Linked Glycoprotein Identification Tool Using a Y1-Ion Pattern Matching Algorithm and <i>in Silico</i> MS <sup>2</sup> Approach. <i>Analytical Chemistry</i> , 2015, 87, 2466-2473.	3.2	67
10	Metabolite Identification for Mass Spectrometry-Based Metabolomics Using Multiple Types of Correlated Ion Information. <i>Analytical Chemistry</i> , 2015, 87, 2143-2151.	3.2	65
11	An Informatics-assisted Label-free Quantitation Strategy that Depicts Phosphoproteomic Profiles in Lung Cancer Cell Invasion. <i>Journal of Proteome Research</i> , 2010, 9, 5582-5597.	1.8	57
12	Predicting helix-helix interactions from residue contacts in membrane proteins. <i>Bioinformatics</i> , 2009, 25, 996-1003.	1.8	56
13	Protein subcellular localization prediction based on compartment-specific features and structure conservation. <i>BMC Bioinformatics</i> , 2007, 8, 330.	1.2	54
14	Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2015, 14, 3415-3431.	1.8	53
15	HYPROSP II-A knowledge-based hybrid method for protein secondary structure prediction based on local prediction confidence. <i>Bioinformatics</i> , 2005, 21, 3227-3233.	1.8	50
16	Rapid High-pH Reverse Phase StageTip for Sensitive Small-Scale Membrane Proteomic Profiling. <i>Analytical Chemistry</i> , 2015, 87, 12016-12023.	3.2	47
17	N-GlyDE: a two-stage N-linked glycosylation site prediction incorporating gapped dipeptides and pattern-based encoding. <i>Scientific Reports</i> , 2019, 9, 15975.	1.6	46
18	BIOSMILE: A semantic role labeling system for biomedical verbs using a maximum-entropy model with automatically generated template features. <i>BMC Bioinformatics</i> , 2007, 8, 325.	1.2	45

#	ARTICLE	IF	CITATIONS
19	Detection of the inferred interaction network in hepatocellular carcinoma from EHCO (Encyclopedia Tj ETQq1 1 0.784314 rgBT /Overlo	1.2	45
20	PSLDoc: Protein subcellular localization prediction based on gapped dipeptides and probabilistic latent semantic analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 693-710.	1.5	44
21	A data-independent acquisition-based global phosphoproteomics system enables deep profiling. <i>Nature Communications</i> , 2021, 12, 2539.	5.8	44
22	Integrating linguistic knowledge into a conditional random field framework to identify biomedical named entities. <i>Expert Systems With Applications</i> , 2006, 30, 117-128.	4.4	39
23	Enhanced Membrane Protein Topology Prediction Using a Hierarchical Classification Method and a New Scoring Function. <i>Journal of Proteome Research</i> , 2008, 7, 487-496.	1.8	35
24	Protein subcellular localization prediction of eukaryotes using a knowledge-based approach. <i>BMC Bioinformatics</i> , 2009, 10, S8.	1.2	35
25	Phosphoproteomics Identifies Oncogenic Ras Signaling Targets and Their Involvement in Lung Adenocarcinomas. <i>PLoS ONE</i> , 2011, 6, e20199.	1.1	35
26	Phosphoproteomics Reveals HMGA1, a CK2 Substrate, as a Drug-Resistant Target in Non-Small Cell Lung Cancer. <i>Scientific Reports</i> , 2017, 7, 44021.	1.6	31
27	Improving protein secondary structure prediction based on short subsequences with local structure similarity. <i>BMC Genomics</i> , 2010, 11, S4.	1.2	29
28	The shuffle-cubes and their generalization. <i>Information Processing Letters</i> , 2001, 77, 35-41.	0.4	27
29	HYPROSP: a hybrid protein secondary structure prediction algorithm—a knowledge-based approach. <i>Nucleic Acids Research</i> , 2004, 32, 5059-5065.	6.5	24
30	Spectrum-based Method to Generate Good Decoy Libraries for Spectral Library Searching in Peptide Identifications. <i>Journal of Proteome Research</i> , 2013, 12, 2305-2310.	1.8	24
31	Mining Missing Membrane Proteins by High-pH Reverse-Phase StageTip Fractionation and Multiple Reaction Monitoring Mass Spectrometry. <i>Journal of Proteome Research</i> , 2015, 14, 3658-3669.	1.8	24
32	Finding the most vital edges with respect to the number of spanning trees. <i>IEEE Transactions on Reliability</i> , 1994, 43, 600-603.	3.5	23
33	Label-free Quantitative Proteomics and N-Glycoproteomics Analysis of KRAS-activated Human Bronchial Epithelial Cells. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 901-915.	2.5	23
