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Targeted data extraction of the MS/MS spectra generated by data-independent acquisition: a new concept for consistent and accurate proteome analysis

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2078	Analytical technologies for identification and characterization of the plant N-glycoproteome. 2012 , 3, 150		18
2077	A computational tool to detect and avoid redundancy in selected reaction monitoring. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 540-9	7.6	79
2076	Exoproteomics: exploring the world around biological systems. 2012 , 9, 561-75		66
2075	Accurate multiplexed proteomics at the MS2 level using the complement reporter ion cluster. 2012 , 84, 9214-21		111
2074	Human serum proteome analysis: new source of markers in metabolic disorders. 2012 , 6, 759-73		19
2073	Proteomics. 2012 , 39, 81-106		3
2072	Mass spectrometry for translational proteomics: progress and clinical implications. 2012 , 4, 63		59
2071	Combination of gas-phase fractionation and MS ⁿ acquisition modes for relative protein quantification with isobaric tagging. 2012 , 11, 5081-9		28
2070	Targeted proteome investigation via selected reaction monitoring mass spectrometry. 2012 , 75, 3495-513		52
2069	Translational proteomics. 2012 , 75, 4571-2		
2068	Beyond hairballs: The use of quantitative mass spectrometry data to understand protein-protein interactions. 2012 , 586, 2723-31		23
2067	Analysis of protein isoforms: can we do it better?. 2012 , 12, 2937-48		50
2066	Quantitative mass spectrometry in proteomics: critical review update from 2007 to the present. 2012 , 404, 939-65		585
2065	Developments in quantitative mass spectrometry for the analysis of proteome dynamics. 2012 , 30, 668-76		18
2064	Automated selected reaction monitoring software for accurate label-free protein quantification. 2012 , 11, 3766-73		25
2063	Molecular analysis of model gut microbiotas by imaging mass spectrometry and nanodesorption electrospray ionization reveals dietary metabolite transformations. 2012 , 84, 9259-67		50
2062	Current status of the plant phosphorylation site database PhosPhAt and its use as a resource for molecular plant physiology. 2012 , 3, 132		14

2061	Mass spectrometry-based proteomics and network biology. 2012 , 81, 379-405	326
2060	Selected reaction monitoring-based proteomics: workflows, potential, pitfalls and future directions. 2012 , 9, 555-66	997
2059	Microbiology and proteomics, getting the best of both worlds!. 2013 , 15, 12-23	62
2058	Availability of MudPIT data for classification of biological samples. 2013 , 3, 1	8
2057	Data-independent microbial metabolomics with ambient ionization mass spectrometry. 2013 , 24, 1167-76	19
2056	Metaproteomics to unravel major microbial players in leaf litter and soil environments: challenges and perspectives. 2013 , 13, 2895-909	46
2055	Data Acquisition Strategy for Mass Spectrometers Applied to Bottom-up-Based Protein Identification. 2013 , 41, 1120-1128	5
2054	Review of software tools for design and analysis of large scale MRM proteomic datasets. 2013 , 61, 287-98	66
2053	Improving qualitative and quantitative performance for MS(E)-based label-free proteomics. 2013 , 12, 2340-53	57
2052	The Human Eye Proteome Project: perspectives on an emerging proteome. 2013 , 13, 2500-11	63
2051	Quantitative Proteomics in Development of Disease Protein Biomarkers. 2013 , 259-278	2
2050	Detection and correction of interference in SRM analysis. 2013 , 61, 299-303	19
2049	An untargeted metabolomic workflow to improve structural characterization of metabolites. 2013 , 85, 7713-9	51
2048	Unifying expression scale for peptide hydrophobicity in proteomic reversed phase high-pressure liquid chromatography experiments. 2013 , 85, 10878-86	8
2047	Mass spectrometric protein maps for biomarker discovery and clinical research. 2013 , 13, 811-25	105
2046	The cancer secretome, current status and opportunities in the lung, breast and colorectal cancer context. 2013 , 1834, 2242-58	72
2045	Mapping differential interactomes by affinity purification coupled with data-independent mass spectrometry acquisition. 2013 , 10, 1239-45	207
2044	Quantifying protein interaction dynamics by SWATH mass spectrometry: application to the 14-3-3 system. 2013 , 10, 1246-53	249

2043	Biomarker discovery and validation: the tide is turning. 2013 , 10, 505-7	5
2042	Liquid Chromatography Coupled to Mass Spectrometry-Based Metabolomics and the Concept of Biomarker. 2013 , 67, 159-218	5
2041	Proteomics meets the scientific method. 2013 , 10, 24-7	123
2040	Targeted proteomics strategy applied to biomarker evaluation. 2013 , 7, 739-47	32
2039	A flexible statistical model for alignment of label-free proteomics data--incorporating ion mobility and product ion information. 2013 , 14, 364	5
2038	Clustering and filtering tandem mass spectra acquired in data-independent mode. 2013 , 24, 1862-71	14
2037	Bottom-Up Mass Spectrometry-Based Proteomics as an Investigative Analytical Tool for Discovery and Quantification of Proteins in Biological Samples. 2013 , 2, 549-557	12
2036	The biology/disease-driven human proteome project (B/D-HPP): enabling protein research for the life sciences community. 2013 , 12, 23-7	87
2035	Novel approaches for the identification of biomarkers of aggressive prostate cancer. 2013 , 5, 56	5
2034	A complete mass-spectrometric map of the yeast proteome applied to quantitative trait analysis. 2013 , 494, 266-70	250
2033	Next-generation proteomics: towards an integrative view of proteome dynamics. 2013 , 14, 35-48	530
2032	Proteomic analysis of an unculturable bacterial endosymbiont (Blochmannia) reveals high abundance of chaperonins and biosynthetic enzymes. 2013 , 12, 704-18	28
2031	Selectivity of LC-MS/MS analysis: implication for proteomics experiments. 2013 , 81, 148-58	103
2030	The emerging field of chemo- and pharmacoproteomics. 2013 , 7, 171-80	14
2029	Recent advances in mass spectrometry: data independent analysis and hyper reaction monitoring. 2013 , 10, 551-66	104
2028	Comprehensive analysis of protein digestion using six trypsins reveals the origin of trypsin as a significant source of variability in proteomics. 2013 , 12, 5666-80	54
2027	Networks in proteomics analysis of cancer. 2013 , 24, 1122-8	19
2026	Proteomic Analysis of Cellular Systems. 2013 , 3-25	13

2025	Next Generation Instruments and Methods for Proteomics. 2013 , 15-67	4
2024	Proteomics in Nutritional Systems Biology: Defining Health. 2013 , 167-189	
2023	Sources of technical variability in quantitative LC-MS proteomics: human brain tissue sample analysis. 2013 , 12, 2128-37	118
2022	Quantitative measurements of N-linked glycoproteins in human plasma by SWATH-MS. 2013 , 13, 1247-56	171
2021	Protein analysis by shotgun/bottom-up proteomics. 2013 , 113, 2343-94	902
2020	Technologies and challenges in large-scale phosphoproteomics. 2013 , 13, 910-31	130
2019	Interaction domains of Sos1/Grb2 are finely tuned for cooperative control of embryonic stem cell fate. 2013 , 152, 1008-20	45
2018	Glycocapture-based proteomics for secretome analysis. 2013 , 13, 512-25	21
2017	Quantitative analysis of peptides and proteins in biomedicine by targeted mass spectrometry. 2013 , 10, 28-34	347
2016	Sum of the parts: mass spectrometry-based metabolomics. 2013 , 52, 3829-40	48
2015	Label-free quantitative proteomics trends for protein-protein interactions. 2013 , 81, 91-101	47
2014	Orbitrap mass spectrometry. 2013 , 85, 5288-96	327
2013	Protein-protein interaction networks: probing disease mechanisms using model systems. 2013 , 5, 37	53
2012	Recent advances in quantitative neuroproteomics. 2013 , 61, 186-218	93
2011	Enhanced detection of ubiquitin isopeptides using reductive methylation. 2013 , 24, 421-30	11
2010	The Mtb proteome library: a resource of assays to quantify the complete proteome of Mycobacterium tuberculosis. 2013 , 13, 602-612	139
2009	Analysis of biopharmaceutical proteins in biological matrices by LC-MS/MS II. LC-MS/MS analysis. 2013 , 48, 52-61	34
2008	Multiplexed MS/MS for improved data-independent acquisition. 2013 , 10, 744-6	215

2007	A proteomics view of the molecular mechanisms and biomarkers of glaucomatous neurodegeneration. 2013 , 35, 18-43		37
2006	A review on recent developments in mass spectrometry instrumentation and quantitative tools advancing bacterial proteomics. 2013 , 97, 4749-62		46
2005	Recognizing the potential benefits and pitfalls of high-resolution MS. 2013 , 5, 1157-60		3
2004	FTDR 2.0: a tool to achieve sub-ppm level recalibrated accuracy in routine LC-MS analysis. 2013 , 12, 3857-64		2
2003	Unlocking the puzzling biology of the black Périgord truffle <i>Tuber melanosporum</i> . 2013 , 12, 5349-56		22
2002	Targeted identification of SUMOylation sites in human proteins using affinity enrichment and paralogue-specific reporter ions. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 2536-50	7.6	36
2001	Effects of traveling wave ion mobility separation on data independent acquisition in proteomics studies. 2013 , 12, 2323-39		70
2000	Mass fingerprinting of complex mixtures: protein inference from high-resolution peptide masses and predicted retention times. 2013 , 12, 5730-41		12
1999	Use of narrow mass-window, high-resolution extracted product ion chromatograms for the sensitive and selective identification of protein modifications. 2013 , 85, 4621-7		14
1998	Multinozzle emitter array chips for small-volume proteomics. 2013 , 85, 816-9		41
1997	The spectrum of circulating RNA: a window into systems toxicology. 2013 , 132, 478-92		29
1996	Pre-analytical and analytical variability in absolute quantitative MRM-based plasma proteomic studies. 2013 , 5, 2837-56		35
1995	Shooting movies of signaling network dynamics with multiparametric cytometry. 2014 , 377, 177-89		3
1994	Label-Free Quantitation and Mapping of the ErbB2 Tumor Receptor by Multiple Protease Digestion with Data-Dependent (MS1) and Data-Independent (MS2) Acquisitions. 2013 , 2013, 791985		20
1993	Application of selected reaction monitoring mass spectrometry to field-grown crop plants to allow dissection of the molecular mechanisms of abiotic stress tolerance. 2013 , 4, 20		16
1992	Neutron-encoded signatures enable product ion annotation from tandem mass spectra. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 3812-23	7.6	18
1991	N-glycoprotein SRMATlas: a resource of mass spectrometric assays for N-glycosites enabling consistent and multiplexed protein quantification for clinical applications. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 1005-16	7.6	42
1990	From a gene-centric to whole-proteome view of differentiation of T helper cell subsets. 2013 , 12, 471-82		6

1989	A new hybrid probability-based method for identifying proteins and protein modifications. 2013,	0
1988	Tissue proteomics in pancreatic cancer study: discovery, emerging technologies, and challenges. 2013, 13, 710-21	31
1987	Recent technological developments in proteomics shed new light on translational research on diabetic microangiopathy. 2013, 280, 5668-81	11
1986	Mass Informatics: From Mass Spectrometry Peaks to Biological Pathways. 2013, 53, 157-165	1
1985	Tpo1-mediated spermine and spermidine export controls cell cycle delay and times antioxidant protein expression during the oxidative stress response. 2013, 14, 1113-9	39
1984	DNA sequencing methods in human genetics and disease research. 2013, 5, 34	6
1983	The Role of Mass Spectrometry in the "Omics" Era. 2013, 17, 2891-2905	48
1982	Molecular biomarkers in glaucoma. 2013, 54, 121-31	38
1981	Structural, kinetic and proteomic characterization of acetyl phosphate-dependent bacterial protein acetylation. 2014, 9, e94816	178
1980	Advances in Proteomic Technologies and Its Contribution to the Field of Cancer. 2014, 2014, 238045	19
1979	Iron promotes protein insolubility and aging in <i>C. elegans</i> . 2014, 6, 975-91	41
1978	A cooperative mechanism drives budding yeast kinetochore assembly downstream of CENP-A. 2014, 206, 509-24	66
1977	Urinary biomarkers of physical activity: candidates and clinical utility. 2014, 11, 91-106	12
1976	Next-generation snake venomomics: protein-locus resolution through venom proteome decomplexation. 2014, 11, 315-29	87
1975	Application of clinical proteomics in acute respiratory distress syndrome. 2014, 3, 34	6
1974	Tomato nuclear proteome reveals the involvement of specific E2 ubiquitin-conjugating enzymes in fruit ripening. 2014, 15, 548	67
1973	An Overview of Quantitative Proteomic Approaches. 2014, 63, 111-135	
1972	Advantages and Applications of Gel-Free Proteomic Approaches in the Study of Prokaryotes. 2014, 64, 157-200	1

1971	MixGF: spectral probabilities for mixture spectra from more than one peptide. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 3688-97	7.6	15
1970	Large-scale label-free phosphoproteomics: from technology to data interpretation. 2014 , 6, 2403-20		6
1969	Biomedical applications of ion mobility-enhanced data-independent acquisition-based label-free quantitative proteomics. 2014 , 11, 675-84		23
1968	Bioinformatic Approaches to Increase Proteome Coverage. 2014 , 385-419		1
1967	The beta cell immunopeptidome. 2014 , 95, 115-44		6
1966	Daily rhythms in the cyanobacterium <i>synechococcus elongatus</i> probed by high-resolution mass spectrometry-based proteomics reveals a small defined set of cyclic proteins. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2042-55	7.6	55
1965	Conserved peptide fragmentation as a benchmarking tool for mass spectrometers and a discriminating feature for targeted proteomics. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2056-71	7.6	65
1964	Multiplexed and data-independent tandem mass spectrometry for global proteome profiling. 2014 , 33, 452-70		174
1963	The top-down, middle-down, and bottom-up mass spectrometry approaches for characterization of histone variants and their post-translational modifications. 2014 , 14, 489-97		103
1962	Comparison of data acquisition strategies on quadrupole ion trap instrumentation for shotgun proteomics. 2014 , 25, 2048-59		27
1961	The Q Exactive HF, a Benchtop mass spectrometer with a pre-filter, high-performance quadrupole and an ultra-high-field Orbitrap analyzer. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 3698-708	7.6	229
1960	High resolution mass spectrometry based techniques at the crossroads of metabolic pathways. 2014 , 33, 471-500		117
1959	Progress in Mass Spectrometry Acquisition Approach for Quantitative Proteomics. 2014 , 42, 1859-1868		6
1958	Quantitative Analysis of Targeted Proteins in Complex Sample Using Novel Data Independent Acquisition. 2014 , 42, 1750-1758		4
1957	Proteomics for systems toxicology. 2014 , 11, 73-90		45
1956	Liquid chromatography, in combination with a quadrupole time-of-flight instrument (LC QTOF), with sequential window acquisition of all theoretical fragment-ion spectra (SWATH) acquisition: systematic studies on its use for screenings in clinical and forensic toxicology and comparison with information-dependent acquisition (IDA). 2014 , 86, 11742-9		97
1955	Hybrid data acquisition and processing strategies with increased throughput and selectivity: pSMART analysis for global qualitative and quantitative analysis. 2014 , 13, 5415-30		24
1954	Quantitative proteomics using the high resolution accurate mass capabilities of the quadrupole-orbitrap mass spectrometer. 2014 , 6, 2159-70		12

1953	Systems cell biology. 2014 , 206, 695-706		29
1952	Human saliva proteome: an overview. 2014 ,		
1951	Proteomics, genomics and transcriptomics: their emerging roles in the discovery and validation of colorectal cancer biomarkers. 2014 , 11, 179-205		21
1950	Phosphoprotein secretome of tumor cells as a source of candidates for breast cancer biomarkers in plasma. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 1034-49	7.6	35
1949	Glycoproteomic analysis of prostate cancer tissues by SWATH mass spectrometry discovers N-acylethanolamine acid amidase and protein tyrosine kinase 7 as signatures for tumor aggressiveness. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 1753-68	7.6	143
1948	Mass Spectrometric Target Analysis and Proteomics in Environmental Toxicology. 2014 , 149-167		
1947	Targeted peptide measurements in biology and medicine: best practices for mass spectrometry-based assay development using a fit-for-purpose approach. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 907-17	7.6	392
1946	Integrating omics technologies to study pulmonary physiology and pathology at the systems level. 2014 , 33, 1239-60		10
1945	Proteomic strategies for the discovery of novel diagnostic and therapeutic targets for infectious diseases. 2014 , 71, 177-89		8
1944	Predicted multiple selected reaction monitoring to screen activated drug-mediated modifications on human serum albumin. 2014 , 449, 59-67		12
1943	Improving the identification rate of data independent label-free quantitative proteomics experiments on non-model crops: a case study on apple fruit. 2014 , 105, 31-45		34
1942	Computational proteomics: designing a comprehensive analytical strategy. 2014 , 19, 266-74		15
1941	Quantitative targeted proteomics for understanding the blood-brain barrier: towards pharmacoproteomics. 2014 , 11, 303-13		32
1940	SWATH and iTRAQ-based quantitative proteomic analyses reveal an overexpression and biological relevance of CD109 in advanced NSCLC. 2014 , 102, 125-36		35
1939	What can proteomics tell us about platelets?. 2014 , 114, 1204-19		76
1938	A <i>Candida albicans</i> PeptideAtlas. 2014 , 97, 62-8		19
1937	Mass spectral enhanced detection of UbIs using SWATH acquisition: MEDUSA--simultaneous quantification of SUMO and ubiquitin-derived isopeptides. 2014 , 25, 767-77		15
1936	Technical considerations for large-scale parallel reaction monitoring analysis. 2014 , 100, 147-59		128

1935	Proteomics in investigation of cancer metastasis: functional and clinical consequences and methodological challenges. 2014 , 14, 426-40	10
1934	Integrated quantification and identification of aldehydes and ketones in biological samples. 2014 , 86, 5089-100	52
1933	Fine tuning of proteomic technologies to improve biological findings: advancements in 2011-2013. 2014 , 86, 176-95	18
1932	Thermoanaerobacter thermohydrosulfuricus WC1 shows protein complement stability during fermentation of key lignocellulose-derived substrates. 2014 , 80, 1602-15	22
1931	Systems approach to neurodegenerative disease biomarker discovery. 2014 , 54, 457-81	38
1930	Exploring intercellular signaling by proteomic approaches. 2014 , 14, 498-512	13
1929	Using PeptideAtlas, SRMAtlas, and PASSEL: Comprehensive Resources for Discovery and Targeted Proteomics. 2014 , 46, 13.25.1-28	45
1928	Evaluation of data-dependent and -independent mass spectrometric workflows for sensitive quantification of proteins and phosphorylation sites. 2014 , 13, 5973-88	38
1927	Label-free quantitative proteomic analysis of the YAP/TAZ interactome. 2014 , 306, C805-18	49
1926	Protein inference using Peptide quantification patterns. 2014 , 13, 3191-9	10
1925	Data for mitochondrial proteomic alterations in the developing rat brain. 2014 , 1, 42-5	2
1924	Separation methodology to improve proteome coverage depth. 2014 , 11, 409-14	9
1923	Exploring skyline for both MS(E) -based label-free proteomics and HRMS quantitation of small molecules. 2014 , 14, 169-80	11
1922	Identification of cardiac myofilament protein isoforms using multiple mass spectrometry based approaches. 2014 , 8, 578-589	8
1921	Variation and quantification among a target set of phosphopeptides in human plasma by multiple reaction monitoring and SWATH-MS2 data-independent acquisition. 2014 , 35, 3487-97	17
1920	Proteomic analysis of the mitochondria from embryonic and postnatal rat brains reveals response to developmental changes in energy demands. 2014 , 109, 228-39	18
1919	Quantitative shotgun proteomics with data-independent acquisition and traveling wave ion mobility spectrometry: a versatile tool in the life sciences. 2014 , 806, 79-91	4
1918	DeMix workflow for efficient identification of cofragmented peptides in high resolution data-dependent tandem mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 3211-23	7.6 44

1917	Panorama: a targeted proteomics knowledge base. 2014 , 13, 4205-10	149
1916	Label-free protein quantification for plant Golgi protein localization and abundance. 2014 , 166, 1033-43	31
1915	A sentinel protein assay for simultaneously quantifying cellular processes. 2014 , 11, 1045-8	52
1914	Targeted proteomics of myofilament phosphorylation and other protein posttranslational modifications. 2014 , 8, 543-53	13
1913	OpenSWATH enables automated, targeted analysis of data-independent acquisition MS data. 2014 , 32, 219-23	508
1912	Targeted protein quantification using sparse reference labeling. 2014 , 11, 301-4	8
1911	Recent advances in mass spectrometry-based glycoproteomics. 2014 , 95, 71-123	14
1910	Expansion of the ion library for mining SWATH-MS data through fractionation proteomics. 2014 , 86, 7242-6	29
1909	High-throughput proteomics. 2014 , 7, 427-54	128
1908	Label-free quantification of differentially expressed proteins in mouse liver cancer cells with high and low metastasis rates by a SWATH acquisition method. 2014 , 57, 718-722	1
1907	Implementation of dipolar resonant excitation for collision induced dissociation with ion mobility/time-of-flight MS. 2014 , 25, 563-71	4
1906	Proteogenomics of selective susceptibility to endotoxin using circulating acute phase biomarkers and bioassay development in sheep: a review. 2014 , 12, 12	10
1905	Quantitative proteomics by SWATH-MS reveals altered expression of nucleic acid binding and regulatory proteins in HIV-1-infected macrophages. 2014 , 13, 2109-19	54
1904	Quantitative proteomics in the field of microbiology. 2014 , 14, 547-65	57
1903	Mass spectrometric analysis of histone proteoforms. 2014 , 7, 113-28	49
1902	A targeted in vivo SILAC approach for quantification of drug metabolism enzymes: regulation by the constitutive androstane receptor. 2014 , 13, 866-74	7
1901	Proteomics for the discovery of biomarkers and diagnosis of periodontitis: a critical review. 2014 , 11, 31-41	15
1900	Twenty years of protein interaction studies for biological function deciphering. 2014 , 107, 93-7	16

1899	Comparison of information-dependent acquisition, SWATH, and MS(All) techniques in metabolite identification study employing ultrahigh-performance liquid chromatography-quadrupole time-of-flight mass spectrometry. 2014 , 86, 1202-9	155
1898	Mass spectrometry-driven phosphoproteomics: patterning the systems biology mosaic. 2014 , 3, 83-112	56
1897	Recent advances in proteomics: towards the human proteome. 2014 , 28, 848-57	20
1896	Drift time-specific collision energies enable deep-coverage data-independent acquisition proteomics. 2014 , 11, 167-70	284
1895	Nano-LC/MALDI-MS using a column-integrated spotting probe for analysis of complex biomolecule samples. 2014 , 86, 2549-58	8
1894	Identification of chemoresistance-related cell-surface glycoproteins in leukemia cells and functional validation of candidate glycoproteins. 2014 , 13, 1593-601	16
1893	Directed network wiring identifies a key protein interaction in embryonic stem cell differentiation. 2014 , 54, 1034-41	29
1892	Data processing methods and quality control strategies for label-free LC-MS protein quantification. 2014 , 1844, 29-41	45
1891	Elucidating the fungal stress response by proteomics. 2014 , 97, 151-63	34
1890	Contemporary network proteomics and its requirements. 2013 , 3, 22-38	5
1889	Mycobacterium tuberculosis in the Proteomics Era. 2014 , 2,	14
1888	iPhos: a toolkit to streamline the alkaline phosphatase-assisted comprehensive LC-MS phosphoproteome investigation. 2014 , 15 Suppl 16, S10	7
1887	A repository of assays to quantify 10,000 human proteins by SWATH-MS. 2014 , 1, 140031	266
1886	A novel targeted proteomics method for identification and relative quantitation of difference in nitration degree of OGDH between healthy and diabetic mouse. 2014 , 14, 2417-26	14
1885	Ariadne's Thread: A Robust Software Solution Leading to Automated Absolute and Relative Quantification of SRM Data. 2015 , 14, 3779-92	2
1884	A decade of metaproteomics: where we stand and what the future holds. 2015 , 15, 3409-17	119
1883	Label-free Quantitative Analysis of Changes in Broiler Liver Proteins under Heat Stress using SWATH-MS Technology. 2015 , 5, 15119	28
1882	Quantitative measurement of intact alpha-synuclein proteoforms from post-mortem control and Parkinson's disease brain tissue by intact protein mass spectrometry. 2014 , 4, 5797	89

1881	Multi-omics approach for comparative studies of monoclonal antibody producing CHO cells. 2015 , 9, O8	1
1880	Evaluation of Proteomic Data: From Profiling to Network Analysis by Way of Biomarker Discovery. 2015 , 163-182	
1879	A maximum-likelihood approach to absolute protein quantification in mass spectrometry. 2015 ,	0
1878	Quantitative mass spectrometric profiling of cancer-cell proteomes derived from liquid and solid tumors. 2015 , e52435	5
1877	The proteome of mouse vestibular hair bundles over development. 2015 , 2, 150047	22
1876	Assessment of global proteome in LNCaP cells by 2D-RP/RP LC-MS/MS following sulforaphane exposure. 2015 , 9, 34-40	2
1875	Unravelling the proteome of degenerative human mitral valves. 2015 , 15, 2934-44	14
1874	Minimal sample requirement for highly multiplexed protein quantification in cell lines and tissues by PCT-SWATH mass spectrometry. 2015 , 15, 3711-21	36
1873	Priorities and trends in the study of proteins in eye research, 1924-2014. 2015 , 9, 1105-22	4
1872	Quantitative proteomics signature profiling based on network contextualization. 2015 , 10, 71	20
1871	Automated measurement of site-specific N-glycosylation occupancy with SWATH-MS. 2015 , 15, 2177-86	56
1870	Analysis of colorectal cancer glyco-secretome identifies laminin β 1 (LAMB1) as a potential serological biomarker for colorectal cancer. 2015 , 15, 3905-20	40
1869	Proteomic analysis of the kidney filtration barrier--Problems and perspectives. 2015 , 9, 1053-68	16
1868	A peptide resource for the analysis of Staphylococcus aureus in host-pathogen interaction studies. 2015 , 15, 3648-61	17
1867	Analytics for Metabolic Engineering. 2015 , 3, 135	59
1866	Low T3 State Is Correlated with Cardiac Mitochondrial Impairments after Ischemia Reperfusion Injury: Evidence from a Proteomic Approach. 2015 , 16, 26687-705	11
1865	Primary Structural Analysis of Cyclotides. 2015 , 113-154	2
1864	From raw data to biological discoveries: a computational analysis pipeline for mass spectrometry-based proteomics. 2015 , 26, 1820-6	11

1863	Advances in plant proteomics toward improvement of crop productivity and stress resistance. 2015 , 6, 209		77
1862	Quantifying ubiquitin signaling. 2015 , 58, 660-76		104
1861	Monitoring host responses to the gut microbiota. 2015 , 9, 1908-15		30
1860	Quantification of biopharmaceuticals and biomarkers in complex biological matrices: a comparison of liquid chromatography coupled to tandem mass spectrometry and ligand binding assays. 2015 , 12, 355-74		28
1859	Processing strategies and software solutions for data-independent acquisition in mass spectrometry. 2015 , 15, 964-80		105
1858	Development of a highly automated and multiplexed targeted proteome pipeline and assay for 112 rat brain synaptic proteins. 2015 , 15, 1202-14		11
1857	Psoriatic arthritis under a proteomic spotlight: application of novel technologies to advance diagnosis and management. 2015 , 17, 35		10
1856	Recent findings from the Human Proteome Project: opening the mass spectrometry toolbox to advance cancer diagnosis, surveillance and treatment. 2015 , 12, 279-93		14
1855	Chromatographic behavior of peptides containing oxidized methionine residues in proteomic LC-MS experiments: Complex tale of a simple modification. 2015 , 125, 131-9		14
1854	The human saliva proteome: overview and emerging methods for characterization. 2015 ,		
1853	Multiplexed peptide analysis using data-independent acquisition and Skyline. 2015 , 10, 887-903		132
1852	Targeted phosphoproteomics of insulin signaling using data-independent acquisition mass spectrometry. 2015 , 8, rs6		43
1851	Analysis of Major Histocompatibility Complex (MHC) Immunopeptidomes Using Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 3105-17	7.6	143
1850	Globally Optimized Targeted Mass Spectrometry: Reliable Metabolomics Analysis with Broad Coverage. 2015 , 87, 12355-62		71
1849	Microbial Proteome Profiling and Systems Biology: Applications to Mycobacterium tuberculosis. 2015 , 883, 235-54		9
1848	Systems analysis of methylerythritol-phosphate pathway flux in E. coli: insights into the role of oxidative stress and the validity of lycopene as an isoprenoid reporter metabolite. 2015 , 14, 193		21
1847	Do hypoxia/normoxia culturing conditions change the neuroregulatory profile of Wharton Jelly mesenchymal stem cell secretome?. 2015 , 6, 133		47
1846	In-depth evaluation of software tools for data-independent acquisition based label-free quantification. 2015 , 15, 3140-51		40

1845	SWATH enables precise label-free quantification on proteome scale. 2015 , 15, 1215-23		103
1844	An enhanced in vivo stable isotope labeling by amino acids in cell culture (SILAC) model for quantification of drug metabolism enzymes. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 750-60	7.6	6
1843	Emerging proteomic technologies for elucidating context-dependent cellular signaling events: A big challenge of tiny proportions. 2015 , 15, 1486-502		8
1842	Albumin decrease is associated with spontaneous preterm delivery within 48 h in women with threatened preterm labor. 2015 , 14, 457-66		6
1841	Neuroproteomics tools in clinical practice. 2015 , 1854, 705-17		25
1840	Data-independent MS/MS quantification of neuropeptides for determination of putative feeding-related neurohormones in microdialysate. 2015 , 6, 174-80		10
1839	Multiplexed quantification for data-independent acquisition. 2015 , 87, 2570-5		25
1838	Quantitative proteomic analysis of histone modifications. 2015 , 115, 2376-418		241
1837	Trans-Proteomic Pipeline, a standardized data processing pipeline for large-scale reproducible proteomics informatics. 2015 , 9, 745-54		222
1836	High-antibody-producing Chinese hamster ovary cells up-regulate intracellular protein transport and glutathione synthesis. 2015 , 14, 609-18		45
1835	MS/MS-based strategies for proteomic profiling of invasive cell structures. 2015 , 15, 272-86		14
1834	Dissecting the proteome of lipoproteins: New biomarkers for cardiovascular diseases?. 2015 , 7, 30-39		13
1833	Using data-independent, high-resolution mass spectrometry in protein biomarker research: perspectives and clinical applications. 2015 , 9, 307-21		130
1832	Mass spectrometry-based proteomic quest for diabetes biomarkers. 2015 , 1854, 519-27		34
1831	Coupling enrichment methods with proteomics for understanding and treating disease. 2015 , 9, 33-47		17
1830	Protein Biomarkers for Detecting Cancer: Molecular Screening. 2015 , 331-346.e5		
1829	Advances in high-resolution accurate mass spectrometry application to targeted proteomics. 2015 , 15, 880-90		78
1828	DIA-Umpire: comprehensive computational framework for data-independent acquisition proteomics. 2015 , 12, 258-64, 7 p following 264		371

