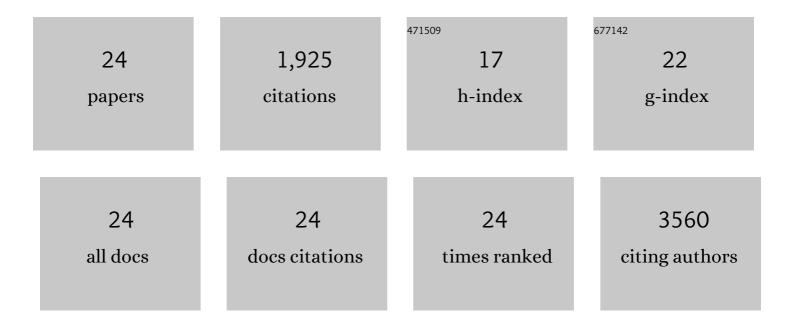
Chih-Chiang Tsou

List of Publications by Year in descending order

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Снин-Снимс Теон

#	Article	IF	CITATIONS
1	Pitfalls in HLA Ligandomics—How to Catch a Li(e)gand. Molecular and Cellular Proteomics, 2021, 20, 100110.	3.8	26
2	Tumor‣elective Altered Glycosylation and Functional Attenuation of CD73 in Human Hepatocellular Carcinoma. Hepatology Communications, 2019, 3, 1400-1414.	4.3	15
3	The HLA ligandome landscape of chronic myeloid leukemia delineates novel T-cell epitopes for immunotherapy. Blood, 2019, 133, 550-565.	1.4	57
4	Functional proteogenomics reveals biomarkers and therapeutic targets in lymphomas. Proceedings of the United States of America, 2017, 114, 6581-6586.	7.1	32
5	New targeted approaches for the quantification of dataâ€independent acquisition mass spectrometry. Proteomics, 2017, 17, 1700021.	2.2	49
6	Untargeted, spectral libraryâ€free analysis of dataâ€independent acquisition proteomics data generated using Orbitrap mass spectrometers. Proteomics, 2016, 16, 2257-2271.	2.2	56
7	Data Independent Acquisition analysis in ProHits 4.0. Journal of Proteomics, 2016, 149, 64-68.	2.4	66
8	A multicenter study benchmarks software tools for label-free proteome quantification. Nature Biotechnology, 2016, 34, 1130-1136.	17.5	321
9	DIA-Umpire: comprehensive computational framework for data-independent acquisition proteomics. Nature Methods, 2015, 12, 258-264.	19.0	561
10	Mining Missing Membrane Proteins by High-pH Reverse-Phase StageTip Fractionation and Multiple Reaction Monitoring Mass Spectrometry. Journal of Proteome Research, 2015, 14, 3658-3669.	3.7	24
11	Large-scale determination of absolute phosphorylation stoichiometries in human cells by motif-targeting quantitative proteomics. Nature Communications, 2015, 6, 6622.	12.8	139
12	QPROT: Statistical method for testing differential expression using protein-level intensity data in label-free quantitative proteomics. Journal of Proteomics, 2015, 129, 121-126.	2.4	66
13	mapDIA: Preprocessing and statistical analysis of quantitative proteomics data from data independent acquisition mass spectrometry. Journal of Proteomics, 2015, 129, 108-120.	2.4	149
14	N-Glycoproteomic Landscape of Human Lymphoid Cancers Reveals Novel Biomarkers and Potential Therapeutic Targets. Blood, 2015, 126, 697-697.	1.4	0
15	Label-free Quantitative Proteomics and N-Glycoproteomics Analysis of KRAS-activated Human Bronchial Epithelial Cells. Molecular and Cellular Proteomics, 2012, 11, 901-915.	3.8	23
16	Label-free quantitative proteomics of CD133-positive liver cancer stem cells. Proteome Science, 2012, 10, 69.	1.7	9
17	An Informatics-assisted Label-free Approach for Personalized Tissue Membrane Proteomics: Case Study on Colorectal Cancer. Molecular and Cellular Proteomics, 2011, 10, M110.003087.	3.8	50
18	Comparative Proteomic Analysis of Proteins Involved in the Tumorigenic Process of Seminal Vesicle Carcinoma in Transgenic Mice. International Journal of Proteomics, 2010, 2010, 1-14.	2.0	14

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#	Article	IF	CITATIONS
19	IDEAL-Q, an Automated Tool for Label-free Quantitation Analysis Using an Efficient Peptide Alignment Approach and Spectral Data Validation. Molecular and Cellular Proteomics, 2010, 9, 131-144.	3.8	114
20	An Informatics-assisted Label-free Quantitation Strategy that Depicts Phosphoproteomic Profiles in Lung Cancer Cell Invasion. Journal of Proteome Research, 2010, 9, 5582-5597.	3.7	57
21	MaXIC-Q Web: a fully automated web service using statistical and computational methods for protein quantitation based on stable isotope labeling and LC–MS. Nucleic Acids Research, 2009, 37, W661-W669.	14.5	10
22	Fast VQ codebook search algorithm for grayscale image coding. Image and Vision Computing, 2008, 26, 657-666.	4.5	75
23	Efficient optimal pixel grouping schemes for AMBTC. Imaging Science Journal, 2008, 56, 217-231.	0.5	10
24	A Remediable Image Authentication Scheme Based on Feature Extraction and Clustered VQ. , 2007, , 446-449.		2