

MultiNotch MS3 Enables Accurate, Sensitive, and Multi- Expression across Cancer Cell Line Proteomes

Analytical Chemistry

86, 7150-7158

DOI: [10.1021/ac502040v](https://doi.org/10.1021/ac502040v)

Citation Report

#	ARTICLE	IF	CITATIONS
7	Quantitative proteomic analysis reveals posttranslational responses to aneuploidy in yeast. <i>ELife</i> , 2014, 3, e03023.	2.8	218
8	Progress in Mass Spectrometry Acquisition Approach for Quantitative Proteomics. <i>Chinese Journal of Analytical Chemistry</i> , 2014, 42, 1859-1868.	0.9	8
9	Isobaric Labeling-Based Relative Quantification in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2014, 13, 5293-5309.	1.8	520
10	Comprehensive and Scalable Highly Automated MS-Based Proteomic Workflow for Clinical Biomarker Discovery in Human Plasma. <i>Journal of Proteome Research</i> , 2014, 13, 3837-3845.	1.8	49
11	The paracaspase MALT1 cleaves HOIL1 reducing linear ubiquitination by LUBAC to dampen lymphocyte NF- κ B signalling. <i>Nature Communications</i> , 2015, 6, 8777.	5.8	139
12	A comprehensive proteomic and phosphoproteomic analysis of yeast deletion mutants of 14 α -orthologs and associated effects of rapamycin. <i>Proteomics</i> , 2015, 15, 474-486.	1.3	49
13	Protein identification and quantification from riverbank grape, <i>Vitis riparia</i> : Comparing SDS-PAGE and FASP-GPF techniques for shotgun proteomic analysis. <i>Proteomics</i> , 2015, 15, 3061-3065.	1.3	14
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21	High-Resolution Enabled 12-Plex DiLeu Isobaric Tags for Quantitative Proteomics. <i>Analytical Chemistry</i> , 2015, 87, 1646-1654.	3.2	117
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23	Sample Multiplexing with Cysteine-Selective Approaches: cysDML and cPILOT. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 615-630.	1.2	26
24	A comprehensive Xist interactome reveals cohesin repulsion and an RNA-directed chromosome conformation. <i>Science</i> , 2015, 349, .	6.0	397

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