1827	Building high-quality assay libraries for targeted analysis of SWATH MS data. 2015 , 10, 426-41		229
1826	Reproducible and consistent quantification of the <i>Saccharomyces cerevisiae</i> proteome by SWATH-mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 739-49	7.6	136
1825	Rapid mass spectrometric conversion of tissue biopsy samples into permanent quantitative digital proteome maps. 2015 , 21, 407-13		250
1824	Absolute Proteome Composition and Dynamics during Dormancy and Resuscitation of <i>Mycobacterium tuberculosis</i> . 2015 , 18, 96-108		155
1823	Biomarker Discovery and Verification of Esophageal Squamous Cell Carcinoma Using Integration of SWATH/MRM. 2015 , 14, 3793-803		35
1822	Proteome signatures--how are they obtained and what do they teach us?. 2015 , 99, 7417-31		10
1821	Targeting breast cancer-associated fibroblasts to improve anti-cancer therapy. 2015 , 24, 532-8		18
1820	Liquid chromatography, in combination with a quadrupole time-of-flight instrument, with sequential window acquisition of all theoretical fragment-ion spectra acquisition: validated quantification of 39 antidepressants in whole blood as part of a simultaneous screening and quantification procedure. 2015 , 87, 3294-301		39
1819	New Challenges and Perspectives in Hair Analysis. 2015 , 337-368		3
1818	Quantification of SAHA-Dependent Changes in Histone Modifications Using Data-Independent Acquisition Mass Spectrometry. 2015 , 14, 3252-62		36
1817	Targeted Data-Independent Acquisition and Mining Strategy for Trace Drug Metabolite Identification Using Liquid Chromatography Coupled with Tandem Mass Spectrometry. 2015 , 87, 7535-9		18
1816	Online Peptide fractionation using a multiphasic microfluidic liquid chromatography chip improves reproducibility and detection limits for quantitation in discovery and targeted proteomics. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 1708-19	7.6	25
1815	Citrullination of myofilament proteins in heart failure. 2015 , 108, 232-42		46
1814	Data-independent-acquisition mass spectrometry for identification of targeted-peptide site-specific modifications. 2015 , 407, 6627-35		15
1813	High resolution parallel reaction monitoring with electron transfer dissociation for middle-down proteomics. 2015 , 87, 8360-6		26
1812	Extending the limits of quantitative proteome profiling with data-independent acquisition and application to acetaminophen-treated three-dimensional liver microtissues. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 1400-10	7.6	471
1811	MS1 Peptide Ion Intensity Chromatograms in MS2 (SWATH) Data Independent Acquisitions. Improving Post Acquisition Analysis of Proteomic Experiments. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 2405-19	7.6	45
1810	Advances in high-resolution quantitative proteomics: implications for clinical applications. 2015 , 12, 489-98		28

1809	Oligonucleotide aptamers: emerging affinity probes for bioanalytical mass spectrometry and biomarker discovery. 2015 , 7, 7416-7430		8
1808	Evolution of Orbitrap Mass Spectrometry Instrumentation. 2015 , 8, 61-80		235
1807	The Impact II, a Very High-Resolution Quadrupole Time-of-Flight Instrument (QTOF) for Deep Shotgun Proteomics. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 2014-29	7.6	116
1806	Proteomics and autoimmune kidney disease. 2015 , 161, 23-30		9
1805	In-depth comparative proteomic analysis of yeast proteome using iTRAQ and SWATH based MS. 2015 , 11, 2135-43		27
1804	Translational value of liquid chromatography coupled with tandem mass spectrometry-based quantitative proteomics for in vitro-in vivo extrapolation of drug metabolism and transport and considerations in selecting appropriate techniques. 2015 , 11, 1357-69		21
1803	An LXR-NCOA5 gene regulatory complex directs inflammatory crosstalk-dependent repression of macrophage cholesterol efflux. 2015 , 34, 1244-58		26
1802	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. 2015 , 12, 725-31		86
1801	Improving spectral library search by redefining similarity measures. 2015 , 55, 963-71		4
1800	mzDB: a file format using multiple indexing strategies for the efficient analysis of large LC-MS/MS and SWATH-MS data sets. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 771-81	7.6	16
1799	Automated Validation of Results and Removal of Fragment Ion Interferences in Targeted Analysis of Data-independent Acquisition Mass Spectrometry (MS) using SWATHProphet. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 1411-8	7.6	26
1798	Large-Scale Targeted Proteomics Using Internal Standard Triggered-Parallel Reaction Monitoring (IS-PRM). <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 1630-44	7.6	124
1797	Simultaneous Quantification of Viral Antigen Expression Kinetics Using Data-Independent (DIA) Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 1361-72	7.6	18
1796	Using the canary genome to decipher the evolution of hormone-sensitive gene regulation in seasonal singing birds. 2015 , 16, 19		44
1795	Proteomics characterization of exosome cargo. 2015 , 87, 75-82		109
1794	Application guide for omics approaches to cell signaling. 2015 , 11, 387-97		52
1793	Plant Proteomics: Technologies and Applications. 2015 , 213-256		0
1792	Proteomics analysis of bodily fluids in pancreatic cancer. 2015 , 15, 2705-15		44

1791	SWATH analysis of the synaptic proteome in Alzheimer's disease. 2015 , 87, 1-12		39
1790	Efficient visualization of high-throughput targeted proteomics experiments: TAPIR. 2015 , 31, 2415-7		11
1789	Cell-secreted signals shape lymphoma identity. 2015 , 34, 81-91		4
1788	specL--an R/Bioconductor package to prepare peptide spectrum matches for use in targeted proteomics. 2015 , 31, 2228-31		9
1787	Multidimensional proteomics for cell biology. 2015 , 16, 269-80		288
1786	Challenges and developments in protein identification using mass spectrometry. 2015 , 69, 76-87		19
1785	Quantitative variability of 342 plasma proteins in a human twin population. 2015 , 11, 786		222
1784	Altered glycosylation in prostate cancer. 2015 , 126, 345-82		70
1783	Sequential Window Acquisition of all Theoretical Mass Spectra (SWATH) Analysis for Characterization and Quantification of Histone Post-translational Modifications. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 2420-8	7.6	76
1782	Evolutionary Engineering Improves Tolerance for Replacement Jet Fuels in <i>Saccharomyces cerevisiae</i> . 2015 , 81, 3316-25		38
1781	Global Phosphoproteomic Analysis of Human Skeletal Muscle Reveals a Network of Exercise-Regulated Kinases and AMPK Substrates. 2015 , 22, 922-35		233
1780	reSpect: software for identification of high and low abundance ion species in chimeric tandem mass spectra. 2015 , 26, 1837-47		12
1779	Multiplexed, Scheduled, High-Resolution Parallel Reaction Monitoring on a Full Scan QqTOF Instrument with Integrated Data-Dependent and Targeted Mass Spectrometric Workflows. 2015 , 87, 10222-9		72
1778	Progress in epigenetic histone modification analysis by mass spectrometry for clinical investigations. 2015 , 12, 499-517		42
1777	Quantitative proteogenomics of human pathogens using DIA-MS. 2015 , 129, 98-107		21
1776	Ranking Fragment Ions Based on Outlier Detection for Improved Label-Free Quantification in Data-Independent Acquisition LC-MS/MS. 2015 , 14, 4581-93		18
1775	Identification of a Set of Conserved Eukaryotic Internal Retention Time Standards for Data-independent Acquisition Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 2800-13	7.6	51
1774	Identification of Acetaminophen Adducts of Rat Liver Microsomal Proteins using 2D-LC-MS/MS. 2015 , 28, 2142-50		12

1773	Applications of targeted proteomics in systems biology and translational medicine. 2015 , 15, 3193-208	134
1772	Mass Spectrometric Analysis of Phospholipids by Target Discovery Approach. 2015 , 349-356	9
1771	Low Resolution Data-Independent Acquisition in an LTQ-Orbitrap Allows for Simplified and Fully Untargeted Analysis of Histone Modifications. 2015 , 87, 11448-54	43
1770	High resolution data-independent acquisition with electron transfer dissociation mass spectrometry: Multiplexed analysis of post-translationally modified proteins. 2015 , 390, 155-162	2
1769	Parallel Accumulation-Serial Fragmentation (PASEF): Multiplying Sequencing Speed and Sensitivity by Synchronized Scans in a Trapped Ion Mobility Device. 2015 , 14, 5378-87	161
1768	Reproducible quantitative proteotype data matrices for systems biology. 2015 , 26, 3926-31	33
1767	Proteomics discovery of radioresistant cancer biomarkers for radiotherapy. 2015 , 369, 289-97	17
1766	QPROT: Statistical method for testing differential expression using protein-level intensity data in label-free quantitative proteomics. 2015 , 129, 121-126	39
1765	Mass Spectrometry for Biomarker Development. 2015 , 17-48	1
1764	Advancing Urinary Protein Biomarker Discovery by Data-Independent Acquisition on a Quadrupole-Orbitrap Mass Spectrometer. 2015 , 14, 4752-62	81
1763	Group-DIA: analyzing multiple data-independent acquisition mass spectrometry data files. 2015 , 12, 1105-6	61
1762	Development of data representation standards by the human proteome organization proteomics standards initiative. 2015 , 22, 495-506	42
1761	Lessons from the proteomic study of osteoarthritis. 2015 , 12, 433-43	13
1760	mapDIA: Preprocessing and statistical analysis of quantitative proteomics data from data independent acquisition mass spectrometry. 2015 , 129, 108-120	101
1759	Simultaneous quantitative determination, identification and qualitative screening of pesticides in fruits and vegetables using LC-Q-OrbitrapMS. 2015 , 32, 1628-36	67
1758	The Use of Variable Q1 Isolation Windows Improves Selectivity in LC-SWATH-MS Acquisition. 2015 , 14, 4359-71	114
1757	Global Metabonomic and Proteomic Analysis of Human Conjunctival Epithelial Cells (IOBA-NHC) in Response to Hyperosmotic Stress. 2015 , 14, 3982-95	22
1756	PredRet: prediction of retention time by direct mapping between multiple chromatographic systems. 2015 , 87, 9421-8	78

1755	Peptide-Centric Proteome Analysis: An Alternative Strategy for the Analysis of Tandem Mass Spectrometry Data. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 2301-7	7.6	104
1754	YPED: an integrated bioinformatics suite and database for mass spectrometry-based proteomics research. 2015 , 13, 25-35		13
1753	Transformative Impact of Proteomics on Cardiovascular Health and Disease: A Scientific Statement From the American Heart Association. 2015 , 132, 852-72		112
1752	Large-scale models of signal propagation in human cells derived from discovery phosphoproteomic data. 2015 , 6, 8033		61
1751	Bioanalytical approaches for characterizing catabolism of antibody-drug conjugates. 2015 , 7, 1583-604		26
1750	Gasdermin D is an executor of pyroptosis and required for interleukin-1 β secretion. 2015 , 25, 1285-98		959
1749	Short GeLC-SWATH: a fast and reliable quantitative approach for proteomic screenings. 2015 , 15, 757-62		53
1748	The role of protein and peptide separation before mass spectrometry analysis in clinical proteomics. 2015 , 1381, 1-12		51
1747	Unraveling the exercise-related proteome signature in heart. 2015 , 110, 454		25
1746	Stressor-induced proteome alterations in zebrafish: a meta-analysis of response patterns. 2015 , 159, 1-12		17
1745	Identifying novel biomarkers through data mining-a realistic scenario?. 2015 , 9, 437-43		14
1744	The application of targeted mass spectrometry-based strategies to the detection and localization of post-translational modifications. 2015 , 34, 595-626		24
1743	Applying 'Sequential Windowed Acquisition of All Theoretical Fragment Ion Mass Spectra' (SWATH) for systematic toxicological analysis with liquid chromatography-high-resolution tandem mass spectrometry. 2015 , 407, 405-14		93
1742	Tools for monitoring system suitability in LC MS/MS centric proteomic experiments. 2015 , 15, 891-902		28
1741	Whole cell, label free protein quantitation with data independent acquisition: quantitation at the MS2 level. 2015 , 15, 16-24		15
1740	Data processing has major impact on the outcome of quantitative label-free LC-MS analysis. 2015 , 14, 676-87		24
1739	State of the art of 2D DIGE. 2015 , 9, 277-88		79
1738	Current approaches and challenges for the metabolite profiling of complex natural extracts. 2015 , 1382, 136-64		332

1737	DIANA--algorithmic improvements for analysis of data-independent acquisition MS data. 2015 , 31, 555-62	65
1736	Toward an integrated pipeline for protein biomarker development. 2015 , 1854, 677-86	41
1735	SWATH-MS: Data Acquisition and Analysis. 2016 , 161-173	3
1734	Mass Spectrometry-Based Metabolomic and Proteomic Strategies in Organic Acidemias. 2016 , 2016, 9210408	24
1733	Human Pituitary Adenoma Proteomics: New Progresses and Perspectives. 2016 , 7, 54	18
1732	Lipidomics-Reshaping the Analysis and Perception of Type 2 Diabetes. 2016 , 17,	35
1731	Personalized Proteomics: The Future of Precision Medicine. 2016 , 4,	67
1730	Phosphoproteome Discovery in Human Biological Fluids. 2016 , 4,	10
1729	SWATH2stats: An R/Bioconductor Package to Process and Convert Quantitative SWATH-MS Proteomics Data for Downstream Analysis Tools. 2016 , 11, e0153160	31
1728	The Chloroplast Proteome Changes in Response to Protoplastation. 2016 , 7, 1661	11
1727	SWATH-MS Quantitative Analysis of Proteins in the Rice Inferior and Superior Spikelets during Grain Filling. 2016 , 7, 1926	14
1726	Technical advances in proteomics: new developments in data-independent acquisition. 2016 , 5,	119
1725	Multi-mode acquisition (MMA): An MS/MS acquisition strategy for maximizing selectivity, specificity and sensitivity of DIA product ion spectra. 2016 , 16, 2284-301	10
1724	A hybrid retention time alignment algorithm for SWATH-MS data. 2016 , 16, 2272-83	4
1723	Meet the neighbors: Mapping local protein interactomes by proximity-dependent labeling with BioID. 2016 , 16, 2503-2518	98
1722	Proteogenomics of rare taxonomic phyla: A prospective treasure trove of protein coding genes. 2016 , 16, 226-40	11
1721	Large-scale multiplex absolute protein quantification of drug-metabolizing enzymes and transporters in human intestine, liver, and kidney microsomes by SWATH-MS: Comparison with MRM/SRM and HR-MRM/PRM. 2016 , 16, 2106-17	93
1720	Assessment of SRM, MRM(3) , and DIA for the targeted analysis of phosphorylation dynamics in non-small cell lung cancer. 2016 , 16, 2193-205	38

1719	SAINTq: Scoring protein-protein interactions in affinity purification - mass spectrometry experiments with fragment or peptide intensity data. 2016 , 16, 2238-45	23
1718	Dynamic reorganization of photosystem II supercomplexes in response to variations in light intensities. 2016 , 1857, 1651-60	40
1717	Common errors in mass spectrometry-based analysis of post-translational modifications. 2016 , 16, 700-14	75
1716	Application of wide selected-ion monitoring data-independent acquisition to identify tomato fruit proteins regulated by the CUTIN DEFICIENT2 transcription factor. 2016 , 16, 2081-94	19
1715	Multiplexed data independent acquisition (MSX-DIA) applied by high resolution mass spectrometry improves quantification quality for the analysis of histone peptides. 2016 , 16, 2095-105	18
1714	Targeted proteomics coming of age - SRM, PRM and DIA performance evaluated from a core facility perspective. 2016 , 16, 2183-92	27
1713	A reference library of peripheral blood mononuclear cells for SWATH-MS analysis. 2016 , 10, 760-4	10
1712	Review on proteomics for food authentication. 2016 , 147, 212-225	110
1711	Advances in targeted proteomics and applications to biomedical research. 2016 , 16, 2160-82	134
1710	Rearrangement of mitochondrial pyruvate dehydrogenase subunit dihydrolipoamide dehydrogenase protein-protein interactions by the MDM2 ligand nutlin-3. 2016 , 16, 2327-44	12
1709	Untargeted, spectral library-free analysis of data-independent acquisition proteomics data generated using Orbitrap mass spectrometers. 2016 , 16, 2257-71	45
1708	Identifying Urinary and Serum Exosome Biomarkers for Radiation Exposure Using a Data Dependent Acquisition and SWATH-MS Combined Workflow. 2016 , 96, 566-77	23
1707	Metaproteomic data analysis at a glance: advances in computational microbial community proteomics. 2016 , 13, 757-69	44
1706	Evaluation of sample extraction methods for proteomics analysis of green algae <i>Chlorella vulgaris</i> . 2016 , 37, 1270-6	12
1705	Exploring novel paths towards protein signatures of chronic pain. 2016 , 12,	1
1704	Modular Assembly of the Bacterial Large Ribosomal Subunit. 2016 , 167, 1610-1622.e15	97
1703	The Advent of Mass Spectrometry-Based Proteomics in Systems Biology Research. 2016 , 166-176	0
1702	A proteomic evaluation of urinary changes associated with cardiopulmonary bypass. 2016 , 13, 17	6

1701	Bursaphelenchus xylophilus and B. mucronatus secretomes: a comparative proteomic analysis. 2016 , 6, 39007		20
1700	Qualification and Verification of Protein Biomarker Candidates. 2016 , 919, 493-514		13
1699	Protocol for Standardizing High-to-Moderate Abundance Protein Biomarker Assessments Through an MRM-with-Standard-Peptides Quantitative Approach. 2016 , 919, 515-530		12
1698	Pooled-matrix protein interaction screens using Barcode Fusion Genetics. 2016 , 12, 863		59
1697	SWATH-MS dataset of heat-shock treated embryos. 2016 , 9, 991-995		1
1696	Undiscovered Physiology of Transcript and Protein Networks. 2016 , 6, 1851-1872		
1695	Mass Spectrometry Applied to Bottom-Up Proteomics: Entering the High-Throughput Era for Hypothesis Testing. 2016 , 9, 449-72		202
1694	Unraveling Mesenchymal Stem Cells' Dynamic Secretome Through Nontargeted Proteomics Profiling. 2016 , 1416, 521-49		15
1693	Data Independent Acquisition analysis in ProHits 4.0. 2016 , 149, 64-68		37
1692	Dinosaur: A Refined Open-Source Peptide MS Feature Detector. 2016 , 15, 2143-51		32
1691	Current state of the art for enhancing urine biomarker discovery. 2016 , 13, 609-26		60
1690	Nested data independent MS/MS acquisition. 2016 , 408, 5031-40		6
1689	From Correlation to Causality: Statistical Approaches to Learning Regulatory Relationships in Large-Scale Biomolecular Investigations. 2016 , 15, 683-90		12
1688	DeMix-Q: Quantification-Centered Data Processing Workflow. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 1467-78	7.6	50
1687	Immunology by numbers: quantitation of antigen presentation completes the quantitative milieu of systems immunology!. 2016 , 40, 88-95		18
1686	A targeted metabolomics assay for cardiac metabolism and demonstration using a mouse model of dilated cardiomyopathy. 2016 , 12, 59		25
1685	Optimizing the SWATH-MS-workflow for label-free proteomics. 2016 , 145, 137-140		18
1684	Standardized Profiling of The Membrane-Enriched Proteome of Mouse Dorsal Root Ganglia (DRG) Provides Novel Insights Into Chronic Pain. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 2152-68	7.6	21

1683	NAD ⁺ repletion improves mitochondrial and stem cell function and enhances life span in mice. 2016 , 352, 1436-43		645
1682	Advances in mass spectrometry-based cancer research and analysis: from cancer proteomics to clinical diagnostics. 2016 , 13, 593-607		12
1681	On the Dependency of Cellular Protein Levels on mRNA Abundance. 2016 , 165, 535-50		1235
1680	A Structures for Lossless Ion Manipulations (SLIM) Module for Collision Induced Dissociation. 2016 , 27, 1285-8		12
1679	Reproducible Tissue Homogenization and Protein Extraction for Quantitative Proteomics Using MicroPestle-Assisted Pressure-Cycling Technology. 2016 , 15, 1821-9		34
1678	Characterization of the porcine seminal plasma proteome comparing ejaculate portions. 2016 , 142, 15-23		60
1677	High-throughput proteomics and the fight against pathogens. 2016 , 12, 2373-84		11
1676	SWATH Mass Spectrometry Performance Using Extended Peptide MS/MS Assay Libraries. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 2501-14	7.6	69
1675	Effects of Lipid-Lowering Drugs on Vancomycin Susceptibility of Mycobacteria. 2016 , 60, 6193-9		27
1674	Loss of Pink1 modulates synaptic mitochondrial bioenergetics in the rat striatum prior to motor symptoms: concomitant complex I respiratory defects and increased complex II-mediated respiration. 2016 , 10, 1205-1217		17
1673	Proteomics discovery of chemoresistant biomarkers for ovarian cancer therapy. 2016 , 13, 905-915		5
1672	Current Proteomic Methods to Investigate the Dynamics of Histone Turnover in the Central Nervous System. 2016 , 574, 331-354		3
1671	Developments for Personalized Medicine of Lung Cancer Subtypes: Mass Spectrometry-Based Clinical Proteogenomic Analysis of Oncogenic Mutations. 2016 , 926, 115-137		8
1670	Advances in proteomic study of cardiac amyloidosis: progress and potential. 2016 , 13, 1017-1027		3
1669	A multicenter study benchmarks software tools for label-free proteome quantification. 2016 , 34, 1130-1136		202
1668	Extensive dataset of boar seminal plasma proteome displaying putative reproductive functions of identified proteins. 2016 , 8, 1370-3		6
1667	TRIC: an automated alignment strategy for reproducible protein quantification in targeted proteomics. 2016 , 13, 777-83		122
1666	Systems-level Proteomics of Two Ubiquitous Leaf Commensals Reveals Complementary Adaptive Traits for Phyllosphere Colonization. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 3256-3269	7.6	28

1665	SWATH acquisition mode for drug metabolism and metabolomics investigations. 2016 , 8, 1735-50	35
1664	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. 2016 , 15, 3961-3970	130
1663	Effect of peptide assay library size and composition in targeted data-independent acquisition-MS analyses. 2016 , 16, 2221-37	24
1662	Advancing Clinical Proteomics via Analysis Based on Biological Complexes: A Tale of Five Paradigms. 2016 , 15, 3167-79	22
1661	Protein Z: A putative novel biomarker for early detection of ovarian cancer. 2016 , 138, 2984-92	35
1660	Proteomics, biomarkers, and HIV-1: A current perspective. 2016 , 10, 110-25	12
1659	Regulation of highly homologous major urinary proteins in house mice quantified with label-free proteomic methods. 2016 , 12, 3005-16	19
1658	Systematic evaluation of data-independent acquisition for sensitive and reproducible proteomics-a prototype design for a single injection assay. 2016 , 51, 1-11	23
1657	Targeted proteomic assays for the verification of global proteomics insights. 2016 , 13, 897-899	7
1656	Advanced Precursor Ion Selection Algorithms for Increased Depth of Bottom-Up Proteomic Profiling. 2016 , 15, 3563-3573	9
1655	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. 2016 , 13, 741-8	337
1654	Applications and Developments in Targeted Proteomics: From SRM to DIA/SWATH. 2016 , 16, 2065-7	48
1653	CCAN Assembly Configures Composite Binding Interfaces to Promote Cross-Linking of Ndc80 Complexes at the Kinetochores. 2016 , 26, 2370-8	43
1652	Identification and Quantification of Histone PTMs Using High-Resolution Mass Spectrometry. 2016 , 574, 3-29	24
1651	Comparing Multiple Reaction Monitoring and Sequential Window Acquisition of All Theoretical Mass Spectra for the Relative Quantification of Barley Gluten in Selectively Bred Barley Lines. 2016 , 88, 9127-35	26
1650	SWATH-MS data of proteome dynamics during embryogenesis. 2016 , 9, 771-775	4
1649	Mass-spectrometric exploration of proteome structure and function. 2016 , 537, 347-55	1070
1648	Untargeted Metabolomics Strategies-Challenges and Emerging Directions. 2016 , 27, 1897-1905	405

1647	MetDIA: Targeted Metabolite Extraction of Multiplexed MS/MS Spectra Generated by Data-Independent Acquisition. 2016 , 88, 8757-64	71
1646	Training in metabolomics research. I. Designing the experiment, collecting and extracting samples and generating metabolomics data. 2016 , 51, 461-75	45
1645	Human SRMATlas: A Resource of Targeted Assays to Quantify the Complete Human Proteome. 2016 , 166, 766-778	236
1644	Discovering Regulated Metabolite Families in Untargeted Metabolomics Studies. 2016 , 88, 8082-90	56
1643	Application of Fragment Ion Information as Further Evidence in Probabilistic Compound Screening Using Bayesian Statistics and Machine Learning: A Leap Toward Automation. 2016 , 88, 7705-14	7
1642	Robust Label-free, Quantitative Profiling of Circulating Plasma Microparticle (MP) Associated Proteins. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 3640-3652	7.6 17
1641	Understanding the dimorphic lifestyles of human gastric pathogen <i>Helicobacter pylori</i> using the SWATH-based proteomics approach. 2016 , 6, 26784	29
1640	Vitamin D Promotes Protein Homeostasis and Longevity via the Stress Response Pathway Genes <i>skn-1</i> , <i>ire-1</i> , and <i>xbp-1</i> . 2016 , 17, 1227-1237	38
1639	Proteomics of thyroid tumours provides new insights into their molecular composition and changes associated with malignancy. 2016 , 6, 23660	28
1638	Proteome-wide association studies identify biochemical modules associated with a wing-size phenotype in <i>Drosophila melanogaster</i> . 2016 , 7, 12649	32
1637	Optimizing of a protein extraction method for <i>Mycobacterium tuberculosis</i> proteome analysis using mass spectrometry. 2016 , 131, 144-147	13
1636	The Deimination of Arginine to Citrulline. 2016 , 275-306	1
1635	Proteomic Studies of HIV-1 and Its Posttranslational Modifications. 2016 , 77-97	
1634	Computational Methods in Mass Spectrometry-Based Proteomics. 2016 , 939, 63-89	7
1633	Comprehensive and quantitative proteomic analyses of zebrafish plasma reveals conserved protein profiles between genders and between zebrafish and human. 2016 , 6, 24329	46
1632	Fast MS/MS acquisition without dynamic exclusion enables precise and accurate quantification of proteome by MS/MS fragment intensity. 2016 , 6, 26392	5
1631	Advanced Mass Spectrometric Technologies as the Key in Novel Drug Development Linked with Clinical Proteomics. 2016 , 64, 65-69	
1630	YphC and YsxC GTPases assist the maturation of the central protuberance, GTPase associated region and functional core of the 50S ribosomal subunit. 2016 , 44, 8442-55	23

1629	Integrating highly quantitative proteomics and genome-scale metabolic modeling to study pH adaptation in the human pathogen. 2016 , 2, 16017	20
1628	Fuzzy-FishNET: a highly reproducible protein complex-based approach for feature selection in comparative proteomics. 2016 , 9, 67	7
1627	Characterisation of the circulating acellular proteome of healthy sheep using LC-MS/MS-based proteomics analysis of serum. 2016 , 15, 11	5
1626	Analysis of dynamic protein carbonylation in rice embryo during germination through AP-SWATH. 2016 , 16, 989-1000	25
1625	Analysis of Drosophila melanogaster proteome dynamics during embryonic development by a combination of label-free proteomics approaches. 2016 , 16, 2068-80	17
1624	Use of captive spray ionization to increase throughput of the data-independent acquisition technique PAcFIC. 2016 , 30, 1101-7	5
1623	Systems proteomics of liver mitochondria function. 2016 , 352, aad0189	193
1622	Urinary proteomics and metabolomics studies to monitor bladder health and urological diseases. 2016 , 16, 11	24
1621	Differential quantification of isobaric phosphopeptides using data-independent acquisition mass spectrometry. 2016 , 12, 2385-8	7
1620	Liver: Phenotypic and genetic variance: a systems approach to the liver. 2016 , 13, 439-40	6
1619	Pseudo isobaric peptide termini labelling for relative proteome quantification by SWATH MS acquisition. 2016 , 141, 4912-8	9
1618	Clinical translation of MS-based, quantitative plasma proteomics: status, challenges, requirements, and potential. 2016 , 13, 673-84	31
1617	Integrating Networks and Proteomics: Moving Forward. 2016 , 34, 951-959	24
1616	High-performance targeted mass spectrometry with precision data-independent acquisition reveals site-specific glycosylation macroheterogeneity. 2016 , 510, 106-113	12
1615	Design principles for clinical network-based proteomics. 2016 , 21, 1130-8	17
1614	Neisseria meningitidis Lacking the Major Porins PorA and PorB Is Viable and Modulates Apoptosis and the Oxidative Burst of Neutrophils. 2016 , 15, 2356-65	16
1613	BatMass: a Java Software Platform for LC-MS Data Visualization in Proteomics and Metabolomics. 2016 , 15, 2500-9	28
1612	A Comprehensive Investigation toward the Indicative Proteins of Bladder Cancer in Urine: From Surveying Cell Secretomes to Verifying Urine Proteins. 2016 , 15, 2164-77	11

1611	The use of proteases complementary to trypsin to probe isoforms and modifications. 2016 , 16, 715-28	20
1610	High-precision iRT prediction in the targeted analysis of data-independent acquisition and its impact on identification and quantitation. 2016 , 16, 2246-56	80
1609	Parallel reaction monitoring using quadrupole-Orbitrap mass spectrometer: Principle and applications. 2016 , 16, 2146-59	165
1608	Proteomics approaches to understanding mitogen-activated protein kinase inhibitor resistance in melanoma. 2016 , 28, 172-9	6
1607	Global discovery of protein kinases and other nucleotide-binding proteins by mass spectrometry. 2016 , 35, 601-19	17
1606	Early Expression of Parkinson's Disease-Related Mitochondrial Abnormalities in PINK1 Knockout Rats. 2016 , 53, 171-186	56
1605	Target identification of natural and traditional medicines with quantitative chemical proteomics approaches. 2016 , 162, 10-22	76
1604	Trans-Omics: How To Reconstruct Biochemical Networks Across Multiple 'Omic' Layers. 2016 , 34, 276-290	162
1603	A Quantitative Proteomic Analysis of In Vitro Assembled Chromatin. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 945-59	7.6 9
1602	Testing Suitability of Cell Cultures for SILAC-Experiments Using SWATH-Mass Spectrometry. 2016 , 1394, 101-108	5
1601	New era of integrated cancer biomarker discovery using reverse-phase protein arrays. 2016 , 31, 35-45	27
1600	Neonatal mitochondrial abnormalities due to PINK1 deficiency: Proteomics reveals early changes relevant to Parkinson's disease. 2016 , 6, 428-32	8
1599	Bottom-Up Proteomics (2013-2015): Keeping up in the Era of Systems Biology. 2016 , 88, 95-121	45
1598	MaRaCluster: A Fragment Rarity Metric for Clustering Fragment Spectra in Shotgun Proteomics. 2016 , 15, 713-20	26
1597	Mining Large Scale Tandem Mass Spectrometry Data for Protein Modifications Using Spectral Libraries. 2016 , 15, 721-31	19
1596	Chemoproteomic profiling of protein modifications by lipid-derived electrophiles. 2016 , 30, 37-45	10
1595	Combinatorial Histone Acetylation Patterns Are Generated by Motif-Specific Reactions. 2016 , 2, 49-58	11
1594	Plug-and-play analysis of the human phosphoproteome by targeted high-resolution mass spectrometry. 2016 , 13, 431-4	77

