

Chia-Feng Tsai

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

2,084
citations

304743

22
h-index

434195

31
g-index

40
all docs

40
docs citations

40
times ranked

2989
citing authors

#	ARTICLE	IF	CITATIONS
1	Circulating ACE2-expressing extracellular vesicles block broad strains of SARS-CoV-2. <i>Nature Communications</i> , 2022, 13, 405.	12.8	92
2	Motif-centric phosphoproteomics to target kinase-mediated signaling pathways. <i>Cell Reports Methods</i> , 2022, 2, 100138.	2.9	10
3	Three-dimensional feature matching improves coverage for single-cell proteomics based on ion mobility filtering. <i>Cell Systems</i> , 2022, 13, 426-434.e4.	6.2	49
4	Determining protein polarization proteome-wide using physical dissection of individual <i>Stentor coeruleus</i> cells. <i>Current Biology</i> , 2022, , .	3.9	4
5	Internal Standard Triggered-Parallel Reaction Monitoring Mass Spectrometry Enables Multiplexed Quantification of Candidate Biomarkers in Plasma. <i>Analytical Chemistry</i> , 2022, 94, 9540-9547.	6.5	11
6	Mass Spectrometry-Based for Analysis of. <i>Methods in Molecular Biology</i> , 2021, 2259, 247-257.	0.9	0
7	Surfactant-assisted one-pot sample preparation for label-free single-cell proteomics. <i>Communications Biology</i> , 2021, 4, 265.	4.4	46
8	The AML microenvironment catalyzes a stepwise evolution to gilteritinib resistance. <i>Cancer Cell</i> , 2021, 39, 999-1014.e8.	16.8	62
9	Nanoscale Solid-Phase Isobaric Labeling for Multiplexed Quantitative Phosphoproteomics. <i>Journal of Proteome Research</i> , 2021, 20, 4193-4202.	3.7	7
10	Facile One-Pot Nanoproteomics for Label-Free Proteome Profiling of 50-1000 Mammalian Cells. <i>Journal of Proteome Research</i> , 2021, 20, 4452-4461.	3.7	12
11	High-throughput and high-efficiency sample preparation for single-cell proteomics using a nested nanowell chip. <i>Nature Communications</i> , 2021, 12, 6246.	12.8	76
12	Transcriptomic and proteomic signatures of stemness and differentiation in the colon crypt. <i>Communications Biology</i> , 2020, 3, 453.	4.4	37
13	Automated Coupling of Nanodroplet Sample Preparation with Liquid Chromatography-Mass Spectrometry for High-Throughput Single-Cell Proteomics. <i>Analytical Chemistry</i> , 2020, 92, 10588-10596.	6.5	105
14	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26.	28.9	296
15	An Improved Boosting to Amplify Signal with Isobaric Labeling (iBASIL) Strategy for Precise Quantitative Single-cell Proteomics. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 828-838.	3.8	121
16	Proteogenomic Characterization of Ovarian HGSC Implicates Mitotic Kinases, Replication Stress in Observed Chromosomal Instability. <i>Cell Reports Medicine</i> , 2020, 1, 100004.	6.5	46
17	Tandem Mass Tag Labeling Facilitates Reversed-Phase Liquid Chromatography-Mass Spectrometry Analysis of Hydrophilic Phosphopeptides. <i>Analytical Chemistry</i> , 2019, 91, 11606-11613.	6.5	22
18	High-Throughput Single Cell Proteomics Enabled by Multiplex Isobaric Labeling in a Nanodroplet Sample Preparation Platform. <i>Analytical Chemistry</i> , 2019, 91, 13119-13127.	6.5	156

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19	Automated Nanoflow Two-Dimensional Reversed-Phase Liquid Chromatography System Enables In-Depth Proteome and Phosphoproteome Profiling of Nanoscale Samples. <i>Analytical Chemistry</i> , 2019, 91, 9707-9715.	6.5	36
20	Phosphoproteome Analysis Reveals Estrogen-ER Pathway as a Modulator of mTOR Activity Via DEPTOR. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1607-1618.	3.8	18
21	Boosting to Amplify Signal with Isobaric Labeling (BASIL) Strategy for Comprehensive Quantitative Phosphoproteomic Characterization of Small Populations of Cells. <i>Analytical Chemistry</i> , 2019, 91, 5794-5801.	6.5	86
22	Inducing hair follicle neogenesis with secreted proteins enriched in embryonic skin. <i>Biomaterials</i> , 2018, 167, 121-131.	11.4	29
23	Phosphoproteomics Reveals HMGA1, a CK2 Substrate, as a Drug-Resistant Target in Non-Small Cell Lung Cancer. <i>Scientific Reports</i> , 2017, 7, 44021.	3.3	31
24	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
25	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
26	Effect of sialylation on EGFR phosphorylation and resistance to tyrosine kinase inhibition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6955-6960.	7.1	102
27	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
28	Rapid High-pH Reverse Phase StageTip for Sensitive Small-Scale Membrane Proteomic Profiling. <i>Analytical Chemistry</i> , 2015, 87, 12016-12023.	6.5	47
29	Informatics View on the Challenges of Identifying Missing Proteins from Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2015, 14, 5396-5407.	3.7	14
30	Sequential Phosphoproteomic Enrichment through Complementary Metal-Directed Immobilized Metal Ion Affinity Chromatography. <i>Analytical Chemistry</i> , 2014, 86, 685-693.	6.5	100
31	Cancer Phosphoproteomics: Tools and Emerging Applications for Mining the Phosphoproteome in Cancer Biology. , 2012, , 161-188.		0
32	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
33	Immobilized Metal Affinity Chromatography Revisited: pH/Acid Control toward High Selectivity in Phosphoproteomics. <i>Journal of Proteome Research</i> , 2008, 7, 4058-4069.	3.7	125