

CITATION REPORT

List of articles citing

Top-down proteomics reveals concerted reductions in myofilament and Z-disc protein phosphorylation after acute myocardial infarction

DOI: 10.1074/mcp.m114.040675

Molecular and Cellular Proteomics, 2014, 13, 2752-64.

Source: <https://exaly.com/paper-pdf/59049411/citation-report.pdf>

Version: 2024-04-27

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper	IF	Citations
87	Multiple proteases to localize oxidation sites. <i>PLoS ONE</i> , 2015 , 10, e0116606	3.7	
86	Phosphorylation of myosin regulatory light chain controls myosin head conformation in cardiac muscle. <i>Journal of Molecular and Cellular Cardiology</i> , 2015 , 85, 199-206	5.8	40
85	New mass-spectrometry-compatible degradable surfactant for tissue proteomics. <i>Journal of Proteome Research</i> , 2015 , 14, 1587-99	5.6	48
84	Affinity proteomics for phosphatase interactions in atrial fibrillation. <i>Journal of the American College of Cardiology</i> , 2015 , 65, 174-6	15.1	2
83	Dissecting human skeletal muscle troponin proteoforms by top-down mass spectrometry. <i>Journal of Muscle Research and Cell Motility</i> , 2015 , 36, 169-81	3.5	5
82	Effective top-down LC/MS+ method for assessing actin isoforms as a potential cardiac disease marker. <i>Analytical Chemistry</i> , 2015 , 87, 8399-8406	7.8	19
81	Three dimensional liquid chromatography coupling ion exchange chromatography/hydrophobic interaction chromatography/reverse phase chromatography for effective protein separation in top-down proteomics. <i>Analytical Chemistry</i> , 2015 , 87, 5363-5371	7.8	52
80	Transformative Impact of Proteomics on Cardiovascular Health and Disease: A Scientific Statement From the American Heart Association. <i>Circulation</i> , 2015 , 132, 852-72	16.7	112
79	Comprehensive assessment of chamber-specific and transmural heterogeneity in myofilament protein phosphorylation by top-down mass spectrometry. <i>Journal of Molecular and Cellular Cardiology</i> , 2015 , 87, 102-12	5.8	21
78	State of the art of 2D DIGE. <i>Proteomics - Clinical Applications</i> , 2015 , 9, 277-88	3.1	79
77	Top-Down Proteomics and Farm Animal and Aquatic Sciences. <i>Proteomes</i> , 2016 , 4,	4.6	9
76	Top-Down Targeted Proteomics Reveals Decrease in Myosin Regulatory Light-Chain Phosphorylation That Contributes to Sarcopenic Muscle Dysfunction. <i>Journal of Proteome Research</i> , 2016 , 15, 2706-16	5.6	35
75	Myosin light chain phosphorylation enhances contraction of heart muscle via structural changes in both thick and thin filaments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E3039-47	11.5	79
74	Myofibril growth during cardiac hypertrophy is regulated through dual phosphorylation and acetylation of the actin capping protein CapZ. <i>Cellular Signalling</i> , 2016 , 28, 1015-24	4.9	16
73	Proteomic changes in human lung epithelial cells (A549) in response to carbon black and titanium dioxide exposures. <i>Journal of Proteomics</i> , 2016 , 149, 53-63	3.9	22
72	Comprehensive analysis of tropomyosin isoforms in skeletal muscles by top-down proteomics. <i>Journal of Muscle Research and Cell Motility</i> , 2016 , 37, 41-52	3.5	21
71	Top-Down Proteomics. 2016 , 187-212		1