1593	A Biologist's Field Guide to Multiplexed Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 1489-97	7.6	44
1592	HIV-1 transgenic rats display mitochondrial abnormalities consistent with abnormal energy generation and distribution. 2016 , 22, 564-574		27
1591	Population-specific renal proteomes of marine and freshwater three-spined sticklebacks. 2016 , 135, 112-131		10
1590	Systems Proteomics View of the Endogenous Human Claudin Protein Family. 2016 , 15, 339-59		17
1589	Pan-proteomics, a concept for unifying quantitative proteome measurements when comparing closely-related bacterial strains. 2016 , 13, 355-65		14
1588	Sperm proteomics: potential impact on male infertility treatment. 2016 , 13, 285-96		21
1587	Quantitation and Identification of Thousands of Human Proteoforms below 30 kDa. 2016 , 15, 976-82		73
1586	Methods and applications of absolute protein quantification in microbial systems. 2016 , 136, 222-33		14
1585	Analytical applications of partitioning in aqueous two-phase systems: Exploring protein structural changes and protein-partner interactions in vitro and in vivo by solvent interaction analysis method. 2016 , 1864, 622-44		32
1584	Proteomic profiling predicts drug response to novel targeted anticancer therapeutics. 2016 , 13, 411-20		5
1583	Discovery of potential protein biomarkers of lung adenocarcinoma in bronchoalveolar lavage fluid by SWATH MS data-independent acquisition and targeted data extraction. 2016 , 138, 106-14		59
1582	Protein Quality Assessment on Saliva Samples for Biobanking Purposes. 2016 , 14, 289-97		12
1581	The secretome signature of malignant mesothelioma cell lines. 2016 , 145, 3-10		18
1580	Human Leukocyte Antigen (HLA) B27 Allotype-Specific Binding and Candidate Arthritogenic Peptides Revealed through Heuristic Clustering of Data-independent Acquisition Mass Spectrometry (DIA-MS) Data. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 1867-76	7.6	26
1579	Developments of mass spectrometry-based technologies for effective drug development linked with clinical proteomes. 2016 , 31, 3-11		7
1578	Large-scale inference of protein tissue origin in gram-positive sepsis plasma using quantitative targeted proteomics. 2016 , 7, 10261		71
1577	Opening a SWATH Window on Posttranslational Modifications: Automated Pursuit of Modified Peptides. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 1151-63	7.6	37
1576	Emerging Proteomic Technologies Provide Enormous and Underutilized Potential for Brain Cancer Research. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 362-7	7.6	3

1575	Generating Sample-Specific Databases for Mass Spectrometry-Based Proteomic Analysis by Using RNA Sequencing. 2016 , 1394, 219-232		4
1574	Autoimmune diseases - connecting risk alleles with molecular traits of the immune system. 2016 , 17, 160-74		124
1573	Proteomic Biomarker Discovery in 1000 Human Plasma Samples with Mass Spectrometry. 2016 , 15, 389-99		67
1572	Adaptation of Skyline for Targeted Lipidomics. 2016 , 15, 291-301		33
1571	The biochemistry of blister fluid from pediatric burn injuries: proteomics and metabolomics aspects. 2016 , 13, 35-53		11
1570	The clinical impact of recent advances in LC-MS for cancer biomarker discovery and verification. 2016 , 13, 99-114		37
1569	High resolution mass spectrometry for structural identification of metabolites in metabolomics. 2016 , 12, 1		60
1568	Peptide-level Robust Ridge Regression Improves Estimation, Sensitivity, and Specificity in Data-dependent Quantitative Label-free Shotgun Proteomics. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 657-68	7.6	40
1567	Genomic variability and protein species - Improving sequence coverage for proteogenomics. 2016 , 134, 25-36		8
1566	Phosphoproteomics in the Age of Rapid and Deep Proteome Profiling. 2016 , 88, 74-94		159
1565	Alzheimer's as a Systems-Level Disease Involving the Interplay of Multiple Cellular Networks. 2016 , 1303, 3-48		24
1564	Advanced DNA- and Protein-based Methods for the Detection and Investigation of Food Allergens. 2016 , 56, 2511-2542		61
1563	Protein complex analysis: From raw protein lists to protein interaction networks. 2017 , 36, 600-614		15
1562	Diabetic retinopathy: Proteomic approaches to help the differential diagnosis and to understand the underlying molecular mechanisms. 2017 , 150, 351-358		15
1561	A timeline of stable isotopes and mass spectrometry in the life sciences. 2017 , 36, 58-85		47
1560	Algorithms and design strategies towards automated glycoproteomics analysis. 2017 , 36, 475-498		68
1559	Applying proteomics to tick vaccine development: where are we?. 2017 , 14, 211-221		15
1558	Peptide Selection for Targeted Protein Quantitation. 2017 , 16, 1376-1380		16

1557	Accelerating the search for the missing proteins in the human proteome. 2017 , 8, 14271		73
1556	Principles of 60S ribosomal subunit assembly emerging from recent studies in yeast. 2017 , 474, 195-214		55
1555	Deciphering lymphoma pathogenesis via state-of-the-art mass spectrometry-based quantitative proteomics. 2017 , 1047, 2-14		0
1554	Feature selection in clinical proteomics: with great power comes great reproducibility. 2017 , 22, 912-918		24
1553	Targeted Proteomics for Multiplexed Verification of Markers of Colorectal Tumorigenesis. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 407-427	7.6	29
1552	An integrated transcriptomics-guided genome-wide promoter analysis and next-generation proteomics approach to mine factor(s) regulating cellular differentiation. 2017 , 24, 143-157		9
1551	Comprehensive mass spectrometry based biomarker discovery and validation platform as applied to diabetic kidney disease. 2017 , 14, 1-10		22
1550	Predicting Electrophoretic Mobility of Tryptic Peptides for High-Throughput CZE-MS Analysis. 2017 , 89, 2000-2008		33
1549	Why proteomics is not the new genomics and the future of mass spectrometry in cell biology. 2017 , 216, 21-24		19
1548	Contribution of Mass Spectrometry-Based Proteomics to the Understanding of TNF- α Signaling. 2017 , 16, 14-33		9
1547	A Golden Age for Working with Public Proteomics Data. 2017 , 42, 333-341		65
1546	A review on mass spectrometry-based quantitative proteomics: Targeted and data independent acquisition. 2017 , 964, 7-23		190
1545	DIA is not a new mass spectrometry acquisition method. 2017 , 17, 1700017		9
1544	Glycation inhibitors extend yeast chronological lifespan by reducing advanced glycation end products and by back regulation of proteins involved in mitochondrial respiration. 2017 , 156, 104-112		20
1543	SWATH-based proteomics identified carbonic anhydrase 2 as a potential diagnosis biomarker for nasopharyngeal carcinoma. 2017 , 7, 41191		22
1542	SWATH-MS as a tool for biomarker discovery: From basic research to clinical applications. 2017 , 17, 1600278		97
1541	Comprehensive and accurate tracking of carbon origin of LC-tandem mass spectrometry collisional fragments for C-MFA. 2017 , 409, 2309-2326		20
1540	Proteome Analysis of Phototrophic Adaptation. 2017 , 225-270		1

1539	Recent mass spectrometry-based proteomics for biomarker discovery in lung cancer, COPD, and asthma. 2017 , 14, 373-386		36
1538	Post-transcriptional regulation of fruit ripening and disease resistance in tomato by the vacuolar protease SLVPE3. 2017 , 18, 47		34
1537	Molecular Techniques [Genomics and Proteomics. 2017 , 325-354		
1536	Quantitative Proteomic Analysis of Human Airway Cilia Identifies Previously Uncharacterized Proteins of High Abundance. 2017 , 16, 1579-1592		37
1535	Missing Value Monitoring Enhances the Robustness in Proteomics Quantitation. 2017 , 16, 1719-1727		8
1534	and Proteome Analysis of Human Immunodeficiency Virus (HIV)-1-infected, Human CD4 T Cells. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, S108-S123	7.6	15
1533	Comprehensive Metaboproteomics of Burkitt's and Diffuse Large B-Cell Lymphoma Cell Lines and Primary Tumor Tissues Reveals Distinct Differences in Pyruvate Content and Metabolism. 2017 , 16, 1105-1120		15
1532	msPurity: Automated Evaluation of Precursor Ion Purity for Mass Spectrometry-Based Fragmentation in Metabolomics. 2017 , 89, 2432-2439		28
1531	Mass spectrometry for the discovery of biomarkers of sepsis. 2017 , 13, 648-664		52
1530	Two-dimensional mass spectrometry in a linear ion trap, an in silico model. 2017 , 31, 674-684		15
1529	Automated SWATH Data Analysis Using Targeted Extraction of Ion Chromatograms. 2017 , 1550, 289-307		23
1528	Relative protein quantification and accessible biology in lung tumor proteomes from four LC-MS/MS discovery platforms. 2017 , 17, 1600300		13
1527	Generation of High-Quality SWATH Acquisition Data for Label-free Quantitative Proteomics Studies Using TripleTOF Mass Spectrometers. 2017 , 1550, 223-233		39
1526	Customized Consensus Spectral Library Building for Untargeted Quantitative Metabolomics Analysis with Data Independent Acquisition Mass Spectrometry and MetaboDIA Workflow. 2017 , 89, 4897-4906		27
1525	An IonStar Experimental Strategy for MS1 Ion Current-Based Quantification Using Ultrahigh-Field Orbitrap: Reproducible, In-Depth, and Accurate Protein Measurement in Large Cohorts. 2017 , 16, 2445-2456		39
1524	Overexpression of the regulatory subunit of glutamate-cysteine ligase enhances monoclonal antibody production in CHO cells. 2017 , 114, 1825-1836		15
1523	Targeted mass spectrometry: An emerging powerful approach to unblock the bottleneck in phosphoproteomics. 2017 , 1055-1056, 29-38		21
1522	Identification of Immunogenic Epitopes by MS/MS. 2017 , 23, 102-107		17

1521	Current trends in quantitative proteomics - an update. 2017 , 52, 319-341	51
1520	Microbial glycoproteomics. 2017 , 44, 143-150	6
1519	Dynamic and temporal assessment of human dried blood spot MS/MS shotgun lipidomics analysis. 2017 , 14, 28	23
1518	Practical application of in silico fragmentation based residue screening with ion mobility high-resolution mass spectrometry. 2017 , 31, 1147-1157	15
1517	Variable-Velocity Traveling-Wave Ion Mobility Separation Enhancing Peak Capacity for Data-Independent Acquisition Proteomics. 2017 , 89, 5669-5672	45
1516	Clinical applications of quantitative proteomics using targeted and untargeted data-independent acquisition techniques. 2017 , 14, 419-429	74
1515	Development of data-independent acquisition workflows for metabolomic analysis on a quadrupole-orbitrap platform. 2017 , 164, 128-136	46
1514	Electron Transfer Dissociation of All Ions at All Times, MS, in a Quadrupole Time-of-Flight (Q-ToF) Mass Spectrometer. 2017 , 28, 384-388	7
1513	Proteomic explorations of autism spectrum disorder. 2017 , 10, 1460-1469	10
1512	Improvements in Mass Spectrometry Assay Library Generation for Targeted Proteomics. 2017 , 16, 2384-2392	14
1511	Definition of a RACK1 Interaction Network in Using SWATH-MS. 2017 , 7, 2249-2258	5
1510	Application of SWATH Proteomics to Mouse Biology. 2017 , 7, 130-143	7
1509	Epithelial proteome profiling suggests the essential role of interferon-inducible proteins in patients with allergic rhinitis. 2017 , 140, 1288-1298	15
1508	Carbonylated Proteins and Their Metabolic Regulation. 2017 , 110-130	
1507	'Omic' Approaches to Study Uropathogenic Escherichia coli Virulence. 2017 , 25, 729-740	14
1506	SWATH-based quantitative proteomics reveals the mechanism of enhanced Bombyx mori nucleopolyhedrovirus-resistance in silkworm reared on UV-B treated mulberry leaves. 2017 , 17, 1600383	4
1505	A Class of Environmental and Endogenous Toxins Induces BRCA2 Haploinsufficiency and Genome Instability. 2017 , 169, 1105-1118.e15	93
1504	Quantitative proteomics: challenges and opportunities in basic and applied research. 2017 , 12, 1289-1294	133

1503	BioInfra.Prot: A comprehensive proteomics workflow including data standardization, protein inference, expression analysis and data publication. 2017 , 261, 116-125		17
1502	Inference and quantification of peptidofoms in large sample cohorts by SWATH-MS. 2017 , 35, 781-788		85
1501	Mining the fecal proteome: from biomarkers to personalised medicine. 2017 , 14, 445-459		32
1500	EDTA-functionalized magnetic nanoparticles: A suitable platform for the analysis of low abundance urinary proteins. 2017 , 170, 81-88		0
1499	Quantitative proteomics by SWATH-MS reveals sophisticated metabolic reprogramming in hepatocellular carcinoma tissues. 2017 , 7, 45913		43
1498	SWATH-ID: An instrument method which combines identification and quantification in a single analysis. 2017 , 17, e1500522		16
1497	A modular and adaptive mass spectrometry-based platform for support of bioprocess development toward optimal host cell protein clearance. 2017 , 9, 654-663		35
1496	Impact of different nitrogen sources on the growth of <i>Arthrospira</i> sp. PCC 8005 under batch and continuous cultivation - A biochemical, transcriptomic and proteomic profile. 2017 , 237, 78-88		19
1495	Precise Temporal Profiling of Signaling Complexes in Primary Cells Using SWATH Mass Spectrometry. 2017 , 18, 3219-3226		23
1494	Adapting Data-Independent Acquisition for Mass Spectrometry-Based Protein Site-Specific N-Glycosylation Analysis. 2017 , 89, 4532-4539		25
1493	Quantitative Age-specific Variability of Plasma Proteins in Healthy Neonates, Children and Adults. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 924-935	7.6	32
1492	LC-MS for Qualitative and Quantitative Proteomic Studies of Psychiatric Disorders. 2017 , 974, 115-129		1
1491	Comprehensive proteome analysis of human skeletal muscle in cachexia and sarcopenia: a pilot study. 2017 , 8, 567-582		27
1490	Locus-specific Retention Predictor (LsRP): A Peptide Retention Time Predictor Developed for Precision Proteomics. 2017 , 7, 43959		10
1489	The Human Proteome Organization-Proteomics Standards Initiative Quality Control Working Group: Making Quality Control More Accessible for Biological Mass Spectrometry. 2017 , 89, 4474-4479		12
1488	The Human Skeletal Muscle Proteome Project: a reappraisal of the current literature. 2017 , 8, 5-18		51
1487	Quantitative Proteomics Based on Optimized Data-Independent Acquisition in Plasma Analysis. 2017 , 16, 665-676		26
1486	Building proteomic tool boxes to monitor MHC class I and class II peptides. 2017 , 17, 1600061		20

1485	Paleomicrobiology to investigate copper resistance in bacteria: isolation and description of <i>Cupriavidus necator</i> B9 in the soil of a medieval foundry. 2017 , 19, 770-787	9
1484	Optimization of Acquisition and Data-Processing Parameters for Improved Proteomic Quantification by Sequential Window Acquisition of All Theoretical Fragment Ion Mass Spectrometry. 2017 , 16, 738-747	23
1483	Model-Based Analysis of Quantitative Proteomics Data with Data Independent Acquisition Mass Spectrometry. 2017 , 125-140	
1482	System-Wide Quantitative Proteomics of the Metabolic Syndrome in Mice: Genotypic and Dietary Effects. 2017 , 16, 831-841	8
1481	Comparison of targeted proteomics approaches for detecting and quantifying proteins derived from human cancer tissues. 2017 , 17, 1600323	15
1480	Choosing an Optimal Database for Protein Identification from Tandem Mass Spectrometry Data. 2017 , 1549, 17-29	15
1479	Optimization of Experimental Parameters in Data-Independent Mass Spectrometry Significantly Increases Depth and Reproducibility of Results. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 2296-2309	7.6 186
1478	Depletion of Myofibril-Associated Proteins Using Selective Protein Extraction as a Tool in Cardiac Proteomics. 2018 , 1788, 1-9	
1477	Quantitative proteomics of model organisms. 2017 , 6, 58-66	7
1476	Data-Independent Mass Spectrometry Approach for Screening and Identification of DNA Adducts. 2017 , 89, 11728-11736	29
1475	Intrinsic Ribosome Destabilization Underlies Translation and Provides an Organism with a Strategy of Environmental Sensing. 2017 , 68, 528-539.e5	30
1474	Systematic proteome and proteostasis profiling in human Trisomy 21 fibroblast cells. 2017 , 8, 1212	59
1473	Data-Independent Acquisition-Based Quantitative Proteomic Analysis Reveals Potential Biomarkers of Kidney Cancer. 2017 , 11, 1700066	26
1472	Multiplex and Label-Free Relative Quantification Approach for Studying Protein Abundance of Drug Metabolizing Enzymes in Human Liver Microsomes Using SWATH-MS. 2017 , 16, 4134-4143	25
1471	HDAC8 Substrates Identified by Genetically Encoded Active Site Photocrosslinking. 2017 , 139, 16222-16227	14
1470	Systems proteomics approaches to study bacterial pathogens: application to <i>Mycobacterium tuberculosis</i> . 2017 , 39, 64-72	21
1469	Data acquisition workflows in liquid chromatography coupled to high resolution mass spectrometry-based metabolomics: Where do we stand?. 2017 , 1526, 1-12	69
1468	Recent progress in mass spectrometry proteomics for biomedical research. 2017 , 60, 1093-1113	52

1467	Recent advances in phosphoproteomics and application to neurological diseases. 2017 , 142, 4373-4387	22
1466	Improving Protein Detection Confidence Using SWATH-Mass Spectrometry with Large Peptide Reference Libraries. 2017 , 17, 1700174	5
1465	<i>Pseudomonas aeruginosa</i> Proteome under Hypoxic Stress Conditions Mimicking the Cystic Fibrosis Lung. 2017 , 16, 3917-3928	23
1464	Statistical control of peptide and protein error rates in large-scale targeted data-independent acquisition analyses. 2017 , 14, 921-927	129
1463	Model for Quality Control of Allergen Products with Mass Spectrometry. 2017 , 16, 3852-3862	5
1462	High Sensitivity Quantitative Proteomics Using Automated Multidimensional Nano-flow Chromatography and Accumulated Ion Monitoring on Quadrupole-Orbitrap-Linear Ion Trap Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 2006-2016	7.6 29
1461	Surveying the sequence diversity of model prebiotic peptides by mass spectrometry. 2017 , 114, E7652-E7659	37
1460	Methylglyoxal attenuates insulin signaling and downregulates the enzymes involved in cholesterol biosynthesis. 2017 , 13, 2338-2349	9
1459	Heterodimeric capping protein is required for stereocilia length and width regulation. 2017 , 216, 3861-3881	26
1458	Spectral Libraries for SWATH-MS Assays for <i>Drosophila melanogaster</i> and <i>Solanum lycopersicum</i> . 2017 , 17, 1700216	18
1457	New Insight of Common Regulatory Pathways in Human Trabecular Meshwork Cells in Response to Dexamethasone and Prednisolone Using an Integrated Quantitative Proteomics: SWATH and MRM-HR Mass Spectrometry. 2017 , 16, 3753-3765	15
1456	Mapping Protein Targets of Bioactive Small Molecules Using Lipid-Based Chemical Proteomics. 2017 , 12, 2671-2681	16
1455	Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. 2017 , 8, 291	252
1454	Comparison of linear intrascan and interscan dynamic ranges of Orbitrap and ion-mobility time-of-flight mass spectrometers. 2017 , 31, 1915-1926	21
1453	Use of monolithic supports for high-throughput protein and peptide separation in proteomics. 2017 , 38, 2851-2869	19
1452	The Human Plasma Proteome Draft of 2017: Building on the Human Plasma PeptideAtlas from Mass Spectrometry and Complementary Assays. 2017 , 16, 4299-4310	119
1451	Proteome-Wide Analysis of N-Glycosylation Stoichiometry Using SWATH Technology. 2017 , 16, 3830-3840	9
1450	The effect of photodamage on the female Caucasian facial stratum corneum corneome using mass spectrometry-based proteomics. 2017 , 39, 637-652	10

1449	PROCAL: A Set of 40 Peptide Standards for Retention Time Indexing, Column Performance Monitoring, and Collision Energy Calibration. 2017 , 17, 1700263		34
1448	A global <i>Staphylococcus aureus</i> proteome resource applied to the in vivo characterization of host-pathogen interactions. 2017 , 7, 9718		34
1447	MdFDIA: A Mass Defect Based Four-Plex Data-Independent Acquisition Strategy for Proteome Quantification. 2017 , 89, 10248-10255		17
1446	Proteomics in Inflammatory Bowel Disease: Approach Using Animal Models. 2017 , 62, 2266-2276		4
1445	What is targeted proteomics? A concise revision of targeted acquisition and targeted data analysis in mass spectrometry. 2017 , 17, 1700180		58
1444	Comparison of fractionation proteomics for local SWATH library building. 2017 , 17, 1700052		13
1443	Identification of Differentially Expressed Splice Variants by the Proteogenomic Pipeline Splicify. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 1850-1863	7.6	22
1442	Quantitation of 87 Proteins by nLC-MRM/MS in Human Plasma: Workflow for Large-Scale Analysis of Biobank Samples. 2017 , 16, 3242-3254		8
1441	Adrenoceptor-induced modulation of transglutaminase 2 transamidase activity in cardiomyoblasts. 2017 , 813, 105-121		8
1440	Enhanced differential expression statistics for data-independent acquisition proteomics. 2017 , 7, 5869		18
1439	Impact of Alternative Splicing on the Human Proteome. 2017 , 20, 1229-1241		74
1438	PECAN: library-free peptide detection for data-independent acquisition tandem mass spectrometry data. 2017 , 14, 903-908		92
1437	Molecular signatures that can be transferred across different omics platforms. 2017 , 33, i333-i340		9
1436	Bioinformatics Resources for Interpreting Proteomics Mass Spectrometry Data. 2017 , 1647, 267-295		1
1435	Nonuniform Sampling Acquisition of Two-Dimensional Fourier Transform Ion Cyclotron Resonance Mass Spectrometry for Increased Mass Resolution of Tandem Mass Spectrometry Precursor Ions. 2017 , 89, 8589-8593		16
1434	Systems Pharmacology Dissection of Cholesterol Regulation Reveals Determinants of Large Pharmacodynamic Variability between Cell Lines. 2017 , 5, 604-619.e7		13
1433	mTORC2 Promotes Tumorigenesis via Lipid Synthesis. 2017 , 32, 807-823.e12		175
1432	New Strategies and Challenges in Lung Proteomics and Metabolomics. An Official American Thoracic Society Workshop Report. 2017 , 14, 1721-1743		26

1431	Clinical veterinary proteomics: Techniques and approaches to decipher the animal plasma proteome. 2017 , 230, 6-12	11
1430	Data-Independent Acquisition and Parallel Reaction Monitoring Mass Spectrometry Identification of Serum Biomarkers for Ovarian Cancer. 2017 , 12, 1177271917710948	15
1429	Neuroproteomics Using Short GeLC-SWATH: From the Evaluation of Proteome Changes to the Clarification of Protein Function. 2017 , 107-138	5
1428	Targeted Approach for Proteomic Analysis of a Hidden Membrane Protein. 2017 , 1619, 151-172	0
1427	SWATH Mass Spectrometry for Proteomics of Non-Depleted Plasma. 2017 , 1619, 373-383	6
1426	Targeted Feature Detection for Data-Dependent Shotgun Proteomics. 2017 , 16, 2964-2974	31
1425	Mass Spectrometry in Environmental Chemistry and Toxicology. 2017 , 159-176	
1424	Protein complex-based analysis is resistant to the obfuscating consequences of batch effects --- a case study in clinical proteomics. 2017 , 18, 142	12
1423	Functional proteomics of cellular mechanosensing mechanisms. 2017 , 71, 118-128	7
1422	ESCMID postgraduate education course: applications of MALDI-TOF mass spectrometry in clinical microbiology. 2017 , 19, 433-442	2
1421	Qualitative and Quantitative Analysis of Proteome and Peptidome of Human Follicular Fluid Using Multiple Samples from Single Donor with LC-MS and SWATH Methodology. 2017 , 16, 3053-3067	20
1420	PIQED: automated identification and quantification of protein modifications from DIA-MS data. 2017 , 14, 646-647	37
1419	Re-examining the role of Cdc14 phosphatase in reversal of Cdk phosphorylation during mitotic exit. 2017 , 130, 2673-2681	13
1418	NetProt: Complex-based Feature Selection. 2017 , 16, 3102-3112	12
1417	Site-specific analysis of changes in the glycosylation of proteins in liver cirrhosis using data-independent workflow with soft fragmentation. 2017 , 409, 619-627	22
1416	Target identification with quantitative activity based protein profiling (ABPP). 2017 , 17, 1600212	26
1415	Proteomic insights into extracellular vesicle biology - defining exosomes and shed microvesicles. 2017 , 14, 69-95	89
1414	Biophysical characterization of the interaction between M2-1 protein of hRSV and quercetin. 2017 , 95, 63-71	6

1413	Towards comprehensive and quantitative proteomics for diagnosis and therapy of human disease. 2017 , 17, 1600079	34
1412	Shedding light on biofilm formation of <i>Halobacterium salinarum</i> R1 by SWATH-LC/MS/MS analysis of planktonic and sessile cells. 2017 , 17, 1600111	15
1411	Determination of differentially regulated proteins upon proteasome inhibition in AML cell lines by the combination of large-scale and targeted quantitative proteomics. 2017 , 17, 1600089	8
1410	Tandem mass spectral libraries of peptides and their roles in proteomics research. 2017 , 36, 634-648	31
1409	Proteomic analysis of synovial fluid in osteoarthritis using SWATH-mass spectrometry. 2018 , 17, 2827-2836	19
1408	Detection of ROS Induced Proteomic Signatures by Mass Spectrometry. 2017 , 8, 470	21
1407	Improved Quantitative Plant Proteomics via the Combination of Targeted and Untargeted Data Acquisition. 2017 , 8, 1669	10
1406	Mass spectrometry-assisted gel-based proteomics in cancer biomarker discovery: approaches and application. 2017 , 7, 3559-3572	40
1405	Identification and Validation of a Salivary Protein Panel to Detect Heart Failure Early. 2017 , 7, 4350-4358	12
1404	Food Authentication of Seafood Species. 2017 , 331-342	2
1403	The Future of DNA Adductomic Analysis. 2017 , 18,	27
1402	A Perspective on Extracellular Vesicles Proteomics. 2017 , 5, 102	67
1401	Chlamyospore Specific Proteins of <i>Candida albicans</i> . 2017 , 2, 26	1
1400	Drug Target Identification Using an iTRAQ-Based Quantitative Chemical Proteomics Approach-Based on a Target Profiling Study of Andrographolide. 2017 , 586, 291-309	9
1399	Systems Biology: Methods and Applications. 2017 , 434-480	
1398	Comparative Proteomics Reveals Differences in Host-Pathogen Interaction between Infectious and Commensal Relationship with. 2017 , 7, 145	11
1397	Current and Emerging Technologies for Probing Molecular Signatures of Traumatic Brain Injury. 2017 , 8, 450	9
1396	Quantitative Mass Spectrometry-Based Proteomic Profiling for Precision Medicine in Prostate Cancer. 2017 , 7, 267	16

1395	Crosstalk between glial and glioblastoma cells triggers the "go-or-grow" phenotype of tumor cells. 2017 , 15, 37	26
1394	Impact of mesenchymal stem cells' secretome on glioblastoma pathophysiology. 2017 , 15, 200	22
1393	Label-Free Quantitative Phosphoproteomics Reveals Regulation of Vasodilator-Stimulated Phosphoprotein upon Stathmin-1 Silencing in a Pair of Isogenic Colorectal Cancer Cell Lines. 2018 , 18, e1700242	7
1392	Data-Independent Acquisition Coupled to Visible Laser-Induced Dissociation at 473 nm (DIA-LID) for Peptide-Centric Specific Analysis of Cysteine-Containing Peptide Subset. 2018 , 90, 3928-3935	5
1391	Identification of Protein Targets of 12/15-Lipoxygenase-Derived Lipid Electrophiles in Mouse Peritoneal Macrophages Using Omega-Alkynyl Fatty Acid. 2018 , 13, 887-893	6
1390	The use of SWATH to analyse the dynamic changes of bacterial proteome of carbapenemase-producing <i>Escherichia coli</i> under antibiotic pressure. 2018 , 8, 3871	13
1389	SWATHtoMRM: Development of High-Coverage Targeted Metabolomics Method Using SWATH Technology for Biomarker Discovery. 2018 , 90, 4062-4070	57
1388	Exploring the Potential of Data-Independent Acquisition Proteomics Using Untargeted All-Ion Quantitation: Application to Tumor Subtype Diagnosis. 2018 , 90, 4380-4388	3
1387	Proteomics of cyanobacteria: current horizons. 2018 , 54, 65-71	13
1386	Proteomic profiling of HIV-infected T-cells by SWATH mass spectrometry. 2018 , 516, 246-257	5
1385	Adapted MS/MS Shotgun Lipidomics Approach for Analysis of Cardiolipin Molecular Species. 2018 , 53, 133-142	17
1384	Advancing translational research and precision medicine with targeted proteomics. 2018 , 189, 1-10	44
1383	Insights into apoptotic proteins in chemotherapy: quantification techniques and informing therapy choice. 2018 , 15, 413-429	2
1382	The role of mass spectrometry in the characterization of biologic protein products. 2018 , 15, 431-449	34
1381	Quantification of Site-specific Protein Lysine Acetylation and Succinylation Stoichiometry Using Data-independent Acquisition Mass Spectrometry. 2018 ,	6
1380	Pseudotargeted MS Method for the Sensitive Analysis of Protein Phosphorylation in Protein Complexes. 2018 , 90, 6214-6221	8
1379	Targeted Proteomics Guided by Label-free Quantitative Proteome Analysis in Saliva Reveal Transition Signatures from Health to Periodontal Disease. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 1392-1409	7.6 41
1378	Influence of white matter injury on gray matter reactive gliosis upon stab wound in the adult murine cerebral cortex. 2018 , 66, 1644-1662	14

