

Chih-Chiang Tsou

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

1,925
citations

471509

17
h-index

677142

22
g-index

24
all docs

24
docs citations

24
times ranked

3560
citing authors

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

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19	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.	3.8	114
20	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.	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. <i>Nucleic Acids Research</i> , 2009, 37, W661-W669.	14.5	10
22	Fast VQ codebook search algorithm for grayscale image coding. <i>Image and Vision Computing</i> , 2008, 26, 657-666.	4.5	75
23	Efficient optimal pixel grouping schemes for AMBTC. <i>Imaging Science Journal</i> , 2008, 56, 217-231.	0.5	10
24	A Remediable Image Authentication Scheme Based on Feature Extraction and Clustered VQ. , 2007, , 446-449.		2