70	An Omics Perspective on Cardiomyopathies and Heart Failure. <i>Trends in Molecular Medicine</i> , 2016 , 22, 813-827	11.5	25
69	Top-down Proteomics: Technology Advancements and Applications to Heart Diseases. <i>Expert Review of Proteomics</i> , 2016 , 13, 717-30	4.2	66
68	Phosphorylation of the regulatory light chain of myosin in striated muscle: methodological perspectives. <i>European Biophysics Journal</i> , 2016 , 45, 779-805	1.9	17
67	Cardiac myosin light chain is phosphorylated by Ca ²⁺ /calmodulin-dependent and -independent kinase activities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E3824-33	11.5	25
66	MASH Suite Pro: A Comprehensive Software Tool for Top-Down Proteomics. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 703-14	7.6	95
65	Protein Sequence Determination: Methodology and Evolutionary Implications. 2016 , 75-83		
64	pTop 1.0: A High-Accuracy and High-Efficiency Search Engine for Intact Protein Identification. <i>Analytical Chemistry</i> , 2016 , 88, 3082-90	7.8	41
63	Comprehensive Characterization of AMP-Activated Protein Kinase Catalytic Domain by Top-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2016 , 27, 220-32	3.5	9
62	Protein species as diagnostic markers. <i>Journal of Proteomics</i> , 2016 , 134, 5-18	3.9	21
61	Online Hydrophobic Interaction Chromatography-Mass Spectrometry for Top-Down Proteomics. <i>Analytical Chemistry</i> , 2016 , 88, 1885-91	7.8	68
60	Top-Down Proteomics of Large Proteins up to 223 kDa Enabled by Serial Size Exclusion Chromatography Strategy. <i>Analytical Chemistry</i> , 2017 , 89, 5467-5475	7.8	78
59	Distinct sequences and post-translational modifications in cardiac atrial and ventricular myosin light chains revealed by top-down mass spectrometry. <i>Journal of Molecular and Cellular Cardiology</i> , 2017 , 107, 13-21	5.8	19
58	Complete Characterization of Cardiac Myosin Heavy Chain (223 kDa) Enabled by Size-Exclusion Chromatography and Middle-Down Mass Spectrometry. <i>Analytical Chemistry</i> , 2017 , 89, 4922-4930	7.8	18
57	Defining Gas-Phase Fragmentation Propensities of Intact Proteins During Native Top-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2017 , 28, 1203-1215	3.5	33
56	Coupling functionalized cobalt ferrite nanoparticle enrichment with online LC/MS/MS for top-down phosphoproteomics. <i>Chemical Science</i> , 2017 , 8, 4306-4311	9.4	25
55	Ubiquitin Chain Enrichment Middle-Down Mass Spectrometry Enables Characterization of Branched Ubiquitin Chains in Cellulo. <i>Analytical Chemistry</i> , 2017 , 89, 4428-4434	7.8	26
54	Proteomic footprint of myocardial ischemia/reperfusion injury: Longitudinal study of the at-risk and remote regions in the pig model. <i>Scientific Reports</i> , 2017 , 7, 12343	4.9	19
53	PP2A-BSholoenzyme substrate recognition, regulation and role in cytokinesis. <i>Cell Discovery</i> , 2017 , 3, 17027	22.3	44