1377	Distinct Proteome Remodeling of Industrial <i>Saccharomyces cerevisiae</i> in Response to Prolonged Thermal Stress or Transient Heat Shock. 2018 , 17, 1812-1825	14
1376	Mechanisms of Persistence of the Ammonia-Oxidizing Bacteria <i>Nitrosomonas</i> to the Biocide Free Nitrous Acid. 2018 , 52, 5386-5397	32
1375	Changes in the mitochondrial proteome of developing maize seed embryos. 2018 , 163, 552-572	4
1374	Removing 4E-BP Enables Synapses to Refine without Postsynaptic Activity. 2018 , 23, 11-22	4
1373	A reference peptide database for proteome quantification based on experimental mass spectrum response curves. 2018 , 34, 2766-2772	0
1372	Cryopreservation and egg yolk medium alter the proteome of ram spermatozoa. 2018 , 181, 73-82	33
1371	Parallel reaction monitoring on a Q Exactive mass spectrometer increases reproducibility of phosphopeptide detection in bacterial phosphoproteomics measurements. 2018 , 189, 60-66	6
1370	Protein Turnover in Aging and Longevity. 2018 , 18, e1700108	44
1369	Distinct Proteomic, Transcriptomic, and Epigenetic Stress Responses in Dorsal and Ventral Hippocampus. 2018 , 84, 531-541	55
1368	Targeted proteomics analyses of phosphorylation-dependent signalling networks. 2018 , 189, 39-47	5
1367	Ion Source Multiplexing on a Single Mass Spectrometer. 2018 , 90, 3576-3583	10
1366	Proteomic Profiling Reveals the Transglutaminase-2 Externalization Pathway in Kidneys after Unilateral Ureteric Obstruction. 2018 , 29, 880-905	22
1365	Metabolomic spectral libraries for data-independent SWATH liquid chromatography mass spectrometry acquisition. 2018 , 410, 1873-1884	28
1364	From the genome sequence via the proteome to cell physiology - Pathoproteomics and pathophysiology of <i>Staphylococcus aureus</i> . 2018 , 308, 545-557	14
1363	Advances in analytical tools for high throughput strain engineering. 2018 , 54, 33-40	23
1362	Nonlinear Regression Improves Accuracy of Characterization of Multiplexed Mass Spectrometric Assays. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 913-924	7.6 14
1361	Insights from Proteomic Studies into Plant Somatic Embryogenesis. 2018 , 18, e1700265	28
1360	Mass spectrometry analysis of plasma from amyotrophic lateral sclerosis and control subjects. 2018 , 19, 362-376	28

1359	Bioinformatics Support for Farm Animal Proteomics. 2018 , 361-386	
1358	Gel-Free Proteomics. 2018 , 55-101	
1357	Phosphoproteomics-Based Profiling of Kinase Activities in Cancer Cells. 2018 , 1711, 103-132	14
1356	Comparison of Proteomic Quantification Approaches for Hepatic Drug Transporters: Multiplexed Global Quantitation Correlates with Targeted Proteomic Quantitation. 2018 , 46, 692-696	22
1355	New In-Depth Analytical Approach of the Porcine Seminal Plasma Proteome Reveals Potential Fertility Biomarkers. 2018 , 17, 1065-1076	37
1354	Proteomics in Prostate Cancer Research. 2018 , 213-236	
1353	Recent advances in the applications of metabolomics in eye research. 2018 , 1037, 28-40	14
1352	Cell-surface proteomics for the identification of novel therapeutic targets in cancer. 2018 , 15, 259-275	29
1351	Identification of candidate serum biomarkers of childhood-onset growth hormone deficiency using SWATH-MS and feature selection. 2018 , 175, 105-113	9
1350	High throughput and accurate serum proteome profiling by integrated sample preparation technology and single-run data independent mass spectrometry analysis. 2018 , 174, 9-16	40
1349	Proteomic analysis of the cardiac extracellular matrix: clinical research applications. 2018 , 15, 105-112	21
1348	Mapping the Polarity Interactome. 2018 , 430, 3521-3544	8
1347	Software ion scan functions in analysis of glycomic and lipidomic MS/MS datasets. 2018 , 53, 264-277	
1346	Integrated Analysis of Protein Abundance, Transcript Level, and Tissue Diversity To Reveal Developmental Regulation of Maize. 2018 , 17, 822-833	6
1345	Pathology, proteomics and the pathway to personalised medicine. 2018 , 15, 231-243	12
1344	Solvent effects on differentiation of mouse brain tissue using laser microdissection 'cut and drop' sampling with direct mass spectral analysis. 2018 , 32, 414-422	9
1343	A Map of Protein-Metabolite Interactions Reveals Principles of Chemical Communication. 2018 , 172, 358-372.e23	192
1342	Identification of stress responsive genes by studying specific relationships between mRNA and protein abundance. 2018 , 4, e00558	2

1341	Mass spectrometry based proteomics as foodomics tool in research and assurance of food quality and safety. 2018 , 77, 100-119	27
1340	Probing the molecular regulation of lipopolysaccharide stress in piglet liver by comparative proteomics analysis. 2018 , 39, 2321-2331	5
1339	Phosphatase mediated bioprecipitation of lead as pyromorphite by <i>Achromobacter xylosoxidans</i> . 2018 , 217, 754-761	11
1338	Broadband ion mobility deconvolution for rapid analysis of complex mixtures. 2018 , 143, 2574-2586	6
1337	Precision Profiling of the Cardiovascular Post-Translationally Modified Proteome: Where There Is a Will, There Is a Way. 2018 , 122, 1221-1237	24
1336	SWATH Tandem Mass Spectrometry Workflow for Quantification of Mass Isotopologue Distribution of Intracellular Metabolites and Fragments Labeled with Isotopic C Carbon. 2018 , 90, 6486-6493	25
1335	AP-SWATH Reveals Direct Involvement of VCP/p97 in Integrated Stress Response Signaling Through Facilitating CREP/PPP1R15B Degradation. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 1295-1307	18
1334	Proteomic Investigation of the Binding Agent between Liver Glycogen IParticles. 2018 , 3, 3640-3645	25
1333	Specter: linear deconvolution for targeted analysis of data-independent acquisition mass spectrometry proteomics. 2018 , 15, 371-378	35
1332	Comparison of protein expression between human livers and the hepatic cell lines HepG2, Hep3B, and Huh7 using SWATH and MRM-HR proteomics: Focusing on drug-metabolizing enzymes. 2018 , 33, 133-140	30
1331	Cost-effective generation of precise label-free quantitative proteomes in high-throughput by microLC and data-independent acquisition. 2018 , 8, 4346	38
1330	Quantification of steroid hormones in plasma using a surrogate calibrant approach and UHPLC-ESI-QTOF-MS/MS with SWATH-acquisition combined with untargeted profiling. 2018 , 1022, 70-80	31
1329	Integrated SWATH-based and targeted-based proteomics provide insights into the retinal emmetropization process in guinea pig. 2018 , 181, 1-15	16
1328	Identification of Single Amino Acid Substitutions in Proteogenomics. 2018 , 83, 250-258	4
1327	Subregion-Specific Proteomic Signature in the Hippocampus for Recognition Processes in Adult Mice. 2018 , 22, 3362-3374	13
1326	Isotope Dilution-Based Targeted and Nontargeted Carbonyl Neurosteroid/Steroid Profiling. 2018 , 90, 5247-5255	10
1325	Deconvolution in mass spectrometry based proteomics. 2018 , 32, 763-774	8
1324	SWATH mass spectrometry as a tool for quantitative profiling of the matrisome. 2018 , 189, 11-22	42

1323	Quantitative proteomic characterization of the lung extracellular matrix in chronic obstructive pulmonary disease and idiopathic pulmonary fibrosis. 2018 , 189, 23-33	40
1322	Evaluation of spectral libraries and sample preparation for DIA-LC-MS analysis of host cell proteins: A case study of a bacterially expressed recombinant biopharmaceutical protein. 2018 , 147, 69-77	10
1321	Identification of small molecules using accurate mass MS/MS search. 2018 , 37, 513-532	194
1320	Clinical Features of Psoriatic Arthritis: a Comprehensive Review of Unmet Clinical Needs. 2018 , 55, 271-294	34
1319	Proteomic and Metaproteomic Approaches to Understand Host-Microbe Interactions. 2018 , 90, 86-109	29
1318	Trichostatin A alters cytoskeleton and energy metabolism of pancreatic adenocarcinoma cells: An in depth proteomic study. 2018 , 119, 2696-2707	23
1317	Ultrafast Peptide Label-Free Quantification with FlashLFQ. 2018 , 17, 386-391	36
1316	Simple strategies to enhance discovery of acetylation post-translational modifications by quadrupole-orbitrap LC-MS/MS. 2018 , 1866, 224-229	3
1315	Effect of the anode potential on the physiology and proteome of <i>Shewanella oneidensis</i> MR-1. 2018 , 119, 172-179	18
1314	Deciphering the electric code of <i>Geobacter sulfurreducens</i> in cocultures with <i>Pseudomonas aeruginosa</i> via SWATH-MS proteomics. 2018 , 119, 150-160	18
1313	Scanning Quadrupole Data-Independent Acquisition, Part A: Qualitative and Quantitative Characterization. 2018 , 17, 770-779	37
1312	Development of a data independent acquisition mass spectrometry workflow to enable glycopeptide analysis without predefined glycan compositional knowledge. 2018 , 172, 68-75	30
1311	Human Gut Microbiome: Function Matters. 2018 , 26, 563-574	241
1310	Enzyme and Chemical Assisted N-Terminal Blocked Peptides Analysis, ENCHANT, as a Selective Proteomics Approach Complementary to Conventional Shotgun Approach. 2018 , 17, 212-221	10
1309	Technical challenges of working with extracellular vesicles. 2018 , 10, 881-906	236
1308	Dual Data-Independent Acquisition Approach Combining Global HCP Profiling and Absolute Quantification of Key Impurities during Bioprocess Development. 2018 , 90, 1241-1247	12
1307	Panomics for Precision Medicine. 2018 , 24, 85-101	47
1306	Direct and indirect approaches to identify drug modes of action. 2018 , 70, 9-22	19

1305	Role of transglutaminase 2 in A adenosine receptor- and Adrenoceptor-mediated pharmacological pre- and post-conditioning against hypoxia-reoxygenation-induced cell death in H9c2 cells. 2018 , 819, 144-160	3
1304	Exploring the chemistry of complex samples by tentative identification and semiquantification: A food contact material case. 2018 , 53, 323-335	9
1303	Measurement of impurities to support process development and manufacture of biopharmaceuticals. 2018 , 101, 120-128	5
1302	Understanding missing proteins: a functional perspective. 2018 , 23, 644-651	8
1301	Comparison of Quantitative Mass Spectrometry Platforms for Monitoring Kinase ATP Probe Uptake in Lung Cancer. 2018 , 17, 63-75	13
1300	An algorithm to correct saturated mass spectrometry ion abundances for enhanced quantitation and mass accuracy in omic studies. 2018 , 427, 91-99	12
1299	Comparative Analyses of Data Independent Acquisition Mass Spectrometric Approaches: DIA, WiSIM-DIA, and Untargeted DIA. 2018 , 18, 1700304	40
1298	Logical MS/MS scans: a new set of operations for tandem mass spectrometry. 2018 , 143, 5438-5452	8
1297	Lost in the crowd: identifying targetable MHC class I neoepitopes for cancer immunotherapy. 2018 , 15, 1065-1077	9
1296	Proteomics goes parallel. 2018 , 36, 1051-1053	9
1295	Data-Independent Acquisition Mass Spectrometry To Quantify Protein Levels in FFPE Tumor Biopsies for Molecular Diagnostics. 2019 , 18, 426-435	11
1294	Ethylene Receptors, CTRs and EIN2 Target Protein Identification and Quantification Through Parallel Reaction Monitoring During Tomato Fruit Ripening. 2018 , 9, 1626	25
1293	Temporal dynamics of liver mitochondrial protein acetylation and succinylation and metabolites due to high fat diet and/or excess glucose or fructose. 2018 , 13, e0208973	26
1292	An Alliance of Gel-Based and Gel-Free Proteomic Techniques Displays Substantial Insight Into the Proteome of a Virulent and an Attenuated Strain. 2018 , 8, 407	7
1291	Fast quantitative urinary proteomic profiling workflow for biomarker discovery in kidney cancer. 2018 , 15, 42	13
1290	Profiling the proteomic inflammatory state of human astrocytes using DIA mass spectrometry. 2018 , 15, 331	11
1289	Proteomic Responses to Cold Stress. 2018 , 111-125	
1288	Proteomic Analysis of Lysosomal Membrane Proteins in Bovine Mammary Epithelial Cells Illuminates Potential Novel Lysosome Functions in Lactation. 2018 , 66, 13041-13049	9

1287	Chromatogram libraries improve peptide detection and quantification by data independent acquisition mass spectrometry. 2018 , 9, 5128	143
1286	Separation of blood microsamples by exploiting sedimentation at the microscale. 2018 , 8, 14101	13
1285	Expanding the Use of Spectral Libraries in Proteomics. 2018 , 17, 4051-4060	26
1284	Exploring the Rampant Expansion of Ubiquitin Proteomics. 2018 , 1844, 345-362	8
1283	Proteomic study of skeletal muscle in obesity and type 2 diabetes: progress and potential. 2018 , 15, 817-828	3
1282	Response of the thylakoid proteome of <i>Synechocystis</i> sp. PCC 6803 to photoinhibitory intensities of orange-red light. 2018 , 132, 524-534	2
1281	DIA+: A Data-Independent Acquisition Method Combining Multiple Precursor Charges to Improve Peptide Signal. 2018 , 90, 12339-12341	3
1280	Identification of Novel Protein Lysine Acetyltransferases in <i>Escherichia coli</i> . 2018 , 9,	39
1279	Time segment scanning-based quasi-multiple reaction monitoring mode by ultra-performance liquid chromatography coupled with quadrupole/time-of-flight mass spectrometry for quantitative determination of herbal medicines: Moutan Cortex, a case study. 2018 , 1581-1582, 33-42	7
1278	Proteomics in Toxicology. 2018 , 375-390	
1277	Estimating the Reliability of Low-Abundant Signals and Limited Replicate Measurements through MS2 Peak Area in SWATH. 2018 , 18, e1800186	3
1276	Multiplex Biomarker Screening Assay for Urinary Extracellular Vesicles Study: A Targeted Label-Free Proteomic Approach. 2018 , 8, 15039	22
1275	Multiple-Enzyme-Digestion Strategy Improves Accuracy and Sensitivity of Label- and Standard-Free Absolute Quantification to a Level That Is Achievable by Analysis with Stable Isotope-Labeled Standard Spiking. 2019 , 18, 217-224	14
1274	The in silico human surfaceome. 2018 , 115, E10988-E10997	94
1273	Free fatty acid profiling in marine algae extract by LC-MS/MS and isolation as well as quantification of the Ω fatty acid hexadeca-4,7,10,13-tetraenoic acid. 2018 , 41, 4286-4295	10
1272	From Molecules to Mechanisms: Functional Proteomics and Its Application to Renal Tubule Physiology. 2018 , 98, 2571-2606	18
1271	Machine Learning Predicts the Yeast Metabolome from the Quantitative Proteome of Kinase Knockouts. 2018 , 7, 269-283.e6	46
1270	Proteomic and functional data sets on synaptic mitochondria from rats with genetic ablation of. 2018 , 20, 568-572	1

1269	Challenges and Opportunities for Biological Mass Spectrometry Core Facilities in the Developing World. 2018 , 29, 4-15		4
1268	Candidate plasma biomarkers for predicting ascending aortic aneurysm in bicuspid aortic valve disease. 2018 , 13, 76		2
1267	Comparative Hippocampal Synaptic Proteomes of Rodents and Primates: Differences in Neuroplasticity-Related Proteins. 2018 , 11, 364		17
1266	Proteomics and Lipidomics in Inflammatory Bowel Disease Research: From Mechanistic Insights to Biomarker Identification. 2018 , 19,		21
1265	Epigenetic Regulation Alters Biofilm Architecture and Composition in Multiple Clinical Isolates of Nontypeable Haemophilus influenzae. 2018 , 9,		21
1264	Proteomic Approaches for the Discovery of Biofluid Biomarkers of Neurodegenerative Dementias. 2018 , 6,		33
1263	Characterization of Cerebrospinal Fluid via Data-Independent Acquisition Mass Spectrometry. 2018 , 17, 3418-3430		19
1262	Detection of Functional Overreaching in Endurance Athletes Using Proteomics. 2018 , 6,		18
1261	Pre- and post-puberty expression of genes and proteins in the uterus of Bos indicus heifers: the luteal phase effect post-puberty. 2018 , 49, 539-549		8
1260	Pull-down Assay on Streptavidin Beads and Surface Plasmon Resonance Chips for SWATH-MS-based Interactomics. 2018 , 15, 395-404		5
1259	The State of "" Research for Farmed Penaeids: Advances in Research and Impediments to Industry Utilization. 2018 , 9, 282		18
1258	Kunitz type protease inhibitor EgKI-1 from the canine tapeworm Echinococcus granulosus as a promising therapeutic against breast cancer. 2018 , 13, e0200433		11
1257	Development of a Gill Assay Library for Ecological Proteomics of Threespine Sticklebacks (). <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 2146-2163	7.6	13
1256	Perspectives on Liquid Chromatography-High-Resolution Mass Spectrometry for Pesticide Screening in Foods. 2018 , 66, 9573-9581		46
1255	Multi-region proteome analysis quantifies spatial heterogeneity of prostate tissue biomarkers. 2018 , 1,		38
1254	EpiProfile 2.0: A Computational Platform for Processing Epi-Proteomics Mass Spectrometry Data. 2018 , 17, 2533-2541		51
1253	Similarities and Differences of Blood N-Glycoproteins in Five Solid Carcinomas at Localized Clinical Stage Analyzed by SWATH-MS. 2018 , 23, 2819-2831.e5		26
1252	Comprehensive Tandem-Mass-Spectrometry Coverage of Complex Samples Enabled by Data-Set-Dependent Acquisition. 2018 , 90, 8020-8027		21

1251	Notch2 and Proteomic Signatures in Mouse Neointimal Lesion Formation. 2018 , 38, 1576-1593		7
1250	Proteomics Study Reveals That Docosahexaenoic and Arachidonic Acids Exert Different In Vitro Anticancer Activities in Colorectal Cancer Cells. 2018 , 66, 6003-6012		14
1249	Quantifying and Localizing the Mitochondrial Proteome Across Five Tissues in A Mouse Population. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 1766-1777	7.6	37
1248	Proteomics in Veterinary Medicine and Animal Science: Neglected Scientific Opportunities with Immediate Impact. 2018 , 18, e1800047		17
1247	Infrared laser ablation sampling coupled with data independent high resolution UPLC-IM-MS/MS for tissue analysis. 2018 , 1034, 102-109		12
1246	Analysis of Staphylococcus aureus proteins secreted inside infected human epithelial cells. 2018 , 308, 664-674		2
1245	Systems pathology analysis identifies neurodegenerative nature of age-related vitreoretinal interface diseases. 2018 , 17, e12809		13
1244	SWATH-Based Metabolomics of Follicular Fluid in Patients Shows That Progesterone Adversely Affects Oocyte Quality. 2018 , 2018, 1780391		5
1243	Serum responsive proteome reveals correlation between oxidative phosphorylation and morphogenesis in <i>Candida albicans</i> ATCC10231. 2018 , 185, 25-38		8
1242	Two-dimensional gel and shotgun proteomics approaches to distinguish fresh and frozen-thawed curled octopus (<i>Eledone cirrhosa</i>). 2018 , 186, 1-7		20
1241	Foodomics Applications. 2018 , 643-685		10
1240	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. 2018 , 34, 211-224.e6		327
1239	Reconstructing phosphorylation signalling networks from quantitative phosphoproteomic data. 2018 , 62, 525-534		21
1238	Discovery of the Consistently Well-Performed Analysis Chain for SWATH-MS Based Pharmacoproteomic Quantification. 2018 , 9, 681		52
1237	Quantitative proteomics using SWATH-MS identifies mechanisms of chloride tolerance in the halophilic acidophile <i>Acidihalobacter prosperus</i> DSM 14174. 2018 , 169, 638-648		7
1236	SWATH-MS based quantitative proteomics analysis reveals that curcumin alters the metabolic enzyme profile of CML cells by affecting the activity of miR-22/IPO7/HIF-1 α axis. 2018 , 37, 170		19
1235	SWATH-MS Proteomic Analysis of Oxygen-Induced Retinopathy Reveals Novel Potential Therapeutic Targets. 2018 , 59, 3294-3306		11
1234	Comprehensive overview and recent advances in proteomics MS based methods for food allergens analysis. 2018 , 106, 21-36		47

1233	Potential Alternative Strategy against Drug Resistant Tuberculosis: A Proteomics Prospect. 2018 , 6,	18
1232	Probing the colorectal cancer proteome for biomarkers: Current status and perspectives. 2018 , 187, 93-105	31
1231	Signal-Targeted Therapies and Resistance Mechanisms in Pancreatic Cancer: Future Developments Reside in Proteomics. 2018 , 10,	7
1230	DIA-SIFT: A Precursor and Product Ion Filter for Accurate Stable Isotope Data-Independent Acquisition Proteomics. 2018 , 90, 8722-8726	5
1229	Lys-C/Arg-C, a More Specific and Efficient Digestion Approach for Proteomics Studies. 2018 , 90, 9700-9707	18
1228	OsDER1 Is an ER-Associated Protein Degradation Factor That Responds to ER Stress. 2018 , 178, 402-412	14
1227	Preservation Method and Phosphate Buffered Saline Washing Affect the Acute Myeloid Leukemia Proteome. 2018 , 19,	2
1226	The phospholipase DDHD1 as a new target in colorectal cancer therapy. 2018 , 37, 82	2
1225	H drives metabolic rearrangements in gas-fermenting. 2018 , 11, 55	62
1224	BoxCar acquisition method enables single-shot proteomics at a depth of 10,000 proteins in 100 minutes. 2018 , 15, 440-448	198
1223	IonStar enables high-precision, low-missing-data proteomics quantification in large biological cohorts. 2018 , 115, E4767-E4776	38
1222	Personalization of prostate cancer therapy through phosphoproteomics. 2018 , 15, 483-497	21
1221	Monitoring of Plant Protein Post-translational Modifications Using Targeted Proteomics. 2018 , 9, 1168	32
1220	Applications of Reactive Cysteine Profiling. 2019 , 420, 375-417	18
1219	Recent advancements, challenges, and practical considerations in the mass spectrometry-based analytics of protein biotherapeutics: A viewpoint from the biosimilar industry. 2018 , 161, 214-238	30
1218	Comparison of iTRAQ and SWATH in a clinical study with multiple time points. 2018 , 15, 24	29
1217	Biology/Disease-Driven Initiative on Protein-Aggregation Diseases of the Human Proteome Project: Goals and Progress to Date. 2018 , 17, 4072-4084	3
1216	Ion-Pair Selection Method for Pseudotargeted Metabolomics Based on SWATH MS Acquisition and Its Application in Differential Metabolite Discovery of Type 2 Diabetes. 2018 , 90, 11401-11408	24

1215	Proteomics of <i>Pseudomonas aeruginosa</i> : the increasing role of post-translational modifications. 2018 , 15, 757-772	8
1214	Data-independent acquisition-based SWATH-MS for quantitative proteomics: a tutorial. 2018 , 14, e8126	389
1213	Proteomic phenotyping of metastatic melanoma reveals putative signatures of MEK inhibitor response and prognosis. 2018 , 119, 713-723	2
1212	The Absence of Thioredoxin m1 and Thioredoxin C in <i>Anabaena</i> sp. PCC 7120 Leads to Oxidative Stress. 2018 , 59, 2432-2441	5
1211	Tailored Use of Targeted Proteomics in Plant-Specific Applications. 2018 , 9, 1204	11
1210	Use of Graph Theory to Characterize Human and Arthropod Vector Cell Protein Response to Infection With. 2018 , 8, 265	16
1209	Relative and Absolute Quantitation in Mass Spectrometry-Based Proteomics. 2018 , 11, 49-77	72
1208	Proteomic Analysis of Zebrafish (<i>Danio rerio</i>) After Chemical Exposure. 2018 , 1797, 443-459	1
1207	Comparative Metaproteomics to Study Environmental Changes. 2018 , 327-363	5
1206	Detecting post-translational modification signatures as potential biomarkers in clinical mass spectrometry. 2018 , 15, 515-535	43
1205	Future Prospects of Spectral Clustering Approaches in Proteomics. 2018 , 18, e1700454	10
1204	Mass spectrometry is a multifaceted weapon to be used in the battle against Alzheimer's disease: Amyloid beta peptides and beyond. 2019 , 38, 34-48	14
1203	Fast and facile preparation of nanostructured silicon surfaces for laser desorption/ionization mass spectrometry of small compounds. 2019 , 33 Suppl 1, 66-74	5
1202	Characterization of smooth muscle cells from human atherosclerotic lesions and their responses to Notch signaling. 2019 , 99, 290-304	16
1201	Mass Spectrometry-Based Metabolomic Analysis. 2019 , 410-425	1
1200	Discovering cellular protein-protein interactions: Technological strategies and opportunities. 2019 , 38, 79-111	32
1199	Discrimination of dried sea cucumber (<i>Apostichopus japonicus</i>) products from different geographical origins by sequential windowed acquisition of all theoretical fragment ion mass spectra (SWATH-MS)-based proteomic analysis and chemometrics. 2019 , 274, 592-602	25
1198	hSWATH: Unlocking SWATH's Full Potential for an Untargeted Histone Perspective. 2019 , 18, 3840-3849	8

1197	Deepening our understanding of HDL proteome. 2019 , 16, 749-760	22
1196	Comprehensive lipidomics of mouse plasma using class-specific surrogate calibrants and SWATH acquisition for large-scale lipid quantification in untargeted analysis. 2019 , 1086, 90-102	16
1195	Enhancing signal and mitigating up-front peptide fragmentation using controlled clustering by gas-phase modifiers. 2019 , 411, 6365-6376	1
1194	Concepts and strategies of soybean seed proteomics using the shotgun proteomics approach. 2019 , 16, 795-804	12
1193	Immunoproteomics Methods and Techniques. 2019 , 2024, 25-58	6
1192	Quantitative mass spectrometry-based proteomics in the era of model-informed drug development: Applications in translational pharmacology and recommendations for best practice. 2019 , 203, 107397	13
1191	Glyco-DIA: a method for quantitative O-glycoproteomics with in silico-boosted glycopeptide libraries. 2019 , 16, 902-910	51
1190	Tandem Mass Spectrometry. 2019 , 231-259	1
1189	Progress on Identifying and Characterizing the Human Proteome: 2019 Metrics from the HUPO Human Proteome Project. 2019 , 18, 4098-4107	32
1188	DecoMetDIA: Deconvolution of Multiplexed MS/MS Spectra for Metabolite Identification in SWATH-MS-Based Untargeted Metabolomics. 2019 , 91, 11897-11904	21
1187	OLFM4 Expression in Ductal Carcinoma In Situ and in Invasive Breast Cancer Cohorts by a SWATH-Based Proteomic Approach. 2019 , 19, e1800446	10
1186	Metaproteomic and Metabolomic Approaches for Characterizing the Gut Microbiome. 2019 , 19, e1800363	14
1185	Inferring Protein-Protein Interaction Networks From Mass Spectrometry-Based Proteomic Approaches: A Mini-Review. 2019 , 17, 805-811	26
1184	Breast Cancer Classification Based on Proteotypes Obtained by SWATH Mass Spectrometry. 2019 , 28, 832-843.e7	40
1183	DART-ID increases single-cell proteome coverage. 2019 , 15, e1007082	23
1182	Mass Spectrometric Determination of Protein Ubiquitination. 2019 , 1934, 191-221	1
1181	Signal Transduction in Diffuse Intrinsic Pontine Glioma. 2019 , 19, e1800479	19
1180	Proteomics and Leishmaniasis: Potential Clinical Applications. 2019 , 13, e1800136	9

1179	Mass Spectrometry-Based Biomarkers in Drug Development. 2019 , 1140, 435-449		2
1178	Contribution of Mass Spectrometry-Based Proteomics to Discoveries in Developmental Biology. 2019 , 1140, 143-154		4
1177	Predictive proteomic signatures for response of pancreatic cancer patients receiving chemotherapy. 2019 , 16, 31		8
1176	The antipsychotic medication, risperidone, causes global immunosuppression in healthy mice. 2019 , 14, e0218937		19
1175	Proteomics Approaches for Biomarker and Drug Target Discovery in ALS and FTD. 2019 , 13, 548		25
1174	Proteomics: Tools of the Trade. 2019 , 1073, 1-22		2
1173	Fast and Accurate Bacterial Species Identification in Urine Specimens Using LC-MS/MS Mass Spectrometry and Machine Learning. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 2492-2505	7.6	16
1172	Toward Integrated Multi-omics Analysis for Improving CHO Cell Bioprocessing. 2019 , 163-184		
1171	Recent Advances in Microalgae Peptides: Cardiovascular Health Benefits and Analysis. 2019 , 67, 11825-11838		17
1170	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 3.0. 2019 , 18, 4108-4116		37
1169	High-throughput proteomic analysis of FFPE tissue samples facilitates tumor stratification. 2019 , 13, 2305-2328		43
1168	Proteome analysis of <i>Candida albicans</i> cells undergoing chlamydosporulation. 2019 , 10, 269-290		2
1167	Stable Isotope-Assisted Plant Metabolomics: Combination of Global and Tracer-Based Labeling for Enhanced Untargeted Profiling and Compound Annotation. 2019 , 10, 1366		7
1166	A novel approach for protein identification from complex cell proteome using modified peptide mass fingerprinting algorithm. 2019 , 40, 3062-3073		
1165	The Response of <i>Haloferax volcanii</i> to Salt and Temperature Stress: A Proteome Study by Label-Free Mass Spectrometry. 2019 , 19, e1800491		18
1164	Proteome and Secretome Dynamics of Human Retinal Pigment Epithelium in Response to Reactive Oxygen Species. 2019 , 9, 15440		11
1163	SWATH-based proteomics reveals processes associated with immune evasion and metastasis in poor prognosis colorectal tumours. 2019 , 23, 8219-8232		6
1162	Sirtuin 5 Regulates Proximal Tubule Fatty Acid Oxidation to Protect against AKI. 2019 , 30, 2384-2398		35

1161	Tracking genome-editing and associated molecular perturbations by SWATH mass spectrometry. 2019 , 9, 15240	6
1160	Prediction and Consequences of Cofragmentation in Metaproteomics. 2019 , 18, 3555-3566	4
1159	Surpassing 10 000 identified and quantified proteins in a single run by optimizing current LC-MS instrumentation and data analysis strategy. 2019 , 15, 348-360	71
1158	Potential early clinical stage colorectal cancer diagnosis using a proteomics blood test panel. 2019 , 16, 34	26
1157	Proteogenomics: From next-generation sequencing (NGS) and mass spectrometry-based proteomics to precision medicine. 2019 , 498, 38-46	25
1156	Experimental data from flesh quality assessment and shelf life monitoring of high pressure processed European sea bass () fillets. 2019 , 26, 104451	3
1155	Barocycler-Based Concurrent Multiomics Method To Assess Molecular Changes Associated with Atherosclerosis Using Small Amounts of Arterial Tissue from a Single Mouse. 2019 , 91, 12670-12679	1
1154	R-MetaboList 2: A Flexible Tool for Metabolite Annotation from High-Resolution Data-Independent Acquisition Mass Spectrometry Analysis. 2019 , 9,	5
1153	Characterisation of hybrid yeasts for the production of varietal Sauvignon blanc wine - A review. 2019 , 165, 105699	9
1152	Proteomics advances for precision therapy in ovarian cancer. 2019 , 16, 841-850	2
1151	Mass Spectrometry for Cancer Biomarkers. 2019 ,	1
1150	Methods and Challenges for Computational Data Analysis for DNA Adductomics. 2019 , 32, 2156-2168	7
1149	The Core Proteome of Biofilm-Grown Clinical Isolates. 2019 , 8,	17
1148	Proteomics and proteoforms: Bottom-up or top-down, how to use high-resolution mass spectrometry to reach the Grail. 2019 , 529-567	1
1147	Dietary Sugars Alter Hepatic Fatty Acid Oxidation via Transcriptional and Post-translational Modifications of Mitochondrial Proteins. 2019 , 30, 735-753.e4	66
1146	Mass Spectrometry-Based Plasma Proteomics: Considerations from Sample Collection to Achieving Translational Data. 2019 , 18, 4085-4097	56
1145	DIALignR Provides Precise Retention Time Alignment Across Distant Runs in DIA and Targeted Proteomics. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 806-817	7.6 10
1144	Progress and Challenges in Ocean Metaproteomics and Proposed Best Practices for Data Sharing. 2019 , 18, 1461-1476	39