34	GANa—a genetic algorithm for NMR backbone resonance assignment. <i>Nucleic Acids Research</i> , 2005, 33, 4593-4601.	6.5	22
35	TMPad: an integrated structural database for helix-packing folds in transmembrane proteins. <i>Nucleic Acids Research</i> , 2011, 39, D347-D355.	6.5	21
36	A semi-automatic method for annotating a biomedical proposition bank. , 2006, , .		21

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37	Subcellular Proteome Landscape of Human Embryonic Stem Cells Revealed Missing Membrane Proteins. <i>Journal of Proteome Research</i> , 2018, 17, 4138-4151.	1.8	19
38	RIBRA—An Error-Tolerant Algorithm for the NMR Backbone Assignment Problem. <i>Journal of Computational Biology</i> , 2006, 13, 229-244.	0.8	18
39	Christmas tree: A versatile 1-fault-tolerant design for token rings. <i>Information Processing Letters</i> , 1999, 72, 55-63.	0.4	17
40	iMet-Q: A User-Friendly Tool for Label-Free Metabolomics Quantitation Using Dynamic Peak-Width Determination. <i>PLoS ONE</i> , 2016, 11, e0146112.	1.1	17
41	Routing and transmitting problems in de Bruijn networks. <i>IEEE Transactions on Computers</i> , 1996, 45, 1056-1062.	2.4	16
42	Multiple-edge-fault tolerance with respect to hypercubes. <i>IEEE Transactions on Parallel and Distributed Systems</i> , 1997, 8, 187-192.	4.0	14
43	The Multi-Q web server for multiplexed protein quantitation. <i>Nucleic Acids Research</i> , 2007, 35, W707-W712.	6.5	14
44	Phosphoproteomic Analysis of Human Mesenchymal Stromal Cells during Osteogenic Differentiation. <i>Journal of Proteome Research</i> , 2012, 11, 586-598.	1.8	14
45	Informatics View on the Challenges of Identifying Missing Proteins from Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2015, 14, 5396-5407.	1.8	14
46	Lipid exposure prediction enhances the inference of rotational angles of transmembrane helices. <i>BMC Bioinformatics</i> , 2013, 14, 304.	1.2	13
47	MAGIC-web: a platform for untargeted and targeted N-linked glycoprotein identification. <i>Nucleic Acids Research</i> , 2016, 44, W575-W580.	6.5	13
48	On the construction of combined $k$ -fault-tolerant Hamiltonian graphs. <i>Networks</i> , 2001, 37, 165-170.	1.6	10
49	MaXIC-Q Web: a fully automated web service using statistical and computational methods for protein quantitation based on stable isotope labeling and LC-MS. <i>Nucleic Acids Research</i> , 2009, 37, W661-W669.	6.5	10
50	Prediction of nuclear proteins using nuclear translocation signals proposed by probabilistic latent semantic indexing. <i>BMC Bioinformatics</i> , 2012, 13, S13.	1.2	10
51	Diameter variability of cycles and tori. <i>Information Sciences</i> , 2008, 178, 2960-2967.	4.0	9
52	Decoding the Disease-Associated Proteins Encoded in the Human Chromosome 4. <i>Journal of Proteome Research</i> , 2013, 12, 33-44.	1.8	9
53	Computational Comparative Study of Tuberculosis Proteomes Using a Model Learned from Signal Peptide Structures. <i>PLoS ONE</i> , 2012, 7, e35018.	1.1	9
54	Fault tolerant token ring embedding in double loop networks. <i>Information Processing Letters</i> , 1998, 66, 201-207.	0.4	8

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55	Decoding the Effect of Isobaric Substitutions on Identifying Missing Proteins and Variant Peptides in Human Proteome. <i>Journal of Proteome Research</i> , 2017, 16, 4415-4424.	1.8	8
56	Efficient and Interpretable Prediction of Protein Functional Classes by Correspondence Analysis and Compact Set Relations. <i>PLoS ONE</i> , 2013, 8, e75542.	1.1	7
57	Calibr improves spectral library search for spectrum-centric analysis of data independent acquisition proteomics. <i>Scientific Reports</i> , 2022, 12, 2045.	1.6	7
58	Construction schemes for fault-tolerant Hamiltonian graphs. <i>Networks</i> , 2000, 35, 233-245.	1.6	6
59	MinProtMaxVP: Generating a minimized number of protein variant sequences containing all possible variant peptides for proteogenomic analysis. <i>Journal of Proteomics</i> , 2020, 223, 103819.	1.2	6
