Thesaurus: quantifying phosphopeptide positional ison

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Citation Report

#	Article	IF	CITATIONS
1	R2â€₽2 rapidâ€robotic phosphoproteomics enables multidimensional cell signaling studies. Molecular Systems Biology, 2019, 15, e9021.	7.2	102
2	diaPASEF: parallel accumulation–serial fragmentation combined with data-independent acquisition. Nature Methods, 2020, 17, 1229-1236.	19.0	387
3	Lysine and Arginine Protein Post-translational Modifications by Enhanced DIA Libraries: Quantification in Murine Liver Disease. Journal of Proteome Research, 2020, 19, 4163-4178.	3.7	18
4	PINE: An Automation Tool to Extract and Visualize Protein-Centric Functional Networks. Journal of the American Society for Mass Spectrometry, 2020, 31, 1410-1421.	2.8	14
5	Rapid and site-specific deep phosphoproteome profiling by data-independent acquisition without the need for spectral libraries. Nature Communications, 2020, 11, 787.	12.8	251
6	Comparing 22 Popular Phosphoproteomics Pipelines for Peptide Identification and Site Localization. Journal of Proteome Research, 2020, 19, 1338-1345.	3.7	30
7	Dataâ€Independent Acquisition Mass Spectrometryâ€Based Proteomics and Software Tools: A Glimpse in 2020. Proteomics, 2020, 20, e1900276.	2.2	222
8	Generating high quality libraries for DIA MS with empirically corrected peptide predictions. Nature Communications, 2020, 11, 1548.	12.8	148
9	Acquiring and Analyzing Data Independent Acquisition Proteomics Experiments without Spectrum Libraries. Molecular and Cellular Proteomics, 2020, 19, 1088-1103.	3.8	164
10	Fragment Mass Spectrum Prediction Facilitates Site Localization of Phosphorylation. Journal of Proteome Research, 2021, 20, 634-644.	3.7	16
11	Global and Site-Specific Effect of Phosphorylation on Protein Turnover. Developmental Cell, 2021, 56, 111-124.e6.	7.0	57
12	Proteomic Approaches to Study SARS-CoV-2 Biology and COVID-19 Pathology. Journal of Proteome Research, 2021, 20, 1133-1152.	3.7	27
13	The Role of Data-Independent Acquisition for Glycoproteomics. Molecular and Cellular Proteomics, 2021, 20, 100042.	3.8	38
14	Posttranslational modifications in systems biology. Advances in Protein Chemistry and Structural Biology, 2021, 127, 93-126.	2.3	16
16	MS Amanda 2.0: Advancements in the standalone implementation. Rapid Communications in Mass Spectrometry, 2021, 35, e9088.	1.5	12
18	A data-independent acquisition-based global phosphoproteomics system enables deep profiling. Nature Communications, 2021, 12, 2539.	12.8	44
19	Recent advances in mass-spectrometry based proteomics software, tools and databases. Drug Discovery Today: Technologies, 2021, 39, 69-79.	4.0	19
20	CsoDIAq Software for Direct Infusion Shotgun Proteome Analysis. Analytical Chemistry, 2021, 93, 12312-12319.	6.5	8

CITATION REPORT

#	Article	IF	CITATIONS
21	Phosphoproteomics: a valuable tool for uncovering molecular signaling in cancer cells. Expert Review of Proteomics, 2021, 18, 661-674.	3.0	15
26	Does Data-Independent Acquisition Data Contain Hidden Gems? A Case Study Related to Alzheimer's Disease. Journal of Proteome Research, 2022, 21, 118-131.	3.7	15
27	Advanced mass spectrometry-based methods for protein molecular-structural biologists. , 2022, , 311-326.		8
28	Ubiquitinomics: History, methods, and applications in basic research and drug discovery. Proteomics, 2022, 22, e2200074.	2.2	11
29	Building Spectral Libraries from Narrow-Window Data-Independent Acquisition Mass Spectrometry Data. Journal of Proteome Research, 2022, 21, 1382-1391.	3.7	6
30	Advances in dataâ€independent acquisition mass spectrometry towards comprehensive digital proteome landscape. Mass Spectrometry Reviews, 2023, 42, 2324-2348.	5.4	42
32	Improving Phosphoproteomics Profiling Using Data-Independent Mass Spectrometry. Journal of Proteome Research, 2022, 21, 1789-1799.	3.7	10
33	Ion mobilityâ€resolved phosphoproteomics with diaâ€PASEF and short gradients. Proteomics, 2023, 23, .	2.2	14
36	The language of posttranslational modifications and deciphering it from proteomics data. , 2023, , 109-136.		1
37	DeepFLR facilitates false localization rate control in phosphoproteomics. Nature Communications, 2023, 14, .	12.8	4
38	The Breast Cancer Proteome and Precision Oncology. Cold Spring Harbor Perspectives in Medicine, 0, , a041323.	6.2	0
40	A Multipathway Phosphopeptide Standard for Rapid Phosphoproteomics Assay Development. Molecular and Cellular Proteomics, 2023, 22, 100639.	3.8	1
41	The regulatory landscape of the yeast phosphoproteome. Nature Structural and Molecular Biology, 2023, 30, 1761-1773.	8.2	8
42	Construction of a linguistically interactive thesaurus for English second language acquisition based on an eigenvalue-fitting superiority algorithm. Applied Mathematics and Nonlinear Sciences, 2024, 9, .	1.6	0
43	Computational approaches to identify sites of phosphorylation. Proteomics, 0, , .	2.2	1
44	Acquisition and Analysis of DIA-Based Proteomic Data: A Comprehensive Survey inÂ2023. Molecular and Cellular Proteomics, 2024, 23, 100712.	3.8	0