1143	Data-independent acquisition-based quantitative proteomic analysis reveals differences in host immune response of peripheral blood mononuclear cells to sepsis. 2019 , 89, e12748		9
1142	Quantitation of Glycopeptides by ESI/MS - size of the peptide part strongly affects the relative proportions and allows discovery of new glycan compositions of Ceruloplasmin. 2019 , 36, 13-26		2
1141	Data Independent Acquisition Mass Spectrometry Can Identify Circulating Proteins That Predict Future Weight Loss with a Diet and Exercise Programme. 2019 , 8,		6
1140	Inhibition of T cell activation and function by the adaptor protein CIN85. 2019 , 12,		11
1139	Prosit: proteome-wide prediction of peptide tandem mass spectra by deep learning. 2019 , 16, 509-518		242
1138	Hybrid SWATH/MS and HR-SRM/MS acquisition for phospholipidomics using QUAL/QUANT data processing. 2019 , 411, 5681-5690		9
1137	Novel interconnections of HOG signaling revealed by combined use of two proteomic software packages. 2019 , 17, 66		6
1136	A quantitative <i>Streptococcus pyogenes</i> -human protein-protein interaction map reveals localization of opsonizing antibodies. 2019 , 10, 2727		18
1135	MS-Empire Utilizes Peptide-level Noise Distributions for Ultra-sensitive Detection of Differentially Expressed Proteins. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 1880-1892	7.6	12
1134	Targeted Proteomics for Studying Pathogenic Bacteria. 2019 , 19, e1800435		20
1133	MS-Based Proteomic Analysis of Serum and Plasma: Problem of High Abundant Components and Lights and Shadows of Albumin Removal. 2019 , 1073, 57-76		26
1132	Comprehensive Target Analysis for 484 Organic Micropollutants in Environmental Waters by the Combination of Tandem Solid-Phase Extraction and Quadrupole Time-of-Flight Mass Spectrometry with Sequential Window Acquisition of All Theoretical Fragment-Ion Spectra Acquisition. 2019 , 91, 7749-7755		31
1131	Assessing the Relationship Between Mass Window Width and Retention Time Scheduling on Protein Coverage for Data-Independent Acquisition. 2019 , 30, 1396-1405		12
1130	Clinical biomarker discovery by SWATH-MS based label-free quantitative proteomics: impact of criteria for identification of differentiators and data normalization method. 2019 , 17, 184		7
1129	Metaproteomics of the human gut microbiota: Challenges and contributions to other OMICS.. 2019 , 14 Pt A, 18-30		19
1128	Boar semen proteomics and sperm preservation. 2019 , 137, 23-29		20
1127	Accurate Precursor Mass Assignment Improves Peptide Identification in Data-Independent Acquisition Mass Spectrometry. 2019 , 91, 8453-8460		3
1126	Mass spectrometry analysis of glycoprotein biomarkers in human blood of hepatocellular carcinoma. 2019 , 16, 553-568		2

1125	Improved segmented-scan spectral stitching for stable isotope resolved metabolomics (SIRM) by ultra-high-resolution Fourier transform mass spectrometry. 2019 , 1080, 104-115			4
1124	Changes in the intestinal mucosal proteome of turkeys (<i>Meleagris gallopavo</i>) infected with haemorrhagic enteritis virus. 2019 , 213, 109880			
1123	Identification of potential metabolic biomarkers of polycystic ovary syndrome in follicular fluid by SWATH mass spectrometry. 2019 , 17, 45			19
1122	Single Cell Proteomics by Data-Independent Acquisition To Study Embryonic Asymmetry in. 2019 , 91, 8891-8899			19
1121	Simultaneous Improvement in the Precision, Accuracy, and Robustness of Label-free Proteome Quantification by Optimizing Data Manipulation Chains. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 1683-1699	7.6		70
1120	Metaproteomic investigation to assess gut microbiota shaping in newborn mice: A combined taxonomic, functional and quantitative approach. 2019 , 203, 103378			7
1119	Development of Targeted Mass Spectrometry-Based Approaches for Quantitation of Proteins Enriched in the Postsynaptic Density (PSD). 2019 , 7,			12
1118	A new class of protein biomarkers based on subcellular distribution: application to a mouse liver cancer model. 2019 , 9, 6913			9
1117	Deeper investigation into the utility of functional class scoring in missing protein prediction from proteomics data. 2019 , 17, 1950013			3
1116	Screening a Resource of Recombinant Protein Fragments for Targeted Proteomics. 2019 , 18, 2706-2718			14
1115	Emerging Technologies in Mass Spectrometry-Based DNA Adductomics. 2019 , 8,			17
1114	High pressure processing of European sea bass (<i>Dicentrarchus labrax</i>) fillets and tools for flesh quality and shelf life monitoring. 2019 , 262, 83-91			21
1113	Evaluation of Urinary Proteome Library Generation Methods on Data-Independent Acquisition MS Analysis and its Application in Normal Urinary Proteome Analysis. 2019 , 13, e1800152			4
1112	Practical Integration of Multi-Run iTRAQ Data. 2019 , 1977, 199-215			
1111	Regulation of UCP1 and Mitochondrial Metabolism in Brown Adipose Tissue by Reversible Succinylation. 2019 , 74, 844-857.e7			58
1110	Challenges and promise at the interface of metaproteomics and genomics: an overview of recent progress in metaproteogenomic data analysis. 2019 , 16, 375-390			33
1109	A Combined Chemical Derivatization/Mass Spectrometric Method for the Enhanced Detection and Relative Quantification of Protein Ubiquitination. 2019 , 1977, 17-24			
1108	Recent insights into <i>Mycobacterium tuberculosis</i> through proteomics and implications for the clinic. 2019 , 16, 443-456			10

1107	Mechanisms, Detection, and Relevance of Protein Acetylation in Prokaryotes. 2019 , 10,		57
1106	Quantitative Proteomics of Presynaptic Mitochondria Reveal an Overexpression and Biological Relevance of Neuronal MitoNEET in Postnatal Brain Development. 2019 , 79, 370-386		8
1105	Recent Advances in MS-Based Plant Proteomics: Proteomics Data Validation Through Integration with Other Classic and -Omics Approaches. 2019 , 77-101		5
1104	Large-Scale Quantitative Comparison of Plasma Transmembrane Proteins between Two Human Blood-Brain Barrier Model Cell Lines, hCMEC/D3 and HBMEC/ci. 2019 , 16, 2162-2171		11
1103	Proteome profiling of <i>Pseudomonas aeruginosa</i> PAO1 identifies novel responders to copper stress. 2019 , 19, 69		11
1102	Cryopreservation Differentially Alters the Proteome of Epididymal and Ejaculated Pig Spermatozoa. 2019 , 20,		18
1101	Reductive Stress Selectively Disrupts Collagen Homeostasis and Modifies Growth Factor-independent Signaling Through the MAPK/Akt Pathway in Human Dermal Fibroblasts. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 1123-1137	7.6	5
1100	A Pathogen and a Non-pathogen Spotted Fever Group Trigger Differential Proteome Signatures in Macrophages. 2019 , 9, 43		17
1099	Combining Rapid Data Independent Acquisition and CRISPR Gene Deletion for Studying Potential Protein Functions: A Case of HMGN1. 2019 , 19, e1800438		14
1098	Sample Preparation for Proteomic Analysis of <i>Neisseria meningitidis</i> . 2019 , 1969, 105-112		1
1097	Instrumentation Applied to Metabolomic Analysis. 2019 , 239-292		
1096	Advancing untargeted metabolomics using data-independent acquisition mass spectrometry technology. 2019 , 411, 4349-4357		53
1095	Comparison of ELISA and HPLC-MS methods for the determination of exenatide in biological and biotechnology-based formulation matrices. 2019 , 9, 143-155		14
1094	MS1 ion current-based quantitative proteomics: A promising solution for reliable analysis of large biological cohorts. 2019 , 38, 461-482		20
1093	A Study into the ADP-Ribosylome of IFN- γ -Stimulated THP-1 Human Macrophage-like Cells Identifies ARTD8/PARP14 and ARTD9/PARP9 ADP-Ribosylation. 2019 , 18, 1607-1622		13
1092	Quantification of Dynamic Protein Interactions and Phosphorylation in LPS Signaling Pathway by SWATH-MS. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 1054-1069	7.6	4
1091	Measuring Amber Initiator tRNA Orthogonality in a Genomically Recoded Organism. 2019 , 8, 675-685		8
1090	Two-dimensional mass spectrometry: new perspectives for tandem mass spectrometry. 2019 , 48, 213-229		19

1089	Discovering Protein Biomarkers from Clinical Peripheral Blood Mononuclear Cells Using Data-Independent Acquisition Mass Spectrometry. 2019 , 1959, 151-161	
1088	Rapid, Untargeted Chemical Profiling of Single Cells in Their Native Environment. 2019 , 91, 6118-6126	23
1087	Bio-derived hydroxystearic acid ameliorates skin age spots and conspicuous pores. 2019 , 41, 240-256	14
1086	Omics: Potential Role in Early Phase Drug Development. 2019 , 309-347	
1085	Integrated Tear Proteome and Metabolome Reveal Panels of Inflammatory-Related Molecules via Key Regulatory Pathways in Dry Eye Syndrome. 2019 , 18, 2321-2330	15
1084	Proteomics Approaches to Define Senescence Heterogeneity and Chemotherapy Response. 2019 , 19, e1800447	4
1083	Next Generation Proteomics for Clinical Biomarker Detection Using SWATH-MS. 2019 , 1977, 3-15	4
1082	Sensitive Quantitative Proteomics of Human Hematopoietic Stem and Progenitor Cells by Data-independent Acquisition Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 1454-1467 ^{7,6}	26
1081	Molecular insights into cancer drug resistance from a proteomics perspective. 2019 , 16, 413-429	12
1080	Improving Precursor Selectivity in Data-Independent Acquisition Using Overlapping Windows. 2019 , 30, 669-684	41
1079	Adipose Tissue Exosomal Proteomic Profile Reveals a Role on Placenta Glucose Metabolism in Gestational Diabetes Mellitus. 2019 , 104, 1735-1752	48
1078	The Case for Proteomics and Phospho-Proteomics in Personalized Cancer Medicine. 2019 , 13, e1800113	56
1077	Chemometrics-assisted optimization of liquid chromatography-quadrupole-time-of-flight mass spectrometry analysis for targeted metabolomics. 2019 , 199, 380-387	7
1076	Multi-Reference Spectral Library Yields Almost Complete Coverage of Heterogeneous LC-MS/MS Data Sets. 2019 , 18, 1553-1566	3
1075	Rapid screening methods for yeast sub-metabolome analysis with a high-resolution ion mobility quadrupole time-of-flight mass spectrometer. 2019 , 33 Suppl 2, 66-74	12
1074	Comparison of Protein Quantification in a Complex Background by DIA and TMT Workflows with Fixed Instrument Time. 2019 , 18, 1340-1351	47
1073	Multiomic Profiling of Tyrosine Kinase Inhibitor-Resistant K562 Cells Suggests Metabolic Reprogramming To Promote Cell Survival. 2019 , 18, 1842-1856	6
1072	Mass Spectrometry and Chemical Biology in Epigenetics Drug Discovery. 2019 , 79-106	

1071	The proteome of frozen-thawed pig spermatozoa is dependent on the ejaculate fraction source. 2019 , 9, 705		10
1070	Range size and growth temperature influence Eucalyptus species responses to an experimental heatwave. 2019 , 25, 1665-1684		26
1069	Multi-omic measurements of heterogeneity in HeLa cells across laboratories. 2019 , 37, 314-322		129
1068	Application of Data-Independent Acquisition Approach to Study the Proteome Change from Early to Later Phases of Tomato Pathogenesis Responses. 2019 , 20,		11
1067	A Multiplex Fragment-Ion-Based Method for Accurate Proteome Quantification. 2019 , 91, 3921-3928		7
1066	Global Lysine Acetylation in Results from Growth Conditions That Favor Acetate Fermentation. 2019 , 201,		13
1065	Advances in Biomarker Studies in Autism Spectrum Disorders. 2019 , 1118, 207-233		18
1064	Development and validation of an analytical method for determination of pharmaceuticals in fish muscle based on QuEChERS extraction and SWATH acquisition using LC-QTOF-MS/MS system. 2019 , 199, 370-379		25
1063	Quantitative Proteomics Uncovers the Interaction between a Virulence Factor and Mutanobactin Synthetases in. 2019 , 4,		2
1062	Proteomics, Glycomics, and Glycoproteomics of Matrisome Molecules. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 2138-2148	7.6	24
1061	Proteomics Recapitulates Ovarian Proteins Relevant to Puberty and Fertility in Brahman Heifers (L.). 2019 , 10,		6
1060	A Multiple Protease Strategy to Optimise the Shotgun Proteomics of Mature Medicinal Cannabis Buds. 2019 , 20,		4
1059	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. 2019 , 21, 664-680		21
1058	Classification of mouse B cell types using surfaceome proteotype maps. 2019 , 10, 5734		10
1057	Why Glycosylation Matters in Building a Better Flu Vaccine. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 2348-2358	7.6	37
1056	Radiation-Stimulated Translocation of CD166 and CRYAB to the Endothelial Surface Provides Potential Vascular Targets on Irradiated Brain Arteriovenous Malformations. 2019 , 20,		3
1055	Optimization of Data-Independent Acquisition Mass Spectrometry for Deep and Highly Sensitive Proteomic Analysis. 2019 , 20,		32
1054	Finding Needles in Haystacks: The Use of Quantitative Proteomics for the Early Detection of Colorectal Cancer. 2019 ,		0

1053	Quantitative Protein Expression in the Human Retinal Pigment Epithelium: Comparison Between Apical and Basolateral Plasma Membranes With Emphasis on Transporters. 2019 , 60, 5022-5034	8
1052	Arabidopsis proteome and the mass spectral assay library. 2019 , 6, 278	24
1051	Sex-dependent and sex-independent regulatory systems of size variation in natural populations. 2019 , 15, e9012	3
1050	SWATH Differential Abundance Proteomics and Cellular Assays Show In Vitro Anticancer Activity of Arachidonic Acid- and Docosahexaenoic Acid-Based Monoacylglycerols in HT-29 Colorectal Cancer Cells. 2019 , 11,	4
1049	Optimization of TripleTOF spectral simulation and library searching for confident localization of phosphorylation sites. 2019 , 14, e0225885	3
1048	Comprehensive MS/MS profiling by UHPLC-ESI-QTOF-MS/MS using SWATH data-independent acquisition for the study of platelet lipidomes in coronary artery disease. 2019 , 1046, 1-15	30
1047	Omentin-regulated proteins combine a pro-inflammatory phenotype with an anti-inflammatory counterregulation in human adipocytes: A proteomics analysis. 2019 , 35, e3074	7
1046	Absolute Quantification of All Identified Plasma Proteins from SWATH Data for Biomarker Discovery. 2019 , 19, e1800135	7
1045	Identification of Blood-Brain Barrier-Permeable Proteins Derived from a Peripheral Organ: In Vivo and in Vitro Evidence of Blood-to-Brain Transport of Creatine Kinase. 2019 , 16, 247-257	3
1044	The role of thermostable proteinaceous α -amylase inhibitors in slowing starch digestion in pasta. 2019 , 90, 241-247	27
1043	Data-Independent Acquisition for the Orbitrap Q Exactive HF: A Tutorial. 2019 , 18, 803-813	20
1042	Ecotoxicoproteomics: A decade of progress in our understanding of anthropogenic impact on the environment. 2019 , 198, 66-77	40
1041	High-Resolution Nano-Liquid Chromatography with Tandem Mass Spectrometric Detection for the Bottom-Up Analysis of Complex Proteomic Samples. 2019 , 82, 101-110	11
1040	On the contribution of mass spectrometry-based platforms to the field of personalized oncology. 2019 , 110, 129-142	3
1039	Proteomics Profiling of Pancreatic Cancer: Roles in Biomarker Discovery. 2019 , 299-311	
1038	Quantitative analysis of chemoresistance-inducing fatty acid in food supplements using UHPLC-ESI-MS/MS. 2019 , 411, 479-491	4
1037	Recent applications of omics-based technologies to main topics in food authentication. 2019 , 110, 221-232	48
1036	MSstatsQC 2.0: R/Bioconductor Package for Statistical Quality Control of Mass Spectrometry-Based Proteomics Experiments. 2019 , 18, 678-686	2

1035	Cluster of Differentiation 46 Is the Major Receptor in Human Blood-Brain Barrier Endothelial Cells for Uptake of Exosomes Derived from Brain-Metastatic Melanoma Cells (SK-Mel-28). 2019 , 16, 292-304	28
1034	Application of Proteomics to Inflammatory Bowel Disease Research: Current Status and Future Perspectives. 2019 , 2019, 1426954	9
1033	A Review on Quantitative Multiplexed Proteomics. 2019 , 20, 1210-1224	110
1032	Complex-centric proteome profiling by SEC-SWATH-MS. 2019 , 15, e8438	61
1031	A Case Study and Methodology for OpenSWATH Parameter Optimization Using the ProCan90 Data Set and 45 810 Computational Analysis Runs. 2019 , 18, 1019-1031	3
1030	Data-independent Acquisition Improves Quantitative Cross-linking Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 786-795	7.6 20
1029	Comparing SRM and SWATH Methods for Quantitation of Bovine Muscle Proteomes. 2019 , 67, 1608-1618	20
1028	Comparison of simple monophasic versus classical biphasic extraction protocols for comprehensive UHPLC-MS/MS lipidomic analysis of Hela cells. 2019 , 1048, 66-74	27
1027	SWATH data independent acquisition mass spectrometry for metabolomics. 2019 , 120, 115278	40
1026	Implementation of normalized retention time (iRT) for bottom-up proteomic analysis of the aminoglycoside phosphotransferase enzyme facilitating method distribution. 2019 , 411, 4701-4708	1
1025	Identification of Protein Abundance Changes in Hepatocellular Carcinoma Tissues Using PCT-SWATH. 2019 , 13, e1700179	19
1024	The Role of Ultra Performance Liquid Chromatography-Mass Spectrometry in Metabolic Phenotyping. 2019 , 97-136	1
1023	Sample Multiplexing Strategies in Quantitative Proteomics. 2019 , 91, 178-189	37
1022	Proteome Analysis of Phase-Separated Condensed Proteins with Ionic Surfactants Revealed Versatile Formation of Artificial Biomolecular Condensates. 2019 , 20, 539-545	3
1021	A Guide to Mass Spectrometry-Based Quantitative Proteomics. 2019 , 1916, 3-39	13
1020	A Data Analysis Protocol for Quantitative Data-Independent Acquisition Proteomics. 2019 , 1871, 455-465	3
1019	Proteome Profiling by Label-Free Mass Spectrometry Reveals Differentiated Response of <i>Campylobacter jejuni</i> 81-176 to Sublethal Concentrations of Bile Acids. 2019 , 13, e1800083	1
1018	An Overview of Mass Spectrometry-Based Methods for Functional Proteomics. 2019 , 1871, 179-196	7

1017	Advanced bioinformatics methods for practical applications in proteomics. 2019 , 20, 347-355		11
1016	Quantification of molecular heterogeneity in kidney tissue by targeted proteomics. 2019 , 193, 85-92		10
1015	Human follicular fluid proteomic and peptidomic composition quantitative studies by SWATH-MS methodology. Applicability of high pH RP-HPLC fractionation. 2019 , 191, 131-142		11
1014	MHC class I presented antigens from malignancies: A perspective on analytical characterization & immunogenicity. 2019 , 191, 48-57		11
1013	Anatomy and evolution of database search engines-a central component of mass spectrometry based proteomic workflows. 2020 , 39, 292-306		60
1012	The Skyline ecosystem: Informatics for quantitative mass spectrometry proteomics. 2020 , 39, 229-244		220
1011	DNA adducts: Formation, biological effects, and new biospecimens for mass spectrometric measurements in humans. 2020 , 39, 55-82		27
1010	Mapping Taste-Relevant Food Peptidomes by Means of Sequential Window Acquisition of All Theoretical Fragment Ion-Mass Spectrometry. 2020 , 68, 10287-10298		4
1009	Evaluation of sample preparation methods for label-free quantitative profiling of salivary proteome. 2020 , 210, 103532		6
1008	Serum proteome of dogs at subclinical and clinical onset of canine leishmaniosis. 2020 , 67, 318-327		4
1007	Lipid Atlas of Keratinocytes and Betulin Effects on its Lipidome Profiled by Comprehensive UHPLC-MS/MS with Data Independent Acquisition Using Targeted Data Processing. 2020 , 20, e1900113		4
1006	A quantitative proteomic and bioinformatics analysis of proteins in metacyclogenesis of <i>Leishmania tropica</i> . 2020 , 202, 105227		8
1005	Proteomic Investigations of In Vitro and In Vivo Models of Periodontal Disease. 2020 , 14, e1900043		2
1004	Automation of mass spectrometric detection of analytes and related workflows: A review. 2020 , 208, 120304		18
1003	Reproducibility, Specificity and Accuracy of Relative Quantification Using Spectral Library-based Data-independent Acquisition. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 181-197	7.6	38
1002	Proteomics. 2020 , 93-118		1
1001	Quantitative proteomics in development of disease protein biomarkers. 2020 , 261-288		2
1000	Proteomic analysis of rat kidney under maleic acid treatment by SWATH-MS technology. 2020 , 34 Suppl 1, e8633		1

999	Proteomic dissection of the chloroplast: Moving beyond photosynthesis. 2020 , 212, 103542	4
998	Comparing Data-Independent Acquisition and Parallel Reaction Monitoring in Their Abilities To Differentiate High-Density Lipoprotein Subclasses. 2020 , 19, 248-259	7
997	Systematic Assessment of the Effect of Internal Library in Targeted Analysis of SWATH-MS. 2020 , 19, 477-492	7
996	Partially overlapping sequential window acquisition of all theoretical mass spectra: A methodology to improve the spectra quality of veterinary drugs present at low concentrations in highly complex biological matrices. 2020 , 34, e8638	0
995	In silico spectral libraries by deep learning facilitate data-independent acquisition proteomics. 2020 , 11, 146	59
994	Robust, reproducible and quantitative analysis of thousands of proteomes by micro-flow LC-MS/MS. 2020 , 11, 157	105
993	iq: an R package to estimate relative protein abundances from ion quantification in DIA-MS-based proteomics. 2020 , 36, 2611-2613	12
992	Rapid determination of isoflavones and other bioactive compounds in soybean using SWATH-MS. 2020 , 1103, 122-133	5
991	Exploring mechanisms of increased cardiovascular disease risk with antipsychotic medications: Risperidone alters the cardiac proteomic signature in mice. 2020 , 152, 104589	11
990	Quantitative Proteomics Analysis by Sequential Window Acquisition of All Theoretical Mass Spectra-Mass Spectrometry Reveals Inhibition Mechanism of Pigments and Citrinin Production of Response to High Ammonium Chloride Concentration. 2020 , 68, 808-817	10
989	An Integrated Mass Spectroscopy Data Processing Strategy for Fast Identification, In-Depth, and Reproducible Quantification of Protein -Glycosylation in a Large Cohort of Human Urine Samples. 2020 , 92, 690-698	14
988	Phase-Variable Glycosylation in Nontypeable. 2020 , 19, 464-476	8
987	The clinical potential of thiol redox proteomics. 2020 , 17, 41-48	2
986	DIA-NN: neural networks and interference correction enable deep proteome coverage in high throughput. 2020 , 17, 41-44	179
985	The use of missing values in proteomic data-independent acquisition mass spectrometry to enable disease activity discrimination. 2020 , 36, 2217-2223	12
984	Comparative analysis of constituents and metabolites for traditional Chinese medicine using IDA and SWATH data acquisition modes on LC-Q-TOF MS. 2020 , 10, 588-596	6
983	Comparative Proteomic Analysis of Nodulated and Non-Nodulated Sieb. ex Spreng. Grown under Salinity Conditions Using Sequential Window Acquisition of All Theoretical Mass Spectra (SWATH-MS). 2019 , 21,	8
982	Identification of gene fusion events in that encode chimeric proteins. 2020 , 2, lqaa033	1

981	Surfaceome dynamics reveal proteostasis-independent reorganization of neuronal surface proteins during development and synaptic plasticity. 2020 , 11, 4990	9
980	Recent advances in analytical strategies for mass spectrometry-based lipidomics. 2020 , 1137, 156-169	29
979	Quantifying Plant Dynamic Proteomes by SWATH-based Mass Spectrometry. 2020 , 25, 1171-1172	8
978	Operational Modes and Speed Considerations of an Acoustic Droplet Dispenser for Mass Spectrometry. 2020 , 92, 15818-15826	11
977	The effects of p53 gene inactivation on mutant proteome expression in a human melanoma cell model. 2020 , 1864, 129722	2
976	PASS-DIA: A Data-Independent Acquisition Approach for Discovery Studies. 2020 , 92, 14466-14475	8
975	Standardization and harmonization of distributed multi-center proteotype analysis supporting precision medicine studies. 2020 , 11, 5248	13
974	Characterization of Phosphopeptide Positional Isomers on the Transcriptional Co-activator TAZ. 2020 , 59, 4148-4154	0
973	DIALib-QC an assessment tool for spectral libraries in data-independent acquisition proteomics. 2020 , 11, 5251	11
972	An assessment of quality assurance/quality control efforts in high resolution mass spectrometry non-target workflows for analysis of environmental samples. 2020 , 133, 116063	25
971	SWATH-MS based proteomic profiling of pancreatic ductal adenocarcinoma tumours reveals the interplay between the extracellular matrix and related intracellular pathways. 2020 , 15, e0240453	3
970	Argonaut: A Web Platform for Collaborative Multi-omic Data Visualization and Exploration. 2020 , 1,	7
969	MSpectraAI: a powerful platform for deciphering proteome profiling of multi-tumor mass spectrometry data by using deep neural networks. 2020 , 21, 439	1
968	Bacterial nanotubes as a manifestation of cell death. 2020 , 11, 4963	12
967	Complex-centric proteome profiling by SEC-SWATH-MS for the parallel detection of hundreds of protein complexes. 2020 , 15, 2341-2386	17
966	Data-Independent Acquisition Proteomics Unravels the Effects of Iron Ions on Coronatine Synthesis in pv. DC3000. 2020 , 11, 1362	4
965	PSMD11, PTPRM and PTPRB as novel biomarkers of pancreatic cancer progression. 2020 , 1864, 129682	9
964	Cytochrome c Reductase is a Key Enzyme Involved in the Extracellular Electron Transfer Pathway towards Transition Metal Complexes in Pseudomonas Putida. 2020 , 13, 5308-5317	4

963	Effects of electron-transfer/higher-energy collisional dissociation (ETHcD) on phosphopeptide analysis by data-independent acquisition. 2020 , 452, 116336	1
962	Multi-layered proteomic analyses decode compositional and functional effects of cancer mutations on kinase complexes. 2020 , 11, 3563	16
961	Application of pseudotargeted method combined with multivariate statistical analysis for the quality assessment of traditional Chinese medicine preparation, Sanhuang Tablet as a case. 2020 , 412, 5863-5872	1
960	Establishment and validation of highly accurate formalin-fixed paraffin-embedded quantitative proteomics by heat-compatible pressure cycling technology using phase-transfer surfactant and SWATH-MS. 2020 , 10, 11271	9
959	Increased C-X-C Motif Chemokine Ligand 12 Levels in Cerebrospinal Fluid as a Candidate Biomarker in Sporadic Amyotrophic Lateral Sclerosis. 2020 , 21,	2
958	Avant-garde: an automated data-driven DIA data curation tool. 2020 , 17, 1237-1244	8
957	diaPASEF: parallel accumulation-serial fragmentation combined with data-independent acquisition. 2020 , 17, 1229-1236	85
956	The Nucleosome Remodeling and Deacetylase Complex Has an Asymmetric, Dynamic, and Modular Architecture. 2020 , 33, 108450	5
955	A Versatile Isobaric Tag Enables Proteome Quantification in Data-Dependent and Data-Independent Acquisition Modes. 2020 , 92, 16149-16157	7
954	A comprehensive spectral assay library to quantify the Escherichia coli proteome by DIA/SWATH-MS. 2020 , 7, 389	7
953	Ubiquitination of phytoene synthase 1 precursor modulates carotenoid biosynthesis in tomato. 2020 , 3, 730	8
952	Bringing New Methods to the Seed Proteomics Platform: Challenges and Perspectives. 2020 , 21,	11
951	DIA-based systems biology approach unveils E3 ubiquitin ligase-dependent responses to a metabolic shift. 2020 , 117, 32806-32815	11
950	Mass spectrometry-based proteomics of single cells and organoids: The new generation of cancer research. 2020 , 130, 116005	1
949	DPHL: A DIA Pan-human Protein Mass Spectrometry Library for Robust Biomarker Discovery. 2020 , 18, 104-119	23
948	Recent advances in autophagic machinery: a proteomic perspective. 2020 , 17, 561-579	1
947	Probing SWATH-MS as a tool for proteome level quantification in a nonmodel fish. 2020 , 20, 1647-1657	4
946	Strategies to enable large-scale proteomics for reproducible research. 2020 , 11, 3793	26