52	The Impact of Phosphorylation on Electron Capture Dissociation of Proteins: A Top-Down Perspective. <i>Journal of the American Society for Mass Spectrometry</i> , 2017 , 28, 1805-1814	3.5	8
51	Region and cell-type resolved quantitative proteomic map of the human heart. <i>Nature Communications</i> , 2017 , 8, 1469	17.4	144
50	The pathophysiology of myocardial infarction-induced heart failure. <i>Pathophysiology</i> , 2018 , 25, 277-284	1.8	36
49	Comprehensive Characterization of Swine Cardiac Troponin T Proteoforms by Top-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2018 , 29, 1284-1294	3.5	9
48	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018 , 14, 206-214	11.7	324
47	Radical solutions: Principles and application of electron-based dissociation in mass spectrometry-based analysis of protein structure. <i>Mass Spectrometry Reviews</i> , 2018 , 37, 750-771	11	46
46	Physiological proteomics of heart failure. <i>Current Opinion in Physiology</i> , 2018 , 1, 185-197	2.6	1
45	Precision Profiling of the Cardiovascular Post-Translationally Modified Proteome: Where There Is a Will, There Is a Way. <i>Circulation Research</i> , 2018 , 122, 1221-1237	15.7	24
44	Reversible Covalent Reaction of Levosimendan with Cardiac Troponin C in Vitro and in Situ. <i>Biochemistry</i> , 2018 , 57, 2256-2265	3.2	6
43	Impact of Phosphorylation on the Mass Spectrometry Quantification of Intact Phosphoproteins. <i>Analytical Chemistry</i> , 2018 , 90, 4935-4939	7.8	14
42	Novel Sarcopenia-related Alterations in Sarcomeric Protein Post-translational Modifications (PTMs) in Skeletal Muscles Identified by Top-down Proteomics. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 1347-1355	7.6	23
41	Large Cardiac Muscle Patches Engineered From Human Induced-Pluripotent Stem Cell-Derived Cardiac Cells Improve Recovery From Myocardial Infarction in Swine. <i>Circulation</i> , 2018 , 137, 1712-1730	16.7	207
40	Top-Down Proteomics: Ready for Prime Time?. <i>Analytical Chemistry</i> , 2018 , 90, 110-127	7.8	116
39	iTRAQ analysis of a mouse acute myocardial infarction model reveals that vitamin D binding protein promotes cardiomyocyte apoptosis after hypoxia. <i>Oncotarget</i> , 2018 , 9, 1969-1979	3.3	6
38	Temperature-sensitive sarcomeric protein post-translational modifications revealed by top-down proteomics. <i>Journal of Molecular and Cellular Cardiology</i> , 2018 , 122, 11-22	5.8	8
37	A perspective view of top-down proteomics in snake venom research. <i>Rapid Communications in Mass Spectrometry</i> , 2019 , 33 Suppl 1, 20-27	2.2	15
36	Intact-Mass Analysis Facilitating the Identification of Large Human Heart Proteoforms. <i>Analytical Chemistry</i> , 2019 , 91, 10937-10942	7.8	8
35	Analysis of cardiac troponin proteoforms by top-down mass spectrometry. <i>Methods in Enzymology</i> , 2019 , 626, 347-374	1.7	5

34	Middle-Down Multi-Attribute Analysis of Antibody-Drug Conjugates with Electron Transfer Dissociation. <i>Analytical Chemistry</i> , 2019 , 91, 11661-11669	7.8	12
33	An Unbiased Proteomics Method to Assess the Maturation of Human Pluripotent Stem Cell-Derived Cardiomyocytes. <i>Circulation Research</i> , 2019 , 125, 936-953	15.7	33
32	Bridged Hybrid Monolithic Column Coupled to High-Resolution Mass Spectrometry for Top-Down Proteomics. <i>Analytical Chemistry</i> , 2019 , 91, 1743-1747	7.8	16
31	The whole transcriptome and proteome changes in the early stage of myocardial infarction. <i>Cell Death Discovery</i> , 2019 , 5, 73	6.9	9
30	A photocleavable surfactant for top-down proteomics. <i>Nature Methods</i> , 2019 , 16, 417-420	21.6	36
29	A Top-Down Proteomics Platform Coupling Serial Size Exclusion Chromatography and Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Analytical Chemistry</i> , 2019 , 91, 3835-3844	7.8	19
28	Deep Intact Proteoform Characterization in Human Cell Lysate Using High-pH and Low-pH Reversed-Phase Liquid Chromatography. <i>Journal of the American Society for Mass Spectrometry</i> , 2019 , 30, 2502-2513	3.5	17
27	Comprehensive Characterization of the Recombinant Catalytic Subunit of cAMP-Dependent Protein Kinase by Top-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2019 , 30, 2561-2570	3.5	5
26	Phosphopeptide Fragmentation and Site Localization by Mass Spectrometry: An Update. <i>Analytical Chemistry</i> , 2019 , 91, 126-141	7.8	49
25	Region-resolved proteomics profiling of monkey heart. <i>Journal of Cellular Physiology</i> , 2019 , 234, 13720-13734	6	6
24	Deletion of Enigma Homologue from the Z-disc slows tension development kinetics in mouse myocardium. <i>Journal of General Physiology</i> , 2019 , 151, 670-679	3.4	2
23	Simultaneous Quantification of Protein Expression and Modifications by Top-down Targeted Proteomics: A Case of the Sarcomeric Subproteome. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 594-605	7.6	16
22	Top-down proteomics: challenges, innovations, and applications in basic and clinical research. <i>Expert Review of Proteomics</i> , 2020 , 17, 719-733	4.2	27
21	Nanoproteomics enables proteoform-resolved analysis of low-abundance proteins in human serum. <i>Nature Communications</i> , 2020 , 11, 3903	17.4	24
20	Proteomic Profiling Reveals Roles of Stress Response, Ca Transient Dysregulation, and Novel Signaling Pathways in Alcohol-Induced Cardiotoxicity. <i>Alcoholism: Clinical and Experimental Research</i> , 2020 , 44, 2187-2199	3.7	4
19	Distinct hypertrophic cardiomyopathy genotypes result in convergent sarcomeric proteoform profiles revealed by top-down proteomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 24691-24700	11.5	31
18	Fourier-transform ion cyclotron resonance mass spectrometry for characterizing proteoforms. <i>Mass Spectrometry Reviews</i> , 2020 ,	11	3
17	Cardiac Tissue Engineering: Inclusion of Non-cardiomyocytes for Enhanced Features. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 653127	5.7	0