60	Evaluating the Possibility of Detecting Variants in Shotgun Proteomics via LeTE-Fusion Analysis Pipeline. <i>Journal of Proteome Research</i> , 2018, 17, 2937-2952.	1.8	5
61	WinProphet: A User-Friendly Pipeline Management System for Proteomics Data Analysis Based on Trans-Proteomic Pipeline. <i>Analytical Chemistry</i> , 2019, 91, 9403-9406.	3.2	5
62	TRANSMEMBRANE HELIX AND TOPOLOGY PREDICTION USING HIERARCHICAL SVM CLASSIFIERS AND AN ALTERNATING GEOMETRIC SCORING FUNCTION. , 2006, , .		5
63	The most vital edges of matching in a bipartite graph. <i>Networks</i> , 1993, 23, 309-313.	1.6	4
64	On the isomorphism between cyclic-cubes and wrapped butterfly networks. <i>IEEE Transactions on Parallel and Distributed Systems</i> , 2000, 11, 864.	4.0	4
65	OPTIMUM CONGESTED ROUTING STRATEGY ON TWISTED CUBES. <i>Journal of Interconnection Networks</i> , 2000, 01, 115-134.	0.6	4
66	A note on edge fault tolerance with respect to hypercubes. <i>Applied Mathematics Letters</i> , 2005, 18, 1125-1128.	1.5	4
67	HYPLOSP: A KNOWLEDGE-BASED APPROACH TO PROTEIN LOCAL STRUCTURE PREDICTION. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 1287-1307.	0.3	4
68	Chromosome-centric Human Proteome Project (C-HPP): Chromosome 12. <i>Journal of Proteome Research</i> , 2014, 13, 3160-3165.	1.8	4
69	Somatic mutation subtypes of lung adenocarcinoma in East Asian reveal divergent biological characteristics and therapeutic vulnerabilities. <i>IScience</i> , 2021, 24, 102522.	1.9	4
70	Improving the Alignment Quality of Consistency Based Aligners with an Evaluation Function Using Synonymous Protein Words. <i>PLoS ONE</i> , 2011, 6, e27872.	1.1	4
71	A new shortest path routing algorithm and embedding cycles of crossed cube. , 0, , .		3
72	The Recognition of Double Euler Trails in Series-Parallel Networks. <i>Journal of Algorithms</i> , 1998, 28, 216-257.	0.9	3

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73	Multi-Q 2 software facilitates isobaric labeling quantitation analysis with improved accuracy and coverage. <i>Scientific Reports</i> , 2021, 11, 2233.	1.6	3
74	PROTEIN SUBCELLULAR LOCALIZATION PREDICTION BASED ON COMPARTMENT-SPECIFIC BIOLOGICAL FEATURES. , 2006, , .		3
75	Protein subcellular localization prediction based on compartment-specific biological features. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2006, , 325-30.	0.4	3
76	Transmitting on various network topologies. <i>Networks</i> , 1996, 27, 145-157.	1.6	2
77	Faithful 1-edge fault tolerant graphs. <i>Information Processing Letters</i> , 1997, 61, 173-181.	0.4	2
78	iTop-Q: an Intelligent Tool for Top-down Proteomics Quantitation Using DYAMOND Algorithm. <i>Analytical Chemistry</i> , 2017, 89, 13128-13136.	3.2	2
79	iHPDM: In Silico Human Proteome Digestion Map with Proteolytic Peptide Analysis and Graphical Visualizations. <i>Journal of Proteome Research</i> , 2019, 18, 4124-4132.	1.8	2
80	Comparison of different variant sequence types coupled with decoy generation methods used in concatenated target-decoy database searches for proteogenomic research. <i>Journal of Proteomics</i> , 2021, 231, 104021.	1.2	2
81	A Two-stage Classifier for Protein B-turn Prediction Using Support Vector Machines. , 0, , .		1
82	A KNOWLEDGE-BASED APPROACH TO PROTEIN LOCAL STRUCTURE PREDICTION. , 2005, , .		1
83	Multiaspect Examinations of Possible Alternative Mappings of Identified Variant Peptides: A Case Study on the HEK293 Cell Line. <i>ACS Omega</i> , 0, , .	1.6	1
84	A response to Volgenant's Addendum on the most vital edges. <i>Networks</i> , 1996, 27, 255-255.	1.6	0
85	Christmas tree: a 1-fault-tolerant network for token rings. , 0, , .		0
86	GANAA Genetic Algorithm for NMR Backbone Resonance Assignment. , 0, , .		0
87	Automated Generic Analysis Tools for Protein Quantitation Using Stable Isotope Labeling. <i>Methods in Molecular Biology</i> , 2010, 604, 257-272.	0.4	0
88	Abstract 5565: Quantitative proteomics identifies phosphorylation targets, modulators and pathway signatures of oncogenic RAS-mediated MAPK signaling in lung adenocarcinoma. , 2010, , .		0