945	Spatially resolved analysis of FFPE tissue proteomes by quantitative mass spectrometry. 2020 , 15, 2956-2979	10
944	The Mitochondrial Proteomic Signatures of Human Skeletal Muscle Linked to Insulin Resistance. 2020 , 21,	3
943	The status of proteomics as we enter the 2020s: Towards personalised/precision medicine. 2020 , 113840	6
942	Generating Proteomic Big Data for Precision Medicine. 2020 , 20, e1900358	6
941	Prostate Cancer Biomarker Development: National Cancer Institute's Early Detection Research Network Prostate Cancer Collaborative Group Review. 2020 , 29, 2454-2462	5
940	PHOSPHO1 is a skeletal regulator of insulin resistance and obesity. 2020 , 18, 149	2
939	Glioma stem-like cells evade interferon suppression through MBD3/NuRD complex-mediated STAT1 downregulation. 2020 , 217,	14
938	Phenotype Classification using Proteome Data in a Data-Independent Acquisition Tensor Format. 2020 , 31, 2296-2304	2
937	The endosomal protein sorting nexin 4 is a synaptic protein. 2020 , 10, 18239	2
936	Utility of Proteomics in Emerging and Re-Emerging Infectious Diseases Caused by RNA Viruses. 2020 , 19, 4259-4274	14
935	Mitochondrial translation and dynamics synergistically extend lifespan in <i>C. elegans</i> through HLH-30. 2020 , 219,	16
934	Molecular insights into the genome dynamics and interactions between core and acquired genomes of. 2020 , 117, 23762-23773	11
933	Challenges and Opportunities in Clinical Applications of Blood-Based Proteomics in Cancer. 2020 , 12,	20
932	Proteomics-Based Methodologies for the Detection and Quantification of Seafood Allergens. 2020 , 9,	13
931	Nonalcoholic Fatty Liver Disease (NAFLD) and Hepatic Cytochrome P450 (CYP) Enzymes. 2020 , 13,	8
930	Comparison of high resolution mrm and sequential window acquisition of all theoretical fragment-ion acquisition modes for the quantitation of 48 wastewater-borne pollutants in lettuce. 2020 , 1631, 461566	9
929	A comprehensive CHO SWATH-MS spectral library for robust quantitative profiling of 10,000 proteins. 2020 , 7, 263	7
928	Isolation Window Optimization of Data-Independent Acquisition Using Predicted Libraries for Deep and Accurate Proteome Profiling. 2020 , 92, 12185-12192	12

927	Longitudinal Plasma Protein Profiling Using Targeted Proteomics and Recombinant Protein Standards. 2020 , 19, 4815-4825	4
926	Application of Proteomics in Sarcoidosis. 2020 , 63, 727-738	4
925	Deadly Proteomes: A Practical Guide to Proteotranscriptomics of Animal Venoms. 2020 , 20, e1900324	10
924	Proteomic Strategies to Evaluate the Impact of Farming Conditions on Food Quality and Safety in Aquaculture Products. 2020 , 9,	8
923	Maturation Kinetics of a Multiprotein Complex Revealed by Metabolic Labeling. 2020 , 183, 1785-1800.e26	13
922	Data-Independent Acquisition for the Quantification and Identification of Metabolites in Plasma. 2020 , 10,	10
921	Parallel Factor Analysis Enables Quantification and Identification of Highly Convolved Data-Independent-Acquired Protein Spectra. 2020 , 1, 100137	0
920	Smelling the Dark Proteome: Functional Characterization of PITH Domain-Containing Protein 1 (C1orf128) in Olfactory Metabolism. 2020 , 19, 4826-4843	3
919	Proteomic signatures of 16 major types of human cancer reveal universal and cancer-type-specific proteins for the identification of potential therapeutic targets. 2020 , 13, 170	7
918	Understanding Mechanisms Underlying Non-Alcoholic Fatty Liver Disease (NAFLD) in Mental Illness: Risperidone and Olanzapine Alter the Hepatic Proteomic Signature in Mice. 2020 , 21,	7
917	Vaccination with Alpha-Gal Protects Against Mycobacterial Infection in the Zebrafish Model of Tuberculosis. 2020 , 8,	15
916	SWATH-MS based quantitative proteomics analysis to evaluate the antileishmanial effect of Commiphora wightii- Guggul and Amphotericin B on a clinical isolate of Leishmania donovani. 2020 , 223, 103800	5
915	Mixed-Data Acquisition: Next-Generation Quantitative Proteomics Data Acquisition. 2020 , 222, 103803	3
914	Salivary proteome signatures in the early and middle stages of human pregnancy with term birth outcome. 2020 , 10, 8022	2
913	PolySTest: Robust Statistical Testing of Proteomics Data with Missing Values Improves Detection of Biologically Relevant Features. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 1396-1408	7.6 6
912	Analytical techniques for multiplex analysis of protein biomarkers. 2020 , 17, 257-273	24
911	The power of proteomics to monitor senescence-associated secretory phenotypes and beyond: toward clinical applications. 2020 , 17, 297-308	14
910	SWATH-MS analysis of cerebrospinal fluid to generate a robust battery of biomarkers for Alzheimer's disease. 2020 , 10, 7423	9

909	Proteome Analysis of Hordein-Null Barley Lines Reveals Storage Protein Synthesis and Compensation Mechanisms. 2020 , 68, 5763-5775	7
908	Redox controls metabolic robustness in the gas-fermenting acetogen. 2020 , 117, 13168-13175	23
907	Multi-in-One: Multiple-Proteases, One-Hour-Shot Strategy for Fast and High-Coverage Phosphoproteomic Investigation. 2020 , 92, 8943-8951	2
906	iSwathX 2.0 for Processing DDA Spectral Libraries for DIA Data Analysis. 2020 , 70, e101	1
905	Ultra-High-Throughput Clinical Proteomics Reveals Classifiers of COVID-19 Infection. 2020 , 11, 11-24.e4	219
904	Platform independent protein-based cell-of-origin subtyping of diffuse large B-cell lymphoma in formalin-fixed paraffin-embedded tissue. 2020 , 10, 7876	2
903	Recent advances in mass spectrometry based clinical proteomics: applications to cancer research. 2020 , 17, 17	65
902	NAGuideR: performing and prioritizing missing value imputations for consistent bottom-up proteomic analyses. 2020 , 48, e83	28
901	High-Throughput and Integrated Chemical Proteomic Approach for Profiling Phosphotyrosine Signaling Complexes. 2020 , 92, 8933-8942	3
900	MetaboKit: a comprehensive data extraction tool for untargeted metabolomics. 2020 , 16, 436-447	7
899	Skin proteomics - analysis of the extracellular matrix in health and disease. 2020 , 17, 377-391	3
898	2D MS/MS Spectra Recorded in the Time Domain Using Repetitive Frequency Sweeps in Linear Quadrupole Ion Traps. 2020 , 92, 10016-10023	7
897	Development of a plasma pseudotargeted metabolomics method based on ultra-high-performance liquid chromatography-mass spectrometry. 2020 , 15, 2519-2537	44
896	A mouse SWATH-mass spectrometry reference spectral library enables deconvolution of species-specific proteomic alterations in human tumour xenografts. 2020 , 13,	6
895	Quantitative Proteomics Analysis by Sequential Window Acquisition of All Theoretical Mass Spectra-Mass Spectrometry Reveals a Cross-Protection Mechanism for To Tolerate High-Concentration Ammonium Chloride. 2020 , 68, 6672-6682	3
894	High throughput generation of a resource of the human secretome in mammalian cells. 2020 , 58, 45-54	7
893	Liquid Chromatography-Tandem Mass Spectrometry (LC-MS/MS)-Based Proteomics of Drug-Metabolizing Enzymes and Transporters. 2020 , 25,	9
892	Impact of the Identification Strategy on the Reproducibility of the DDA and DIA Results. 2020 , 19, 3153-3161	14

891	MealTime-MS: A Machine Learning-Guided Real-Time Mass Spectrometry Analysis for Protein Identification and Efficient Dynamic Exclusion. 2020 , 31, 1459-1472	3
890	Lon Protease Is Important for Growth Under Stressful Conditions and Pathogenicity of the Phytopathogen, Bacterium. 2020 , 21,	4
889	Isoform-resolved correlation analysis between mRNA abundance regulation and protein level degradation. 2020 , 16, e9170	14
888	Identification of Novel Biomarkers in Pancreatic Tumor Tissue to Predict Response to Neoadjuvant Chemotherapy. 2020 , 10, 237	11
887	Glycopeptide variable window SWATH for improved data independent acquisition glycoprotein analysis. 2020 , 597, 113667	14
886	Abundances of transcripts, proteins, and metabolites in the cell cycle of budding yeast reveal coordinate control of lipid metabolism. 2020 , 31, 1069-1084	10
885	Comparative Analysis of Quantitative Mass Spectrometric Methods for Subcellular Proteomics. 2020 , 19, 1718-1730	6
884	Monitoring protein communities and their responses to therapeutics. 2020 , 19, 414-426	19
883	Omics technologies for kidney disease research. 2020 , 303, 2729-2742	3
882	Orthogonal Proteomic Platforms and Their Implications for the Stable Classification of High-Grade Serous Ovarian Cancer Subtypes. 2020 , 23, 101079	10
881	Proteomics and Informatics for Understanding Phases and Identifying Biomarkers in COVID-19 Disease. 2020 , 19, 4219-4232	48
880	Synthesizing Systems Biology Knowledge from Omics Using Genome-Scale Models. 2020 , 20, e1900282	14
879	The development and clinical applications of proteomics: an Indian perspective. 2020 , 17, 433-451	0
878	Hyphenations of one-dimensional capillary liquid chromatography with mass spectrometry. 2020 , 319-367	
877	A Comprehensive Proteomic SWATH-MS Workflow for Profiling Blood Extracellular Vesicles: A New Avenue for Glioma Tumour Surveillance. 2020 , 21,	15
876	Discrimination of meat from fur-producing and food-providing animals using mass spectrometry-based proteomics. 2020 , 137, 109446	2
875	Recent advances in non-targeted screening analysis using liquid chromatography - high resolution mass spectrometry to explore new biomarkers for human exposure. 2020 , 219, 121339	13
874	Mass Defect-Based DiLeu Tagging for Multiplexed Data-Independent Acquisition. 2020 , 92, 11119-11126	9

873	Down syndrome. 2020 , 6, 9	120
872	A protocol for studying structural dynamics of proteins by quantitative crosslinking mass spectrometry and data-independent acquisition. 2020 , 218, 103721	5
871	Highly Parallel Quantification and Compartment Localization of Transcription Factors and Nuclear Proteins. 2020 , 30, 2463-2471.e5	8
870	Machine Learning in Mass Spectrometric Analysis of DIA Data. 2020 , 20, e1900352	10
869	DIALib: an automated ion library generator for data independent acquisition mass spectrometry analysis of peptides and glycopeptides. 2020 , 16, 100-112	7
868	Germ-free and microbiota-associated mice yield small intestinal epithelial organoids with equivalent and robust transcriptome/proteome expression phenotypes. 2020 , 22, e13191	15
867	Effects of increased scrotal temperature on semen quality and seminal plasma proteins in Brahman bulls. 2020 , 87, 574-597	3
866	Mass Spectrometry of Human Transporters. 2020 , 13, 223-247	3
865	The bio-chemically selective interaction of hydrogenated and oxidized ultra-small nanodiamonds with proteins and cells. 2020 , 162, 650-661	12
864	Hybrid Spectral Library Combining DIA-MS Data and a Targeted Virtual Library Substantially Deepens the Proteome Coverage. 2020 , 23, 100903	15
863	A Proteogenomic Resource Enabling Integrated Analysis of Genotype-Proteotype-Phenotype Relationships. 2020 , 19, 1647-1662	6
862	Accelerated Protein Biomarker Discovery from FFPE Tissue Samples Using Single-Shot, Short Gradient Microflow SWATH MS. 2020 , 19, 2732-2741	12
861	Click Chemistry in Proteomic Investigations. 2020 , 180, 605-632	92
860	Enhancing protein discoverability by data independent acquisition assisted by ion mobility mass spectrometry. 2020 , 213, 120812	6
859	Deep Proteomics Using Two Dimensional Data Independent Acquisition Mass Spectrometry. 2020 , 92, 4217-4225	15
858	High-throughput quantitative top-down proteomics. 2020 , 16, 91-99	34
857	A proteomic atlas of senescence-associated secretomes for aging biomarker development. 2020 , 18, e3000599	269
856	Developing front-end devices for improved sample preparation in MS-based proteome analysis. 2020 , 55, e4494	1

855	SWATH data independent acquisition mass spectrometry for screening of xenobiotics in biological fluids: Opportunities and challenges for data processing. 2020 , 211, 120747	13
854	Occurrences of microorganic pollutants in the Kumho River by a comprehensive target analysis using LC-Q/TOF-MS with sequential window acquisition of all theoretical fragment ion spectra (SWATH). 2020 , 713, 136508	6
853	Lipidomic profiling of non-mineralized dental plaque and biofilm by untargeted UHPLC-QTOF-MS/MS and SWATH acquisition. 2020 , 412, 2303-2314	2
852	Advancing serum peptidomic profiling by data-independent acquisition for clear-cell renal cell carcinoma detection and biomarker discovery. 2020 , 215, 103671	9
851	Activating transcription factor 4 (ATF4) promotes skeletal muscle atrophy by forming a heterodimer with the transcriptional regulator C/EBP β . 2020 , 295, 2787-2803	15
850	Deciphering tissue-based proteome signatures revealed novel subtyping and prognostic markers for thymic epithelial tumors. 2020 , 14, 721-741	3
849	Beyond mass spectrometry, the next step in proteomics. 2020 , 6, eaax8978	107
848	Advances and applications of stable isotope labeling-based methods for proteome relative quantitation. 2020 , 124, 115815	3
847	SWATH-MS Analysis of FFPE Tissues Identifies Stathmin as a Potential Marker of Endometrial Cancer in Patients Exposed to Tamoxifen. 2020 , 19, 2617-2630	5
846	ProteoViz: a tool for the analysis and interactive visualization of phosphoproteomics data. 2020 , 16, 316-326	8
845	Proteomics-based Predictive Model for the Early Detection of Metastasis and Recurrence in Head and Neck Cancer. 2020 , 17, 259-269	6
844	Glycomics and glycoproteomics of viruses: Mass spectrometry applications and insights toward structure-function relationships. 2020 , 39, 371-409	21
843	Data-Independent Acquisition Mass Spectrometry-Based Proteomics and Software Tools: A Glimpse in 2020. 2020 , 20, e1900276	74
842	Generating high quality libraries for DIA MS with empirically corrected peptide predictions. 2020 , 11, 1548	50
841	Generation of a murine SWATH-MS spectral library to quantify more than 11,000 proteins. 2020 , 7, 104	6
840	The Iron Deficiency Response of <i>Corynebacterium glutamicum</i> and a Link to Thiamine Biosynthesis. 2020 , 86,	5
839	Comprehensive Map of the <i>Artemisia annua</i> Proteome and Quantification of Differential Protein Expression in Chemotypes Producing High versus Low Content of Artemisinin. 2020 , 20, e1900310	3
838	Performance test methods for near-infrared fluorescence imaging. 2020 , 47, 3389-3401	9

837	The Wonderful World of Poo: The Turdome and Beyond. 2020 , 73, 257		
836	Comparative Evaluation of Data Dependent and Data Independent Acquisition Workflows Implemented on an Orbitrap Fusion for Untargeted Metabolomics. 2020 , 10,		24
835	Revealing Dynamic Protein Acetylation across Subcellular Compartments. 2020 , 19, 2404-2418		15
834	Mouse models of neutropenia reveal progenitor-stage-specific defects. 2020 , 582, 109-114		36
833	Acquiring and Analyzing Data Independent Acquisition Proteomics Experiments without Spectrum Libraries. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 1088-1103	7.6	45
832	Selection of Features with Consistent Profiles Improves Relative Protein Quantification in Mass Spectrometry Experiments. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 944-959	7.6	7
831	A circulating extracellular vesicles-based novel screening tool for colorectal cancer revealed by shotgun and data-independent acquisition mass spectrometry. 2020 , 9, 1750202		25
830	PGRMC1 phosphorylation affects cell shape, motility, glycolysis, mitochondrial form and function, and tumor growth. 2020 , 21, 24		17
829	Tick and Host Derived Compounds Detected in the Cement Complex Substance. 2020 , 10,		22
828	Combining Precursor and Fragment Information for Improved Detection of Differential Abundance in Data Independent Acquisition. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 421-430	7.6	14
827	Grass to Glass: Better Beer Through Proteomics. 2021 , 407-416		1
826	GLOBAL AND TARGETED PROFILING OF GTP-BINDING PROTEINS IN BIOLOGICAL SAMPLES BY MASS SPECTROMETRY. 2021 , 40, 215-235		6
825	Single-cell protein analysis by mass spectrometry. 2021 , 60, 1-9		45
824	Mass spectrometry-based lipidomics as a powerful platform in foodomics research. 2021 , 107, 358-376		24
823	Proteomic approaches for the profiling of ubiquitylation events and their applications in drug discovery. 2021 , 231, 103996		5
822	Optimized Sample Preparation and Data Processing of Data-Independent Acquisition Methods for the Robust Quantification of Trace-Level Host Cell Protein Impurities in Antibody Drug Products. 2021 , 20, 923-931		8
821	The tissue proteome in the multi-omic landscape of kidney disease. 2021 , 17, 205-219		12
820	SWATH-MS-Based Proteomics: Strategies and Applications in Plants. 2021 , 39, 433-437		18

819	PulseDIA: Data-Independent Acquisition Mass Spectrometry Using Multi-Injection Pulsed Gas-Phase Fractionation. 2021 , 20, 279-288	5
818	The separation sciences, the front end to proteomics: An historical perspective. 2021 , 35, e4995	4
817	Quantitative mass spectrometry-based analysis of proteins related to cattle and their products - Focus on cows' milk beta-casein proteoforms. 2021 , 186, 112-118	4
816	Data-independent acquisition mass spectrometry (DIA-MS) for proteomic applications in oncology. 2021 , 17, 29-42	23
815	Proteomics in Food Quality. 2021 , 699-717	0
814	Global and Site-Specific Effect of Phosphorylation on Protein Turnover. 2021 , 56, 111-124.e6	16
813	Species and tissue specific analysis based on quantitative proteomics from allotetraploid and the parents. 2021 , 232, 104073	0
812	A simultaneous exploratory and quantitative amino acid and biogenic amine metabolic profiling platform for rapid disease phenotyping via UPLC-QToF-MS. 2021 , 223, 121872	4
811	Mass defect-based carbonyl activated tags (mdCATs) for multiplex data-independent acquisition proteome quantification. 2021 , 57, 737-740	3
810	Development of an Ocean Protein Portal for Interactive Discovery and Education. 2021 , 20, 326-336	4
809	OP7, a novel influenza A virus defective interfering particle: production, purification, and animal experiments demonstrating antiviral potential. 2021 , 105, 129-146	11
808	Selective Labeling and Identification of the Tumor Cell Proteome of Pancreatic Cancer. 2021 , 20, 858-866	0
807	QuantPipe: A User-Friendly Pipeline Software Tool for DIA Data Analysis Based on the OpenSWATH-PyProphet-TRIC Workflow. 2021 , 20, 1096-1102	8
806	Data independent acquisition of plasma biomarkers of response to neoadjuvant chemotherapy in pancreatic ductal adenocarcinoma. 2021 , 231, 103998	3
805	Leveraging Immonium Ions for Targeting Acyl-Lysine Modifications in Proteomic Datasets. 2021 , 21, e2000111	3
804	Synergistic optimization of Liquid Chromatography and Mass Spectrometry parameters on Orbitrap Tribrid mass spectrometer for high efficient data-dependent proteomics. 2021 , 56, e4653	6
803	Mass spectrometry-based forest tree metabolomics. 2021 , 40, 126-157	7
802	Data Treatment in Food Proteomics. 2021 , 324-338	1

801	A Systems-Based Approach to Toxicity Testing. 2021 , 189-206		
800	Cross-Linking MS of the Complement System MAC Assembled on Live Gram-Positive Bacteria. 2020 , 11, 612475		3
799	System-Wide Profiling of Protein Complexes Via Size Exclusion Chromatography-Mass Spectrometry (SEC-MS). 2021 , 2259, 269-294		1
798	Methods for Proteogenomics Data Analysis, Challenges, and Scalability Bottlenecks: A Survey. 2021 , 9, 5497-5516		3
797	Anti-allergic drug azelastine suppresses colon tumorigenesis by directly targeting ARF1 to inhibit IQGAP1-ERK-Drp1-mediated mitochondrial fission. 2021 , 11, 1828-1844		12
796	Trapped Ion Mobility Spectrometry and Parallel Accumulation-Serial Fragmentation in Proteomics. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100138	7.6	13
795	Human obese white adipose tissue sheds depot-specific extracellular vesicles and reveals candidate biomarkers for monitoring obesity and its comorbidities. 2021 ,		11
794	Quantitative Mass Spectrometry-Based Proteomics: An Overview. 2021 , 2228, 85-116		9
793	Mass spectrometry-based protein-protein interaction networks for the study of human diseases. 2021 , 17, e8792		30
792	Data-independent acquisition method for ubiquitinome analysis reveals regulation of circadian biology. 2021 , 12, 254		24
791	Proteomic Profiling of Gastric Signet Ring Cell Carcinoma Tissues Reveals Characteristic Changes of the Complement Cascade Pathway. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100068	7.6	2
790	The Role of Data-Independent Acquisition for Glycoproteomics. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100042	7.6	15
789	In Vivo Protein Lifetime Measurements Across Multiple Organs in the Zebrafish. 2021 , 2218, 291-302		
788	Complement Activation Induces Excessive T Cell Cytotoxicity in Severe COVID-19.		1
787	Proteomics of exhaled breath condensate in lung cancer and controls using data-independent acquisition (DIA): a pilot study. 2020 ,		3
786	Comparative Proteomic Analysis of sensu lato (Acari: Ixodidae) Tropical and Temperate Lineages: Uncovering Differences During Infection. 2020 , 10, 611113		3
785	Chapter 3: Ion Pair Liquid Chromatography-Mass Spectrometry for Probing the Polar Metabolome. 2021 , 41-68		
784	Urinary proteome profiling for stratifying patients with familial Parkinson's disease. 2021 , 13, e13257		19

783	Automated Workflow for Peptide-Level Quantitation from DIA/SWATH-MS Data. 2021 , 2228, 453-468	2
782	Introduction to Data Analysis in Omics Sciences. 2021 , 226-240	
781	Targeted Proteomics for Rapid and Sensitive Detection of Foodborne Pathogens. 2021 , 123-136	
780	Current Approaches in Quantitative Proteomics. 2021 , 642-650	
779	Quantification and Identification of Post-Translational Modifications Using Modern Proteomics Approaches. 2021 , 2228, 225-235	2
778	Molecular pathogenesis of rhegmatogenous retinal detachment. 2021 , 11, 966	6
777	Dynamic Alteration in the Vaginal Secretory Proteome across the Early and Mid-Trimesters of Pregnancy. 2021 , 20, 1190-1205	0
776	Quantification of Changes in Protein Expression Using SWATH Proteomics. 2021 , 2361, 75-94	0
775	DaDIA: Hybridizing Data-Dependent and Data-Independent Acquisition Modes for Generating High-Quality Metabolomic Data. 2021 , 93, 2669-2677	8
774	Sensitive Immunopeptidomics by Leveraging Available Large-Scale Multi-HLA Spectral Libraries, Data-Independent Acquisition, and MS/MS Prediction. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100080 ⁷⁶	10
773	SWATH-MS Protocols in Human Diseases. 2021 , 2259, 105-141	1
772	Exosomal Cargo May Hold the Key to Improving Reproductive Outcomes in Dairy Cows. 2021 , 22,	1
771	Quantitative Proteomic Analysis of the Senescence-Associated Secretory Phenotype by Data-Independent Acquisition. 2021 , 1, e32	5
770	BoxCarMax: A High-Selectivity Data-Independent Acquisition Mass Spectrometry Method for the Analysis of Protein Turnover and Complex Samples. 2021 , 93, 3103-3111	4
769	Assessing technical and biological variation in SWATH-MS-based proteomic analysis of chronic lymphocytic leukaemia cells. 2021 , 11, 2932	2
768	Tissue Proteomic Approaches to Understand the Pathogenesis of Inflammatory Bowel Disease. 2021 , 27, 1184-1200	0
767	The rise of single-cell proteomics. 2021 , 2, 84-94	10
766	Cannabis Use Induces Distinctive Proteomic Alterations in Olfactory Neuroepithelial Cells of Schizophrenia Patients. 2021 , 11,	4

765	N-terminal acetylation of proteins by NatA and NatB serves distinct physiological roles in <i>Saccharomyces cerevisiae</i> . 2021 , 34, 108711	3
764	Single-Cell RNA Sequencing and Quantitative Proteomics Analysis Elucidate Marker Genes and Molecular Mechanisms in Hypoplastic Left Heart Patients With Heart Failure. 2021 , 9, 617853	1
763	Advances in Analytical Technologies for Extracellular Vesicles. 2021 , 93, 4739-4774	14
762	Comparative proteome signatures of trace samples by multiplexed Data-Independent Acquisition.	4
761	SWATH-MS Based Proteomic Profiling of Prostate Cancer Cells Reveals Adaptive Molecular Mechanisms in Response to Anti-Androgen Therapy. 2021 , 13,	3
760	Untargeted approaches in food-omics: The potential of comprehensive two-dimensional gas chromatography/mass spectrometry. 2021 , 135, 116162	10
759	Proteomic insights into synaptic signaling in the brain: the past, present and future. 2021 , 14, 37	5
758	Alternative LC-MS/MS Platforms and Data Acquisition Strategies for Proteomic Genotyping of Human Hair Shafts.	
757	Advances in drugs of abuse testing. 2021 , 514, 40-47	6
756	Combining label-free and label-based accurate quantifications with SWATH-MS: Comparison with SRM and PRM for the evaluation of bovine muscle type effects. 2021 , 21, e2000214	4
755	Is there a serum proteome signature to predict mortality in severe COVID-19 patients?.	
754	A proteome signature for acute incisional pain in dorsal root ganglia of mice. 2021 , 162, 2070-2086	4
753	Proteomic approaches to drive advances in helminth extracellular vesicle research. 2021 , 131, 1-5	4
752	Corneal proteome and differentially expressed corneal proteins in highly myopic chicks using a label-free SWATH-MS quantification approach. 2021 , 11, 5495	4
751	Analyzing Assay Specificity in Metabolomics using Unique Ion Signature Simulations.	
750	PIONEER: Pipeline for Generating High-Quality Spectral Libraries for DIA-MS Data. 2021 , 1, e69	0
749	Gefitinib Results in Robust Host-Directed Immunity Against Infection Through Proteo-Metabolomic Reprogramming. 2021 , 12, 648710	1
748	Proteomics Data Analysis for the Identification of Proteins and Derived Proteotypic Peptides of Potential Use as Putative Drought Tolerance Markers for. 2021 , 22,	5

747	Discovery and Identification of Arsenolipids Using a Precursor-Finder Strategy and Data-Independent Mass Spectrometry. 2021 , 55, 3836-3844	4
746	GproDIA enables data-independent acquisition glycoproteomics with comprehensive statistical control.	
745	Proteogenomic characterization of hepatocellular carcinoma.	0
744	PHONEMeS: Efficient Modeling of Signaling Networks Derived from Large-Scale Mass Spectrometry Data. 2021 , 20, 2138-2144	4
743	Critical role of mass spectrometry proteomics in tear biomarker discovery for multifactorial ocular diseases (Review). 2021 , 47,	6
742	Proteomics Landscape of Alzheimer's Disease. 2021 , 9,	2
741	Ultra-High-Resolution IonStar Strategy Enhancing Accuracy and Precision of MS1-Based Proteomics and an Extensive Comparison with State-of-the-Art SWATH-MS in Large-Cohort Quantification. 2021 , 93, 4884-4893	3
740	Data processing strategies for non-targeted analysis of foods using liquid chromatography/high-resolution mass spectrometry. 2021 , 136, 116188	12
739	Discovery and validation of PZP as a novel serum biomarker for screening lung adenocarcinoma in type 2 diabetes mellitus patients. 2021 , 21, 162	4
738	Improved SILAC Quantification with Data-Independent Acquisition to Investigate Bortezomib-Induced Protein Degradation. 2021 , 20, 1918-1927	3
737	Use of a Recombinant Biomarker Protein DDA Library Increases DIA Coverage of Low Abundance Plasma Proteins. 2021 , 20, 2374-2389	0
736	High sensitivity dia-PASEF proteomics with DIA-NN and FragPipe.	11
735	Chemoproteomic-enabled phenotypic screening. 2021 , 28, 371-393	7
734	Coagulation factor IX analysis in bioreactor cell culture supernatant predicts quality of the purified product. 2021 , 4, 390	4
733	Ultra-fast proteomics with Scanning SWATH. 2021 , 39, 846-854	47
732	Discovery of Screening Biomarkers for Major Depressive Disorder in Remission by Proteomic Approach. 2021 , 11,	0
731	CIDer: A Statistical Framework for Interpreting Differences in CID and HCD Fragmentation. 2021 , 20, 1951-1965	3
730	The Tumor Profiler Study: integrated, multi-omic, functional tumor profiling for clinical decision support. 2021 , 39, 288-293	21

729	OpenTIMS, TimsPy, and TimsR: Open and Easy Access to timsTOF Raw Data. 2021 , 20, 2122-2129	4
728	Cerebrospinal fluid proteome maps detect pathogen-specific host response patterns in meningitis. 2021 , 10,	3
727	[Development of Novel Methodology and Its Application for Clarifying the Transport Function of the Blood-brain Barrier]. 2021 , 141, 447-462	
726	DIA-based Proteomics Identifies IDH2 as a Targetable Regulator of Acquired Drug Resistance in Chronic Myeloid Leukemia.	
725	Towards comprehensive plasma proteomics by orthogonal protease digestion.	
724	Mass Spectrometry Techniques: Principles and Practices for Quantitative Proteomics. 2021 , 22, 121-133	1
723	Differential sperm proteomic profiles according to pregnancy achievement in intracytoplasmic sperm injection cycles: a pilot study. 2021 , 38, 1507-1521	0
722	Alpha-Frag: a deep neural network for fragment presence prediction improves peptide identification.	0
721	Proteogenomic interrogation of cancer cell lines: an overview of the field. 2021 , 18, 221-232	1
720	Comprehensive Proteomic Quantification of Bladder Stone Progression in a Cystinuric Mouse Model Using Data-Independent Acquisitions.	
719	Generation of a mouse SWATH-MS spectral library to quantify 10148 proteins involved in cell reprogramming. 2021 , 8, 118	3
718	Molecular pathways behind acquired obesity: Adipose tissue and skeletal muscle multiomics in monozygotic twin pairs discordant for BMI. 2021 , 2, 100226	6
717	Alpha-XIC: a deep neural network for scoring the coelution of peak groups improves peptide identification by data-independent acquisition mass spectrometry.	
716	Proteomics: A Tool to Study Platelet Function. 2021 , 22,	5
715	Discovery-Versus Hypothesis-Driven Detection of Protein-Protein Interactions and Complexes. 2021 , 22,	2
714	Proteogenomic Workflow Reveals Molecular Phenotypes Related to Breast Cancer Mammographic Appearance. 2021 , 20, 2983-3001	1
713	Trapped Ion Mobility Spectrometry Reduces Spectral Complexity in Mass Spectrometry Based Workflow.	
712	SWATH Based Quantitative Proteomics Reveals Significant Lipid Metabolism in Early Myopic Guinea Pig Retina. 2021 , 22,	5