16	Novel Strategies to Address the Challenges in Top-Down Proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2021 , 32, 1278-1294	3.5	23
15	Characterizing Endogenous Protein Complexes with Biological Mass Spectrometry. <i>Chemical Reviews</i> , 2021 ,	68.1	5
14	Pyroptosis inhibition improves the symptom of acute myocardial infarction. <i>Cell Death and Disease</i> , 2021 , 12, 852	9.8	9
13	Proteomics as a Tool to Decipher Novel Mechanistic Candidates in Cardiac Pathophysiology. 2015 , 1, 1-5		2
12	Compound-Protein Interaction Analysis in Condition Following Cardiac Arrest. <i>Galen</i> , 2018 , 7, e1380	0.3	
11	Protein phosphatase 2A in the healthy and failing heart: New insights and therapeutic opportunities.. <i>Cellular Signalling</i> , 2021 , 91, 110213	4.9	○
10	A bibliometric review of peripartum cardiomyopathy compared to other cardiomyopathies using artificial intelligence and machine learning.. <i>Biophysical Reviews</i> , 2022 , 14, 381-401	3.7	○
9	Sbk2, a Newly Discovered Atrium-Enriched Regulator of Sarcomere Integrity.. <i>Circulation Research</i> , 2022 , 101161CIRCRESAHA121319300	15.7	
8	Size Exclusion Chromatography Strategies and MASH Explorer for Large Proteoform Characterization. <i>Methods in Molecular Biology</i> , 2022 , 15-30	1.4	○
7	Protein Sequence Determination: Methodology and Evolutionary Implications. 2022 ,		○
6	Targeted Bottom-Up Mass Spectrometry Approach for the Relative Quantification of Post-Translational Modification of Bovine β -Casein during Milk Fermentation. 2022 , 27, 5834		○
5	TopFD - A Proteoform Feature Detection Tool for Top-Down Proteomics.		○
4	Myofilament-associated proteins with intrinsic disorder (MAPIDs) and their resolution by computational modeling. 1-79		○
3	High Sensitivity Top-down Proteomics Captures Single Muscle Cell Heterogeneity in Large Proteoforms.		○
2	Top-down Proteomics of Myosin Light Chain Isoforms Define Chamber-Specific Expression in the Human Heart.		○
1	Defining the Sarcomeric Proteoform Landscape in Ischemic Cardiomyopathy by Top-Down Proteomics. 2023 , 22, 931-941		○