711	The biological fate of the polymer nanocarrier material monomethoxy poly(ethylene glycol)-poly(D,L-lactic acid) in rat. 2021 , 11, 1003-1009	2
710	Discovery of plasma biomarkers with data-independent acquisition mass spectrometry and antibody microarray for diagnosis and risk stratification of pulmonary embolism. 2021 , 19, 1738-1751	1
709	Serum proteomes of Santa Gertrudis cattle before and after infestation with <i>Rhipicephalus australis</i> ticks. 2021 , 43, e12836	0
708	DreamDIA-XMBD: deep representation features improve the analysis of data-independent acquisition proteomics.	
707	Data Independent Acquisition Mass Spectrometry of the Human Lens Enhances Spatiotemporal Measurement of Fiber Cell Aging.	0
706	Quantitative Mass Spectrometry-Based Proteomics for Biomarker Development in Ovarian Cancer. 2021 , 26,	4
705	A Simple Optimization Workflow to Enable Precise and Accurate Imputation of Missing Values in Proteomic Data Sets. 2021 , 20, 3214-3229	5
704	The Isotopic Ac-IP Tag Enables Multiplexed Proteome Quantification in Data-Independent Acquisition Mode. 2021 , 93, 8196-8202	1
703	CsoDIAq Software for Direct Infusion Shotgun Proteome Analysis (DISPA).	
702	Universal Spectrum Explorer: A Standalone (Web-)Application for Cross-Resource Spectrum Comparison. 2021 , 20, 3388-3394	6
701	SWATH-MS proteomics of PANC-1 and MIA PaCa-2 pancreatic cancer cells allows identification of drug targets alternative to MEK and PI3K inhibition. 2021 , 552, 23-29	2
700	Principles of gene regulation quantitatively connect DNA to RNA and proteins in bacteria.	3
699	Proteomics, Personalized Medicine and Cancer. 2021 , 13,	9
698	Transcriptional signature in microglia associated with A β plaque phagocytosis. 2021 , 12, 3015	18
697	Ultra-high-performance liquid chromatography high-resolution mass spectrometry variants for metabolomics research. 2021 , 18, 733-746	28
696	Comparative Analysis of Secretome Under and Stimuli. 2021 , 12, 668064	3
695	Imbalanced post- and extrasynaptic SHANK2A functions during development affect social behavior in SHANK2-mediated neuropsychiatric disorders. 2021 ,	1
694	A multifactorial proteomics approach to sex-specific effects of diet composition and social environment in an omnivorous insect. 2021 , 11, 8623-8639	1

693	Identification of a Novel Ciprofloxacin Tolerance Gene, , Which Contributes to Filamentation in <i>Acinetobacter baumannii</i> . 2021 , 65,	2
692	A comprehensive mass spectral library for human thyroid tissues.	0
691	A data-independent acquisition-based global phosphoproteomics system enables deep profiling. 2021 , 12, 2539	11
690	Absolute proteome quantification in the gas-fermenting acetogen <i>Clostridium autoethanogenum</i> .	1
689	Deciphering the signaling network of breast cancer improves drug sensitivity prediction. 2021 , 12, 401-418.e126	
688	Label free-based proteomic analysis of the food spoiler <i>Pseudomonas fluorescens</i> response to lactobionic acid by SWATH-MS. 2021 , 123, 107834	6
687	From coarse to fine: the absolute <i>Escherichia coli</i> proteome under diverse growth conditions. 2021 , 17, e9536	9
686	DIAproteomics: A Multifunctional Data Analysis Pipeline for Data-Independent Acquisition Proteomics and Peptidomics. 2021 , 20, 3758-3766	6
685	Eight key rules for successful data-dependent acquisition in mass spectrometry-based metabolomics. 2021 ,	8
684	Advances in sample preparation for membrane proteome quantification.. 2021 , 39, 23-29	3
683	OsFes1C, a potential nucleotide exchange factor for OsBiP1, is involved in the ER and salt stress responses. 2021 , 187, 396-408	2
682	Proteome analysis of human adipocytes identifies depot-specific heterogeneity at metabolic control points. 2021 , 320, E1068-E1084	5
681	Two-Dimensional Mass Spectrometry Analysis of IgG1 Antibodies. 2021 , 32, 1716-1724	4
680	Acetate overflow metabolism regulates a major metabolic shift after glucose depletion in <i>Escherichia coli</i> . 2021 , 595, 2047-2056	2
679	Implementing the re-use of public DIA proteomics datasets: from the PRIDE database to Expression Atlas.	5
678	A Systems Approach to Brain Tumor Treatment. 2021 , 13,	9
677	A data-independent acquisition (DIA) assay library for quantitation of environmental effects on the kidney proteome of <i>Oreochromis niloticus</i> . 2021 , 21, 2486-2503	2
676	Proteomic Approaches to Study Cysteine Oxidation: Applications in Neurodegenerative Diseases. 2021 , 14, 678837	3

- 675 Potential biomarkers for inherited thrombocytopenia 2 identified by plasma proteomics. **2021**, 1-8 0
- 674 Twenty years of proteomics in radiation biology - a look back. **2021**, 1-5
- 673 Complement activation induces excessive T cell cytotoxicity in severe COVID-19.
- 672 Systematic detection of functional proteoform groups from bottom-up proteomic datasets. **2021**, 12, 3810 6
- 671 Next-Generation Mass Spectrometry Metabolomics Revives the Functional Analysis of Plant Metabolic Diversity. **2021**, 72, 867-891 16
- 670 Identification and Validation of Combination Plasma Biomarker of Afamin, Fibronectin and Sex Hormone-Binding Globulin to Predict Pre-eclampsia. **2021**, 44, 804-815 3
- 669 Multiregional profiling of the brain transmembrane proteome uncovers novel regulators of depression. **2021**, 7, 1
- 668 Application of Mass Spectrometry-Based Proteomics to Barley Research. **2021**, 69, 8591-8609 4
- 667 Toward Comprehensive Plasma Proteomics by Orthogonal Protease Digestion. **2021**, 20, 4031-4040 0
- 666 Skeletal muscle proteomes reveal downregulation of mitochondrial proteins in transition from prediabetes into type 2 diabetes. **2021**, 24, 102712 1
- 665 Dysregulated protein phosphorylation: A determining condition in the continuum of brain aging and Alzheimer's disease. **2021**, 31, e12996 4
- 664 Proteomic and Glyco(proteo)mic tools in the profiling of cardiac progenitors and pluripotent stem cell derived cardiomyocytes: Accelerating translation into therapy. **2021**, 49, 107755 3
- 663 Strategy for Nontargeted Metabolomic Annotation and Quantitation Using a High-Resolution Spectral-Stitching Nano-electrospray Direct-Infusion Mass Spectrometry with Data-Independent Acquisition. **2021**, 93, 10528-10537 2
- 662 A review on recent trends in the phosphoproteomics workflow. From sample preparation to data analysis.. **2022**, 1199, 338857 6
- 661 Function of cofactor Akirin2 in the regulation of gene expression in model human Caucasian neutrophil-like HL60 cells. **2021**, 41, 0
- 660 A serum proteome signature to predict mortality in severe COVID-19 patients. **2021**, 4, 14
- 659 BFG-PCA: tools and resources that expand the potential for binary protein interaction discovery.
- 658 On the feasibility of deep learning applications using raw mass spectrometry data. **2021**, 37, i245-i253 0

657	Developing mass spectrometry for the quantitative analysis of neuropeptides. 2021 , 18, 607-621	1
656	Proteome Profiling of Cerebrospinal Fluid Reveals Novel Biomarker Candidates for Parkinson's Disease.	0
655	Compatibility of Distinct Label-Free Proteomic Workflows in Absolute Quantification of Proteins Linked to the Oocyte Quality in Human Follicular Fluid. 2021 , 22,	1
654	Data-independent acquisition (DIA): An emerging proteomics technology for analysis of drug-metabolizing enzymes and transporters.. 2021 , 39, 49-56	2
653	Cloud-based DIA data analysis module for signal refinement improves accuracy and throughput of large datasets.	
652	MS2Planner: improved fragmentation spectra coverage in untargeted mass spectrometry by iterative optimized data acquisition. 2021 , 37, i231-i236	0
651	Honey proteomic signatures for the identification of honey adulterated with syrup, producing country, and nectar source using SWATH-MS approach. 2021 , 354, 129590	5
650	Metabolic, structural, and proteomic changes in <i>Candida albicans</i> cells induced by the protein-carbohydrate fraction of <i>Dendrobaena veneta</i> coelomic fluid. 2021 , 11, 16711	1
649	Proteomes Are of Proteoforms: Embracing the Complexity. 2021 , 9,	15
648	Changes in the Proteome Profile of People Achieving Remission of Type 2 Diabetes after Bariatric Surgery. 2021 , 10,	1
647	Distinct brain regional proteome changes in the rTg-DI rat model of cerebral amyloid angiopathy. 2021 , 159, 273-291	2
646	Evaluation of the Sensitivity and Reproducibility of Targeted Proteomic Analysis Using Data-Independent Acquisition for Serum and Cerebrospinal Fluid Proteins. 2021 , 20, 4284-4291	1
645	Pipelines and Systems for Threshold-Avoiding Quantification of LC-MS/MS Data. 2021 , 93, 11215-11224	1
644	AlphaMap: An open-source Python package for the visual annotation of proteomics data with sequence specific knowledge.	1
643	Puf6 primes 60S pre-ribosome nuclear export at low temperature. 2021 , 12, 4696	5
642	Alpha-XIC: a deep neural network for scoring the coelution of peak groups improves peptide identification by data-independent acquisition mass spectrometry. 2021 ,	0
641	Analyzing Assay Specificity in Metabolomics Using Unique Ion Signature Simulations. 2021 , 93, 11415-11423	
640	A time-resolved proteomic and prognostic map of COVID-19. 2021 , 12, 780-794.e7	32

639	A data-independent acquisition approach based on HRMS to explore the biodegradation process of organic micropollutants involved in a biological ion-exchange drinking water filter. 2021 , 277, 130216	3
638	Quantitative Proteomics and Relative Enzymatic Activities Reveal Different Mechanisms in Two Peanut Cultivars (<i>L.</i>) Under Waterlogging Conditions. 2021 , 12, 716114	1
637	Use of Linear Ion Traps in Data-Independent Acquisition Methods Benefits Low-Input Proteomics. 2021 , 93, 11649-11653	1
636	Substrate-mediated regulation of the arginine transporter of <i>Toxoplasma gondii</i> . 2021 , 17, e1009816	4
635	Robust optimization of SWATH-MS workflow for human blood serum proteome analysis using a quality by design approach. 2021 , 18, 20	0
634	Characterization by Quantitative Serum Proteomics of Immune-Related Prognostic Biomarkers for COVID-19 Symptomatology. 2021 , 12, 730710	4
633	Time-resolved in vivo ubiquitinome profiling by DIA-MS reveals USP7 targets on a proteome-wide scale. 2021 , 12, 5399	6
632	Proteomic characterization of primary and metastatic prostate cancer reveals reduced proteinase activity in aggressive tumors. 2021 , 11, 18936	2
631	CsoDIAq Software for Direct Infusion Shotgun Proteome Analysis. 2021 , 93, 12312-12319	0
630	Development and application of sequential window acquisition of all theoretical mass spectra data acquisition modes on ultra-high-performance liquid chromatography triple-quadrupole/time-of-flight mass spectrometry for metabolic profiling of amino acids in human plasma. 2021 , 44, 4209-4221	0
629	Differences in proteomic profiles between yak and three cattle strains provide insights into molecular mechanisms underlying high-altitude adaptation. 2021 ,	0
628	High-throughput proteomics and AI for cancer biomarker discovery. 2021 , 176, 113844	7
627	Peroxide antimalarial drugs target redox homeostasis in <i>Plasmodium falciparum</i> infected red blood cells.	
626	Biomarkers for Adverse Lung Injury Following Pediatric Cardiopulmonary Bypass. 2021 , 3, e0528	1
625	Integrating Clinical Data and Tear Proteomics to Assess Efficacy, Ocular Surface Status, and Biomarker Response After Orthokeratology Lens Wear. 2021 , 10, 18	1
624	Alternative LC-MS/MS Platforms and Data Acquisition Strategies for Proteomic Genotyping of Human Hair Shafts. 2021 , 20, 4655-4666	1
623	Integrative analysis allows a global and precise identification of functional miRNA target genes in mESCs.	1
622	SWATH-MS for prospective identification of protein blood biomarkers of rtPA-associated intracranial hemorrhage in acute ischemic stroke: a pilot study. 2021 , 11, 18765	

621	Extensive and Accurate Benchmarking of DIA Acquisition Methods and Software Tools Using a Complex Proteomic Standard. 2021 , 20, 4801-4814	14
620	Narrow Precursor Mass Range for DIA-MS Enhances Protein Identification and Quantification in Arabidopsis. 2021 , 11,	2
619	Proteome and Nutritional Shifts Observed in Hordein Double-Mutant Barley Lines. 2021 , 12, 718504	
618	Proteomic response and molecular regulatory mechanisms of Bacillus cereus spores under ultrasound treatment. 2021 , 78, 105732	1
617	Proteomic analysis of differentially expressed whey proteins in Saanen goat milk from different provinces in China using a data-independent acquisition technique. 2021 , 104, 10513-10527	1
616	Leveraging homologies for cross-species plasma proteomics in ungulates using data-independent acquisition. 2022 , 250, 104384	0
615	Thylakoid proteome variation of Eutrema salsugineum in response to drought and salinity combined stress. 2021 , 1862, 148482	1
614	Proteomics for Quality and Safety in Fishery Products. 2022 , 45-78	
613	Development and validation of qualitative screening, quantitative determination and post-targeted pesticide analysis in tropical fruits and vegetables by LC-HRMS. 2022 , 367, 130714	1
612	Benchmarking Quantitative Performance in Label-Free Proteomics. 2021 , 6, 2494-2504	5
611	Data-independent acquisition-based proteome and phosphoproteome profiling across six melanoma cell lines reveals determinants of proteotypes. 2021 , 17, 413-425	9
610	ProteomeExpert: a docker image based web-server for exploring, modeling, visualizing, and mining quantitative proteomic data sets. 2021 ,	4
609	Cell autonomous and noncell-autonomous role of NF- κ B p50 in astrocyte-mediated fate specification of adult neural progenitor cells. 2017 , 65, 169-181	25
608	The SystemMHC Atlas: a Computational Pipeline, a Website, and a Data Repository for Immunopeptidomic Analyses. 2020 , 2120, 173-181	4
607	What Is New in (Plant) Proteomics Methods and Protocols: The 2015-2019 Quinquennium. 2020 , 2139, 1-10	6
606	Combining Targeted and Untargeted Data Acquisition to Enhance Quantitative Plant Proteomics Experiments. 2020 , 2139, 169-178	2
605	The Proteomic Characterization of Plasma or Serum from HIV-Infected Patients. 2016 , 1354, 293-310	6
604	Introduction to Proteomics Technologies. 2016 , 1362, 3-27	6

603	Methods for SWATH-MS Data Independent Acquisition on TripleTOF Mass Spectrometers. 2016 , 1410, 265-79	16
602	Mapping Biological Networks from Quantitative Data-Independent Acquisition Mass Spectrometry: Data to Knowledge Pipelines. 2017 , 1558, 395-413	5
601	Data-Independent Acquisition for Yeast Glycoproteomics. 2019 , 2049, 191-202	5
600	Considerations in the Analysis of Hydrogen Exchange Mass Spectrometry Data. 2020 , 2051, 407-435	2
599	Mass Western for absolute quantification of target proteins and considerations about the instrument of choice. 2014 , 1072, 199-208	2
598	Selected reaction monitoring mass spectrometry: a methodology overview. 2014 , 1072, 209-22	17
597	The expanding universe of mass analyzer configurations for biological analysis. 2014 , 1072, 61-81	7
596	Global Proteomics of Extremophilic Fungi: Mission Accomplished?. 2019 , 205-249	3
595	Label-Free Quantification by Data Independent Acquisition Mass Spectrometry to Map Cardiovascular Proteomes. 2016 , 227-245	1
594	Bottom-Up Proteomics. 2016 , 155-185	1
593	Mass Spectrometry-Based Protein Sequencing Platforms. 2014 , 69-99	4
592	A Global Screen for Assembly State Changes of the Mitotic Proteome by SEC-SWATH-MS. 2020 , 10, 133-155.e624	
591	From fuzziness to precision medicine: on the rapidly evolving proteomics with implications in mitochondrial connectivity to rare human disease. 2021 , 24, 102030	3
590	Effects of differences in pre-analytical processing on blood protein profiles determined with SWATH-MS. 2020 , 223, 103824	4
589	BAC-DROP: Rapid Digestion of Proteome Fractionated via Dissolvable Polyacrylamide Gel Electrophoresis and Its Application to Bottom-Up Proteomics Workflow. 2021 , 20, 1535-1543	10
588	Generation of a zebrafish SWATH-MS spectral library to quantify 10,000 proteins. 2019 , 6, 190011	23
587	CHAPTER 4: Getting Absolute: Determining Absolute Protein Quantities via Selected Reaction Monitoring Mass Spectrometry. 2014 , 80-109	14
586	CHAPTER 8: Label-free Quantification of Proteins Using Data-Independent Acquisition. 2014 , 175-184	2

585	CHAPTER 9: Spatial Proteomics: Practical Considerations for Data Acquisition and Analysis in Protein Subcellular Localisation Studies. 2014 , 185-210	2
584	Emerging mass spectrometry-based proteomics methodologies for novel biomedical applications. 2020 , 48, 1953-1966	8
583	Comparative 'omics analyses differentiate Mycobacterium tuberculosis and Mycobacterium bovis and reveal distinct macrophage responses to infection with the human and bovine tubercle bacilli. 2018 , 4,	25
582	Precise label-free quantitative proteomes in high-throughput by microLC and data-independent SWATH acquisition.	2
581	Deciphering the Signaling Network Landscape of Breast Cancer Improves Drug Sensitivity Prediction.	2
580	Automated Workflow For Peptide-level Quantitation From DIA/ SWATH-MS Data.	2
579	A mouse SWATH-MS reference spectral library enables deconvolution of species-specific proteomic alterations in human tumour xenografts.	2
578	Phenotype Prediction using a Tensor Representation and Deep Learning from Data Independent Acquisition Mass Spectrometry.	1
577	Global impact of phosphorylation on protein endurance.	1
576	Protein Classifier for Thyroid Nodules Learned from Rapidly Acquired Proteotypes.	5
575	Gut microbiota may underlie the predisposition of healthy individuals to COVID-19.	65
574	Clinical classifiers of COVID-19 infection from novel ultra-high-throughput proteomics.	7
573	FLEXIQuant-LF: Robust Regression to Quantify Protein Modification Extent in Label-Free Proteomics Data.	1
572	Quantitative secretome analysis establishes the cell type-resolved mouse brain secretome.	1
571	Development of an Ocean Protein Portal for Interactive Discovery and Education.	1
570	Data-independent acquisition method for ubiquitinome analysis reveals regulation of circadian biology.	2
569	MSImpute: Imputation of label-free mass spectrometry peptides by low-rank approximation.	0
568	Multi-Omic Profiling of the Liver Across Diets and Age in a Diverse Mouse Population.	3

567	Universal Spectrum Explorer: A standalone (web-)application for cross-resource spectrum comparison.	2
566	Extensive and accurate benchmarking of DIA acquisition methods and software tools using a complex proteomic standard.	3
565	Library-free BoxCarDIA solves the missing value problem in label-free quantitative proteomics.	4
564	A time-resolved proteomic and diagnostic map characterizes COVID-19 disease progression and predicts outcome.	6
563	DIAproteomics: A multi-functional data analysis pipeline for data-independent-acquisition proteomics and peptidomics.	3
562	Multi-Omic Profiling Reveals the Opposing Forces of Excess Dietary Sugar and Fat on Liver Mitochondria Protein Acetylation and Succinylation.	1
561	Rapid proteotyping reveals cancer biology and drug response determinants in the NCI-60 cells.	3
560	Comprehensive peptide quantification for data independent acquisition mass spectrometry using chromatogram libraries.	6
559	A generic normalization method for proper quantification in untargeted proteomics screening.	2
558	Identification of novel protein lysine acetyltransferases in <i>Escherichia coli</i> .	1
557	The human secretome [The proteins secreted from human cells.	6
556	Revealing dynamic protein acetylation across subcellular compartments.	1
555	PGC1 β and Exercise Adaptations in Zebrafish.	4
554	A Proteomic Atlas of Senescence-Associated Secretomes for Aging Biomarker Development.	1
553	De novo Classification of Mouse B Cell Types using Surfaceome Proteotype Maps	1
552	Mouse and human microglial phenotypes in Alzheimer's disease are controlled by amyloid plaque phagocytosis through Hif1 β	5
551	Parallel accumulation [Serial fragmentation combined with data-independent acquisition (diaPASEF): Bottom-up proteomics with near optimal ion usage.	18
550	Scanning SWATH acquisition enables high-throughput proteomics with chromatographic gradients as fast as 30 seconds.	7

549	Accelerated Protein Biomarker Discovery from FFPE tissue samples using Single-shot, Short Gradient Microflow SWATH MS.	2
548	Piezo1 Induces Local Curvature in a Mammalian Membrane and Forms Specific Protein-Lipid Interactions.	3
547	Orthogonal proteomic platforms and their implications for the stable classification of high-grade serous ovarian cancer subtypes.	2
546	Substrate-mediated regulation of the arginine transporter of <i>Toxoplasma gondii</i> .	3
545	Seven perspectives on GPCR H/D-exchange proteomics methods. 2017 , 6, 89	1
544	Needle lost in the haystack: multiple reaction monitoring fails to detect candidate protein biomarkers in plasma and urine samples from individuals with syphilis. 2018 , 7, 336	2
543	The beauty of being (label)-free: sample preparation methods for SWATH-MS and next-generation targeted proteomics. 2, 272	38
542	The beauty of being (label)-free: sample preparation methods for SWATH-MS and next-generation targeted proteomics. 2013 , 2, 272	49
541	Differential Protein Expression in the Hemolymph of <i>Bithynia siamensis goniomphalos</i> Infected with <i>Opisthorchis viverrini</i> . 2016 , 10, e0005104	7
540	Fast and Efficient XML Data Access for Next-Generation Mass Spectrometry. 2015 , 10, e0125108	10
539	Evaluation of iTRAQ and SWATH-MS for the Quantification of Proteins Associated with Insulin Resistance in Human Duodenal Biopsy Samples. 2015 , 10, e0125934	37
538	Genetically and Phenotypically Distinct <i>Pseudomonas aeruginosa</i> Cystic Fibrosis Isolates Share a Core Proteomic Signature. 2015 , 10, e0138527	20
537	Identification of blood biomarkers in glioblastoma by SWATH mass spectrometry and quantitative targeted absolute proteomics. 2018 , 13, e0193799	51
536	An optimized quantitative proteomics method establishes the cell type-resolved mouse brain secretome. 2020 , 39, e105693	19
535	Proteome profiling in cerebrospinal fluid reveals novel biomarkers of Alzheimer's disease. 2020 , 16, e9356	47
534	Integrative proteomics reveals principles of dynamic phosphosignaling networks in human erythropoiesis. 2020 , 16, e9813	8
533	Metabolic drift in the aging brain. 2016 , 8, 1000-20	56
532	Proteomic profiling of mitochondria: what does it tell us about the ageing brain?. 2016 , 8, 3161-3179	16

531	Pyruvate kinase is a dosage-dependent regulator of cellular amino acid homeostasis. 2012 , 3, 1356-69	21
530	Biomarkers of tumor invasiveness in proteomics (Review). 2020 , 57, 409-432	10
529	Human biological monitoring of suspected endocrine-disrupting compounds. 2014 , 16, 5-16	34
528	In-Depth, Proteomic Analysis of Nasal Secretions from Patients With Chronic Rhinosinusitis and Nasal Polyps. 2019 , 11, 691-708	17
527	An open-source computational and data resource to analyze digital maps of immunopeptidomes. 2015 , 4,	68
526	The GTPase Nog1 co-ordinates the assembly, maturation and quality control of distant ribosomal functional centers. 2020 , 9,	18
525	FLEXIQuant-LF to quantify protein modification extent in label-free proteomics data. 2020 , 9,	2
524	Proteomics (SWATH-MS) informed by transcriptomics approach of tropical herb leaves upon methyl jasmonate elicitation. 2018 , 6, e5525	10
523	Amphiregulin Mediates Non-Cell-Autonomous Effect of Senescence on Reprogramming.	
522	Biological Applications for LC-MS-Based Proteomics. 2021 , 1336, 17-29	3
521	The state of the art in plant lipidomics. 2021 , 17, 894-910	3
520	[Advances in high-throughput proteomic analysis]. 2021 , 39, 112-117	
519	Data-independent acquisition mass spectrometry for site-specific glycoproteomics characterization of SARS-CoV-2 spike protein. 2021 , 413, 7305-7318	5
518	Molecular characterization of triple negative breast cancer formaldehyde-fixed paraffin-embedded samples by data-independent acquisition proteomics. 2021 , e2100110	0
517	Exploration of novel biomarkers for hypertensive disorders of pregnancy by comprehensive analysis of peptide fragments in blood: their potential and technologies supporting quantification. 2021 ,	
516	Relationship between the Plasma Proteome and Changes in Inflammatory Markers after Bariatric Surgery. 2021 , 10,	0
515	Effects of High Temperature on Rice Grain Development and Quality Formation Based on Proteomics Comparative Analysis Under Field Warming. 2021 , 12, 746180	3
514	Mass spectrometry based approaches and strategies in bioanalysis for qualitative and quantitative analysis of pharmaceutically relevant molecules.. 2021 , 40, 64-68	1

513	GproDIA enables data-independent acquisition glycoproteomics with comprehensive statistical control. 2021 , 12, 6073	5
512	PRM-LIVE with Trapped Ion Mobility Spectrometry and Its Application in Selectivity Profiling of Kinase Inhibitors. 2021 , 93, 13791-13799	3
511	Deep representation features from DreamDIA improve the analysis of data-independent acquisition proteomics. 2021 , 4, 1190	1
510	CHD1 controls H3.3 incorporation in adult brain chromatin to maintain metabolic homeostasis and normal lifespan. 2021 , 37, 109769	0
509	Multiomic profiling of the liver across diets and age in a diverse mouse population. 2021 ,	2
508	Identification of tumor antigens with immunopeptidomics. 2021 ,	9
507	Extending the Proteomic Characterization of <i>Candida albicans</i> Exposed to Stress and Apoptotic Inducers through Data-Independent Acquisition Mass Spectrometry. 2021 , 6, e0094621	0
506	CHAPTER 5:Sample Preparation and Profiling: Mass-Spectrometry-Based Profiling Strategies. 2013 , 136-161	
505	Proteomics in the Systems-Level Study of the Metabolic Syndrome. 2014 , 185-212	
504	CHAPTER 7:MS1 Label-free Quantification Using Ion Intensity Chromatograms in Skyline (Research and Clinical Applications). 2014 , 154-174	0
503	Mass Spectrometry for Biomarker Development. 2014 , 1-25	
502	Sphingoproteomics: Proteomic Strategies to Examine Sphingolipid Biology. 2015 , 359-384	
501	<i>Mycobacterium tuberculosis</i> in the Proteomics Era. 239-260	
500	Chapter 10:Data Analysis for Data Independent Acquisition. 2016 , 200-228	
499	Chapter 4:PSM Scoring and Validation. 2016 , 69-92	1
498	A Historical Perspective on Cardiovascular Proteomics. 2016 , 1-14	
497	System-wide quantitative proteomics of the metabolic syndrome in mice: genotypic and dietary effects.	
496	Towards comprehensive and quantitative proteomics for diagnosis and therapy of human disease.	2

495	Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry.	3
494	Proteomic Analysis of Neuronal Mitochondria. 2017 , 299-319	
493	High sensitivity quantitative proteomics using accumulated ion monitoring and automated multidimensional nano-flow chromatography.	0
492	DIA-Pipe: Identification and Quantification of Post-Translational Modifications using exclusively Data-Independent Acquisition.	
491	Metabolomics and Proteomics. 2017 , 473-484	
490	Multi-region proteome analysis quantifies spatial heterogeneity of prostate tissue biomarkers.	2
489	Needle lost in the haystack: multiple reaction monitoring fails to detect <i>Treponema pallidum</i> candidate protein biomarkers in plasma and urine samples from individuals with syphilis. 2018 , 7, 336	1
488	DIA-NN: Deep neural networks substantially improve the identification performance of Data-independent acquisition (DIA) in proteomics.	1
487	Identification of protein abundance changes in biopsy-level hepatocellular carcinoma tissues using PCT-SWATH.	1
486	Multi-omic profiling of tyrosine kinase inhibitor-resistant K562 cells suggests metabolic reprogramming to promote cell survival.	
485	Kunitz type protease inhibitor EgKI-1 from the canine tapeworm <i>Echinococcus granulosus</i> as a promising anti-cancer therapeutic.	0
484	Ultra-sensitive proteome profiling of FACS-isolated cell populations by data-independent acquisition-MS: Application to human hematopoietic stem and progenitor cells.	1
483	DIAAlignR provides precise retention time alignment across distant runs in DIA and targeted proteomics.	
482	Data-Independent Acquisition Mass Spectrometry to Localize Phosphosites.	
481	Screening a Resource of Recombinant Protein Fragments for Targeted Proteomics.	1
480	Rapid Proteomic Screen of CRISPR Experiment Outcome by Data Independent Acquisition Mass Spectrometry: A Case Study for HMG1.	
479	A Proteomic Atlas of Senescence-Associated Secretomes for Aging Biomarker Development.	0
478	Quantitative Analysis of Mass Spectrometry-Based Proteomics Data. 2019 , 129-142	0

- 477 Identification of Human Blood Plasma Proteins Using Spike-In Peptides in Shotgun Proteomics. **2019**, 2, e00093
- 476 Advances in Mass Spectrometry-Based Proteomics and Its Application in Cancer Research. **2019**, 89-112
- 475 Proteome and Secretome Dynamics of Stem Cell-Derived Retinal Pigmented Epithelium in Response to Acute and Chronic ROS.
- 474 Measuring amber initiator tRNA orthogonality in a genomically recoded organism.
- 473 Data-Independent Acquisition (SWATH) Mass Spectrometry Analysis of Protein Content in Primary Neuronal Cultures. **2019**, 119-127 0
- 472 Sample Fractionation Techniques for CSF Peptide Spectral Library Generation. **2019**, 2044, 69-77 1
- 471 Avant-garde: An automated data-driven DIA data curation tool. 2
- 470 A global screen for assembly state changes of the mitotic proteome by SEC-SWATH-MS. 1
- 469 Arabidopsis Proteome and the Mass Spectral Assay Library. 0
- 468 Generating high-quality libraries for DIA-MS with empirically-corrected peptide predictions. 1
- 467 DIALib: an automated ion library generator for data independent acquisition mass spectrometry analysis of peptides and glycopeptides. 0
- 466 Mass Spectrometry-Based Plasma Proteomics: Considerations from Sample Collection to Achieving Translational Data. 1
- 465 Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 3.0.
- 464 Surfaceome dynamics during neuronal development and synaptic plasticity reveal system-wide surfaceome reorganization independent of global proteostasis.
- 463 Phase variable glycosylation in non-typeable *Haemophilus influenzae*.
- 462 Review of Issues and Solutions to Data Analysis Reproducibility and Data Quality in Clinical Proteomics. **2020**, 2051, 345-371 0
- 461 N-terminal acetylation of proteins by NatA and NatB serves distinct physiological roles in *Saccharomyces cerevisiae*.
- 460 The endosomal protein sorting nexin 4 is a novel synaptic protein.

- 459 Probing SWATH-MS as a tool for proteome level quantification in a non-model fish.
- 458 DPHL: A pan-human protein mass spectrometry library for robust biomarker discovery. 1
- 457 Parallel factor analysis enables quantification and identification of highly-convolved data independent-acquired protein spectra.
- 456 Current Status and Future Prospects of Biomarker Strategy for Drug Development. **2020**, 51, 151-160
- 455 Proteogenomic workflow reveals distinct molecular phenotypes related to breast cancer appearance
- 454 Liquid-Phase Ion Trap for Ion Trapping, Transfer, and Sequential Ejection in Solutions. **2020**, 92, 9065-9071 1
- 453 Selective Labeling and Identification of the Tumor Cell Proteome of Pancreatic Cancer In Vivo.
- 452 MealTime-MS: A Machine Learning-Guided Real-Time Mass Spectrometry Analysis for Protein Identification and Efficient Dynamic Exclusion.
- 451 PHOSPHO1, a novel skeletal regulator of insulin resistance and obesity.
- 450 Analysis of coagulation factor IX in bioreactor cell culture medium predicts yield and quality of the purified product.
- 449 Urinary proteome profiling for stratifying patients with familial Parkinson disease. 1
- 448 DIAFree enables untargeted open-search identification for Data-Independent Acquisition data.
- 447 DIA-based systems biology approach unveils novel E3-dependent responses to a metabolic shift.
- 446 Data-Independent Acquisition Mass Spectrometry of the Human Lens Enhances Spatiotemporal Measurement of Fiber Cell Aging. **2021**, 32, 2755-2765 0
- 445 Dissecting Host-Pathogen Interactions in TB Using Systems-Based Omic Approaches. **2021**, 12, 762315 2
- 444 Data-Independent Identification of Suspected Organic Pollutants Using Gas Chromatography-Atmospheric Pressure Chemical Ionization-Mass Spectrometry. **2021**, 93, 1498-1506 2
- 443 Extending the proteomic characterization of *Candida albicans* exposed to stress and apoptotic inducers through data-independent acquisition mass spectrometry.
- 442 Data-independent Acquisition-based Proteome and Phosphoproteome Profiling across Six Melanoma Cell Lines Reveals Determinants of Proteotypes. 0

441	PROTREC: A probability-based approach for recovering missing proteins based on biological networks. 2022 , 250, 104392	4
440	Introduction to proteomics for chemical biology. 2022 , 3-45	
439	Mass spectrometry for human kinome analysis. 2022 , 191-216	0
438	Salivary Bioscience and Periodontal Medicine. 2020 , 419-447	0
437	A hybrid spectral library combining DIA-MS data and a targeted virtual library substantially deepens the proteome coverage.	0
436	CHAPTER 10:Applications for Mass Spectrometry-based Proteomics and Phosphoproteomics in Precision Medicine. 2020 , 191-222	
435	Selected Reaction Monitoring Mass Spectrometry. 2020 , 53-88	1
434	Mass Spectrometry Methods for Food Safety/Detection of Toxins in Food. 2020 , 47-60	
433	Synthetic drugs of abuse. 2021 , 103, 191-214	5
432	Network analysis identifies regulators of lineage-specific phenotypes in Mycobacterium tuberculosis.	
431	Increasing proteome coverage using cysteine-specific DIA Mass spectrometry [Cys-DIA.	
430	Standardization and Harmonization of Distributed Multi-National Proteotype Analysis supporting Precision Medicine Studies.	1
429	A comprehensive proteomic SWATH-MS workflow for profiling blood extracellular vesicles: a new avenue for glioma tumour surveillance.	0
428	Leveraging immonium ions for identifying and targeting acyl-lysine modifications in proteomic datasets.	
427	Reproducible Determination of High-Density Lipoprotein Proteotypes. 2021 , 20, 4974-4984	3
426	Computational Optimization of Spectral Library Size Improves DIA-MS Proteome Coverage and Applications to 15 Tumors. 2021 , 20, 5392-5401	2
425	Increasing the throughput of sensitive proteomics by plexDIA.	1
424	A Prostate Cancer Proteomics Database for SWATH-MS Based Protein Quantification. 2021 , 13,	1

423	Cerebrospinal fluid proteome maps detect pathogen-specific host response patterns in meningitis.	
422	Molecular characterization of triple negative breast cancer formaldehyde-fixed paraffin-embedded samples by data-independent acquisition proteomics.	
421	A Recombinant Protein Biomarker DDA Library Increases DIA Coverage of Low Abundance Plasma Proteins.	
420	Improved SILAC quantification with data independent acquisition to investigate bortezomib-induced protein degradation.	0
419	Proteomics for the Investigation of Mycobacteria. 2017 , 9, 15-25	1
418	Molecular Aspects of Wound Healing and the Rise of Venous Leg Ulceration: Omics Approaches to Enhance Knowledge and Aid Diagnostic Discovery. 2017 , 38, 35-55	11
417	Propafenone suppresses esophageal cancer proliferation through inducing mitochondrial dysfunction. 2017 , 7, 2245-2256	4
416	Investigation of cattle plasma proteome in response to pain and inflammation using next generation proteomics technique, SWATH-MS. 2021 ,	0
415	Proteomics analysis reveals suppression of IL-17 signaling pathways contributed to the therapeutic effects of Jia-Wei Bu-Shen-Yi-Qi formula in a murine asthma model. 2021 , 95, 153803	1
414	Chemometric Approaches to Evaluate Interspecies Relationships and Extrapolation in Aquatic Toxicity. 2021 , 181-199	
413	A comprehensive LFQ benchmark dataset on modern day acquisition strategies in proteomics.	1
412	DeepPhospho accelerates DIA phosphoproteome profiling through in silico library generation. 2021 , 12, 6685	4
411	Spatial mapping of cancer tissues by OMICS technologies. 2021 , 188663	1
410	Nontargeted Screening Using Gas Chromatography-Atmospheric Pressure Ionization Mass Spectrometry: Recent Trends and Emerging Potential. 2021 , 26,	3
409	Automated proteomic sample preparation: The key component for high throughput and quantitative mass spectrometry analysis. 2021 , e21750	3
408	A flexible workflow for building spectral libraries from narrow window data independent acquisition mass spectrometry data.	
407	Investigation of the Proteomes of the Truffles , , , , and. 2021 , 22,	2
406	Proteomic and metabolomic analysis of <i>Nicotiana benthamiana</i> under dark stress. 2021 , 12, 231	1

405	Comparative proteome signatures of trace samples by multiplexed Data-Independent Acquisition. <i>Molecular and Cellular Proteomics</i> , 2021 , 100177	7.6	2
404	The Extracellular Matrix Environment of Clear Cell Renal Cell Carcinoma Determines Cancer Associated Fibroblast Growth. 2021 , 13,		4
403	The metabolic growth limitations of petite cells lacking the mitochondrial genome. 2021 , 3, 1521-1535		3
402	Comprehensive kinomic study via a chemical proteomic approach reveals kinome reprogramming in hepatocellular carcinoma tissues.. 2021 , e2100141		
401	Peroxide Antimalarial Drugs Target Redox Homeostasis in Infected Red Blood Cells.. 2022 ,		2
400	l-Asparaginase and HCP quantification by SWATH LC-MS/MS for new and improved purification step in <i>Erwinia chrysanthemil</i> -asparaginase manufacture.. 2021 , 209, 114537		0
399	Spacer length and serum protein adsorption affect active targeting of trastuzumab-modified nanoparticles. 2022 , 5, 100032		0
398	Activation of Annexin A2 signaling at the blood-brain barrier in a mouse model of multiple sclerosis.. 2022 ,		1
397	Barcode fusion genetics-protein-fragment complementation assay (BFG-PCA): tools and resources that expand the potential for binary protein interaction discovery.. 2022 ,		
396	Complexome Profiling-Exploring Mitochondrial Protein Complexes in Health and Disease.. 2021 , 9, 796128		1
395	Urinary Retinol-Binding Protein 4 is Associated With Renal Function and Rapid Renal Function Decline in Kidney Transplant Recipients.. 2022 , 54, 362-362		1
394	Quantitative Proteomic Study Unmasks Fibrinogen Pathway in Polycystic Liver Disease.. 2022 , 10,		0
393	MSLibrarian: Optimized Predicted Spectral Libraries for Data-Independent Acquisition Proteomics.. 2022 ,		0
392	Bottom-up/cross-linking mass spectrometry simplified sample processing on anion-exchange solid-phase extraction spin column.. 2021 ,		2
391	Deep Proteome Profiling Enabled Functional Annotation and Data-Independent Quantification of Proline Hydroxylation Targets.		1
390	Methods for Quantification of Glycopeptides by Liquid Separation and Mass Spectrometry.. 2022 ,		0
389	Advanced mass spectrometry-based methods for protein molecular-structural biologists. 2022 , 311-326		2
388	Alpha-Tri: a deep neural network for scoring the similarity between predicted and measured spectra improves peptide identification of DIA data.. 2022 ,		

387	Streamlined single-cell proteomics by an integrated microfluidic chip and data-independent acquisition mass spectrometry.. 2022 , 13, 37		12
386	The Periplasmic Oxidoreductase DsbA Is Required for Virulence of the Phytopathogen .. 2022 , 23,		1
385	Recent Developments in Clinical Plasma Proteomics-Applied to Cardiovascular Research.. 2022 , 10,		1
384	The Transglutaminase-2 Interactome in the APP23 Mouse Model of Alzheimer's Disease.. 2022 , 11,		0
383	Data-Independent Acquisition Approach to Proteome: A Case Study and a Spectral Library for Mass Spectrometry-Based Investigation of .. 2022 ,		
382	Identification of novel proteins and mechanistic pathways associated with early-onset hypertension by deep proteomic mapping of resistance arteries.. 2021 , 101512		1
381	Three Microbial Musketeers of the Seas: , and , and Their Adaptation to Different Salinity Probed by a Proteomic Approach.. 2022 , 23,		
380	BoxCar and Library-Free Data-Independent Acquisition Substantially Improve the Depth, Range, and Completeness of Label-Free Quantitative Proteomics.. 2022 ,		3
379	Alteration of EIF2 Signaling, Glycolysis, and Dopamine Secretion in Form-Deprived Myopia in Response to 1% Atropine Treatment: Evidence From Interactive iTRAQ-MS and SWATH-MS Proteomics Using a Guinea Pig Model.. 2022 , 13, 814814		0
378	Comparative Proteomic Analysis Reveals Metformin Improves the Expression of Biomarkers of Endometrial Receptivity in Infertile Women with Minimal/Mild Endometriosis.. 2022 , 1		0
377	Metabolic dyshomeostasis induced by SARS-CoV-2 structural proteins reveals immunological insights into viral olfactory interactions.		
376	A practical guide to interpreting and generating bottom-up proteomics data visualizations.. 2022 , e2100103		2
375	DIA-based Proteomics Identifies IDH2 as a Targetable Regulator of Acquired Drug Resistance in Chronic Myeloid Leukemia.. <i>Molecular and Cellular Proteomics</i> , 2021 , 100187	7.6	0
374	Comprehensive biochemical and proteomic characterization of seasonal Australian camel milk.. 2022 , 381, 132297		0
373	Bacterial growth monitored by two-dimensional tandem mass spectrometry.. 2022 ,		1
372	SWATH-MS Proteomic Approach to Discover Novel Protein Targets and Pathways in Response to Abscisic Acid.. 2022 , 2462, 191-200		
371	SWATH-Based Comprehensive Determination of the Localization of Apical and Basolateral Membrane Proteins Using Mouse Liver as a Model Tissue.. 2022 , 10,		0
370	Longitudinal Plasma Proteomics Analysis Reveals Novel Candidate Biomarkers in Acute COVID-19.. 2022 ,		4

369	Complement activation induces excessive T cell cytotoxicity in severe COVID-19.. 2021 ,	9
368	Virulence Biomarkers of : A Proteomic Approach.. 2021 , 12, 822289	2
367	Impact of the Glycemic Level on the Salivary Proteome of Middle-Aged and Elderly People With Type 2 Diabetes Mellitus: An Observational Study.. 2021 , 8, 790091	1
366	[Research progress and application of retention time prediction method based on deep learning]. 2021 , 39, 211-218	2
365	Democratizing data-independent acquisition proteomics analysis on public cloud infrastructures via the Galaxy framework.. 2022 , 11,	4
364	A new mass spectral library for high-coverage and reproducible analysis of the Plasmodium falciparum-infected red blood cell proteome.. 2022 , 11,	2
363	Rapid tryptic peptide mapping of human serum albumin using DI-MS/MS.. 2022 , 12, 9868-9882	
362	Coupling suspension trapping-based sample preparation and data-independent acquisition mass spectrometry for sensitive exosomal proteomic analysis.. 2022 , 414, 2585-2595	3
361	Review of Liquid Chromatography-Mass Spectrometry-Based Proteomic Analyses of Body Fluids to Diagnose Infectious Diseases.. 2022 , 23,	0
360	Data-Independent Acquisition Enables Robust Quantification of 400 Proteins in Non-Depleted Canine Plasma.. 2022 , 10,	1
359	Deletion of the microglial transmembrane immune signaling adaptor TYROBP ameliorates Huntington's disease mouse phenotype.	
358	Defective mitochondrial-lysosomal axis promotes extracellular vesicles release of mitochondrial components in Huntington's Disease.	0
357	Dual data and motif clustering improves the modeling and interpretation of phosphoproteomic data.. 2022 , 2,	1
356	Development of simple, scalable protease production from Botrytis cinerea.. 2022 , 106, 2219	
355	Automated Annotation of Untargeted All-Ion Fragmentation LC-MS Metabolomics Data with MetaboAnnotatoR.. 2022 ,	0
354	Study of Dimorphism Transition Mechanism of Based on Comparative Proteomics.. 2022 , 8,	
353	Mapping Protein-Protein Interactions Using Data-Dependent Acquisition Without Dynamic Exclusion.	
352	All Driven by Energy Demand? Integrative Comparison of Metabolism of Enterococcus faecalis Wildtype and a Glutamine Synthase Mutant.. 2022 , e0240021	1

351	Data-independent acquisition mass spectrometry in severe rheumatic heart disease (RHD) identifies a proteomic signature showing ongoing inflammation and effectively classifying RHD cases.. 2022 , 19, 7	1
350	Pan-cancer proteomic map of 949 human cell lines reveals principles of cancer vulnerabilities.	1
349	All-Ion Monitoring-Directed Low-Abundance Protein Quantification Reveals CALB2 as a Key Promoter in Hepatocellular Carcinoma Metastasis.. 2022 ,	0
348	SWATH-MS identification of CXCL7, LBP, TGF β and PDGFR β s novel biomarkers in human systemic mastocytosis.. 2022 , 12, 5087	0
347	The emerging role of mass spectrometry-based proteomics in drug discovery.. 2022 ,	10
346	Quantitative proteomics analysis of human vitreous in rhegmatogenous retinal detachment associated with choroidal detachment by data-independent acquisition mass spectrometry.. 2022 , 1	0
345	Comparing Machine Learning Architectures for the Prediction of Peptide Collisional Cross Section.	
344	Profiling Mouse Brown and White Adipocytes to Identify Metabolically Relevant Small ORFs and Functional Microproteins.	
343	Data-Independent Acquisition Protease-Multiplexing Enables Increased Proteome Sequence Coverage Across Multiple Fragmentation Modes.. 2022 ,	0
342	Hyperphosphorylated Human Tau Accumulates at the Synapse, Localizing on Synaptic Mitochondrial Outer Membranes and Disrupting Respiration in a Mouse Model of Tauopathy.. 2022 , 15, 852368	0
341	Stratification of follicular thyroid tumors using data-independent acquisition proteomics and a comprehensive thyroid tissue spectral library.. 2022 ,	2
340	Striatal synaptic bioenergetic and autophagic decline in premotor experimental parkinsonism.. 2022 ,	2
339	A comprehensive LFQ benchmark dataset on modern day acquisition strategies in proteomics.. 2022 , 9, 126	3
338	Emergent White Matter Degeneration in the rTg-DI Rat Model of Cerebral Amyloid Angiopathy Exhibits Unique Proteomic Changes.. 2021 ,	0
337	DIA-MS proteome analysis of formalin-fixed paraffin-embedded glioblastoma tissues.. 2022 , 1204, 339695	0
336	The natural diversity of the yeast proteome reveals chromosome-wide dosage compensation in aneuploids.	2
335	Proteome dataset of sea bass (<i>Lateolabrax japonicus</i>) skin-scales exposed to fluoxetine and estradiol.. 2022 , 41, 107971	
334	SWATH-based quantitative proteomic analysis of <i>Morus alba</i> L. leaves after exposure to ultraviolet-B radiation and incubation in the dark.. 2022 , 230, 112443	1

333	Absolute Proteome Quantification in the Gas-Fermenting Acetogen .. 2022 , e0002622	0
332	Absolute quantification of viral proteins during single-round replication of MDCK suspension cells.. 2022 , 259, 104544	0
331	MSSort-DIA: A deep learning classification tool of the peptide precursors quantified by OpenSWATH.. 2022 , 104542	0
330	Identification and characterisation of sPEPs in <i>Cryptococcus neoformans</i> .. 2022 , 160, 103688	
329	Generation of a CHIP isogenic human iPSC-derived cortical neuron model for functional proteomics.. 2022 , 3, 101247	
328	Application of liquid chromatography mass spectrometry-based lipidomics to dairy products research: An emerging modulator of gut microbiota and human metabolic disease risk. 2022 , 157, 111206	3
327	Background ions into exclusion list: A new strategy to enhance the efficiency of DDA data collection for high-throughput screening of chemical contaminations in food.. 2022 , 385, 132669	0
326	Fast Screening and Identification of Illegal Adulterated Glucocorticoids in Dietary Supplements and Herbal Products Using UHPLC-QTOF-MS With All-Ion Fragmentation Acquisition Combined With Characteristic Fragment Ion List Classification.. 2021 , 9, 785475	0
325	Identification and Quantitation of Taste-Active Compounds in Dried Scallops by Combined Application of the Sensomics and a Quantitative NMR Approach.. 2021 ,	1
324	Deep learning approaches for data-independent acquisition proteomics.. 2021 ,	2
323	On the Road to Accurate Protein Biomarkers in Prostate Cancer Diagnosis and Prognosis: Current Status and Future Advances.. 2021 , 22,	2
322	An Atlas of the Quantitative Protein Expression of Anti-Epileptic-Drug Transporters, Metabolizing Enzymes and Tight Junctions at the Blood-Brain Barrier in Epileptic Patients.. 2021 , 13,	0
321	Investigation of Effects of the Spectral Library on Analysis of diaPASEF Data.. 2021 ,	1
320	A peptidiform based proteomic strategy for studying functions of post-translational modifications. 2021 , e2100316	3
319	Anterior gradient protein 2 is a marker of tumor aggressiveness in breast cancer and favors chemotherapy-induced senescence escape.. 2022 , 60,	0
318	Spotted Fever Group Trigger Species-Specific Alterations in Macrophage Proteome Signatures with Different Impacts in Host Innate Inflammatory Responses.. 2021 , e0081421	0
317	Generation of HLA Allele-Specific Spectral Libraries to Identify and Quantify Immunopeptidomes by SWATH/DIA-MS.. 2022 , 2420, 137-147	0
316	Rapid profiling of protein complex re-organization in perturbed systems.	0

315	Phosphoproteomics Sample Preparation Impacts Biological Interpretation of Phosphorylation Signaling Outcomes.. 2021 , 10,	1
314	The Small Open Reading Frame-Encoded Peptides: Advances in Methodologies and Functional Studies. 2021 ,	1
313	A Sensitive and Controlled Data-Independent Acquisition Method for Proteomic Analysis of Cell Therapies.. 2022 ,	0
312	Computational Methods for the Study of Peroxisomes in Health and Disease.	
311	High-throughput proteomics of nanogram-scale samples with Zeno SWATH DIA.	2
310	Obtaining Complete Human Proteomes.. 2022 ,	0
309	Omics-based ecosurveillance for the assessment of ecosystem function, health, and resilience.. 2022 , 6, 185-199	1
308	Meiotic Nuclear Pore Complex Remodeling Provides Key Insights into Nuclear Basket Organization.	
307	Proteome changes associated with the VEGFR pathway and immune system in diabetic macular edema patients at different diabetic retinopathy stages.. 2022 , 1-35	0
306	Multilayered omics reveal sex- and depot-dependent adipose progenitor cell heterogeneity.. 2022 ,	0
305	Lentil allergens identification and quantification: An update from omics perspective.. 2022 , 4, 100109	0
304	Data_Sheet_1.XLSX. 2018 ,	
303	Data_Sheet_2.xlsx. 2018 ,	
302	Data_Sheet_3.ZIP. 2018 ,	
301	Image_1.PDF. 2018 ,	
300	Image_2.PDF. 2018 ,	
299	Image_3.PDF. 2018 ,	
298	Image_4.PDF. 2018 ,	

297 Table_1.PDF. **2018**,

296 Table_2.PDF. **2018**,

295 Presentation_1.PPTX. **2018**,

294 Presentation_2.PPTX. **2018**,

293 Presentation_3.pptx. **2018**,

292 Presentation_4.pptx. **2018**,

291 Presentation_5.PPTX. **2018**,

290 Presentation_6.pptx. **2018**,

289 Presentation_7.pptx. **2018**,

288 Presentation_8.pptx. **2018**,

287 Presentation_9.pptx. **2018**,

286 Table_1.DOCX. **2018**,

285 Table_2.DOCX. **2018**,

284 Table_3.docx. **2018**,

283 Data_Sheet_1.PDF. **2019**,

282 Data_Sheet_2.PDF. **2019**,

281 Data_Sheet_3.PDF. **2019**,

280 Table_1.DOCX. **2019**,

279 Table_2.XLSX. 2019,

278 Table_3.XLSX. 2019,

277 Data_Sheet_1.pdf. 2020,

276 Table_1.DOCX. 2020,

275 Table_2.DOCX. 2020,

274 Image_1.TIFF. 2018,

273 Image_2.TIFF. 2018,

272 Image_3.TIFF. 2018,

271 Image_4.TIFF. 2018,

270 Image_5.TIFF. 2018,

269 Image_6.TIFF. 2018,

268 Image_7.TIFF. 2018,

267 Table_1.XLS. 2018,

266 Table_2.XLS. 2018,

265 Table_3.XLS. 2018,

264 Table_4.XLS. 2018,

263 Table_5.XLS. 2018,

262 Data_Sheet_1.PDF. 2018,

261 Presentation_1.pptx. **2018,**

260 Presentation_2.PPTX. **2018,**

259 Presentation_3.pptx. **2018,**

258 Table_1.xlsx. **2018,**

257 Table_2.xlsx. **2018,**

256 Table_3.xlsx. **2018,**

255 Table_4.docx. **2018,**

254 Table_5.docx. **2018,**

253 DataSheet_1.zip. **2019,**

252 Image_1.tif. **2019,**

251 Table_1.xlsx. **2019,**

250 Table_2.xlsx. **2019,**

249 Table_3.xlsx. **2019,**

248 Proteomics as a tool to understand the biology of agricultural crops. **2022,** 107-122

247 Proteomics in thrombosis research.. **2022,** 6, e12706

246 Emerging Function of Ecotype-Specific Splicing in the Recruitment of Commensal Microbiome.. **2022,** 23,

1

245 Novel trans-translation-associated gene regulation revealed by prophage excision-triggered switching of ribosome rescue pathway.

0

244 Analytical Considerations of Large-Scale Aptamer-Based Datasets for Translational Applications.. **2022,** 14,

0

243	Global, distinctive, and personal changes in molecular and microbial profiles by specific fibers in humans.. 2022 ,	4
242	Building Spectral Libraries from Narrow-Window Data-Independent Acquisition Mass Spectrometry Data.. 2022 ,	0
241	Comprehensive Assessment of Host Cell Protein Expression after Extended Culture and Bioreactor Production of CHO Cell Lines.. 2022 ,	0
240	The Use of Bacteriophages in Biotechnology and Recent Insights into Proteomics. 2022 , 11, 653	0
239	Clinical applications of plasma proteomics and peptidomics: Towards precision medicine.. 2022 , e2100097	1
238	Integrative proteogenomic characterization of hepatocellular carcinoma across etiologies and stages.. 2022 , 13, 2436	1
237	Zinc transport via ZNT5-6 and ZNT7 is critical for cell surface glycosylphosphatidylinositol-anchored protein expression.. 2022 , 102011	1
236	Benchmarking of analysis strategies for data-independent acquisition proteomics using a large-scale dataset comprising inter-patient heterogeneity.. 2022 , 13, 2622	2
235	A data-independent acquisition (DIA)-based quantification workflow for proteome analysis of 5000 cells.. 2022 , 216, 114795	0
234	The heart-brain axis: A proteomics study of meditation on the cardiovascular system of Tibetan Monks.. 2022 , 80, 104026	0
233	Proteomic Analysis of Human Neural Stem Cell Differentiation by SWATH-MS.. 2022 ,	
232	The impact of genomic variation on protein phosphorylation states and regulatory networks.. 2022 , 18, e10712	0
231	Application of proteomics and metabolomics in microbiology research. 2022 , 107-129	
230	Blood-Arachnoid Barrier as a Dynamic Physiological and Pharmacological Interface Between Cerebrospinal Fluid and Blood. 2022 , 93-121	0
229	Novel Bioinformatics Strategies Driving Dynamic Metaproteomic Studies. 2022 , 319-338	
228	High-Throughput Mass Spectrometry-Based Proteomics with dia-PASEF. 2022 , 15-27	1
227	A natural variation-based screen in mouse cells reveals USF2 as a regulator of the DNA damage response and cellular senescence.	
226	Salivary Proteomics Markers for Preclinical Sjögren's Syndrome: A Pilot Study. 2022 , 12, 738	1

225	Secreted Amyloid Precursor Protein Alpha, a Neuroprotective Protein in the Brain Has Widespread Effects on the Transcriptome and Proteome of Human Inducible Pluripotent Stem Cell-Derived Glutamatergic Neurons Related to Memory Mechanisms. 2022 , 16,	2
224	MS-based technologies for untargeted single-cell proteomics. 2022 , 76, 102736	0
223	Advances in data-independent acquisition mass spectrometry towards comprehensive digital proteome landscape.	2
222	Acoustic ejection mass spectrometry: fundamentals and applications in high-throughput drug discovery. 1-13	1
221	Prediction and Experimental Validation of a New Salinity-Responsive Cis-Regulatory Element (CRE) in a Tilapia Cell Line. 2022 , 12, 787	
220	Proteomic Dynamics of Breast Cancers Identifies Potential Therapeutic Protein Targets.	
219	Determination of adulteration, geographical origins, and species of food by mass spectrometry.	1
218	OxoScan-MS: Oxonium ion scanning mass spectrometry facilitates plasma glycoproteomics in large scale.	
217	Untargeted SWATH mass spectrometry-based metabolomics for studying chronic and intermittent exposure to xenobiotics in cohort studies. 2022 , 165, 113188	0
216	Proteomics of Fish White Muscle and Western Blotting to Detect Putative Allergens. 2022 , 397-411	1
215	The Proteomic Landscape of Genome-Wide Genetic Perturbations.	2
214	Omics technologies in allergy and asthma research: an EAACI position paper.	0
213	Integrated Multilayer Omics Reveals the Genomic, Proteomic, and Metabolic Influences of Histidyl Dipeptides on the Heart.	0
212	Unbiased spatial proteomics with single-cell resolution in tissues. 2022 , 82, 2335-2349	5
211	Multiple and Single Reaction Monitoring Mass Spectrometry for Absolute Quantitation of Proteins.	
210	A streamlined platform for analyzing tera-scale DDA and DIA mass spectrometry data enables highly sensitive immunopeptidomics. 2022 , 13,	0
209	Mass spectrometry-based retina proteomics.	
208	Proteomics and glycoproteomics of beer and wine. 2100329	1

- 207 A Periplasmic Lanthanide Mediator, Lanmodulin, in *Methylobacterium aquaticum* Strain 22A. 13,
- 206 Shotgun Proteomics Revealed Preferential Degradation of Misfolded In Vivo Obligate GroE Substrates by Lon Protease in *Escherichia coli*. **2022**, 27, 3772 1
- 205 Implementing the reuse of public DIA proteomics datasets: from the PRIDE database to Expression Atlas. **2022**, 9, 1
- 204 Proteome profiling of cerebrospinal fluid reveals biomarker candidates for Parkinson's disease. **2022**, 3, 100661 1
- 203 Comparative Transcriptome and Proteome Analysis Provides New Insights Into the Mechanism of Protein Synthesis in Kenaf (*Hibiscus cannabinus* L.) Leaves. 13, 1
- 202 Plasma proteomic changes in response to surgical trauma and a novel transdermal analgesic treatment in dogs. **2022**, 265, 104648 0
- 201 Proteomic profile of *Candida albicans* biofilm. **2022**, 265, 104661
- 200 Technological developments of food peptidomics. **2022**, 49-76
- 199 Horizontal Integration: OMICS [Mass Spectrometry-Based Proteomics in Systems Biology Research. **2022**,
- 198 Application of proteomics to the identification of foodborne pathogens. **2022**, 337-362
- 197 Improved profiling of low molecular weight serum proteome for gastric carcinoma by data-independent acquisition.
- 196 Evaluation of Volumetric Absorptive Microsampling and Mass Spectrometry Data-Independent Acquisition of Hemoglobin-Related Clinical Markers.
- 195 Comprehensive proteomic quantification of bladder stone progression in a cystinuric mouse model using data-independent acquisitions. **2022**, 17, e0250137 0
- 194 Mass spectrometry in the discovery of peptides involved in intercellular communication: From targeted to untargeted peptidomics approaches. 0
- 193 One-Week Dynamic Changes in Cardiac Proteomes After Cardiac Radioablation in Experimental Rat Model. 9, 0
- 192 Proteotype Co-evolution and Diversity in Mammals.
- 191 Upregulation of ribosome complexes at the blood-brain barrier in Alzheimer's disease patients. 0271678X2211116
- 190 Strategy of combining offline 2D LC-MS with LC-DIA-MS/MS to accurately identify chemical compounds and for quality control of *Dioscorea septemloba* Thunb.

189	Signal Alignment Enables Analysis of DIA Proteomics Data from Multisite Experiments.	
188	Cerebrospinal Fluid Proteomics in Friedreich Ataxia Reveals Markers of Neurodegeneration and Neuroinflammation. 16,	0
187	Resolving missing protein problems using functional class scoring. 2022 , 12,	
186	Temporal resolution of gene derepression and proteome changes upon PROTAC-mediated degradation of BCL11A protein in erythroid cells. 2022 ,	1
185	Targeted proteomics on its way to discovery. 2100330	0
184	Mapping Protein-Protein Interactions Using Data-Dependent Acquisition without Dynamic Exclusion.	0
183	Deep Phosphoproteomic Elucidation of Metformin-Signaling in Heterogenous Colorectal Cancer Cells.	
182	Network-based quantitative proteomics identified significant proteins associated with growth heterosis in triploid fish.	
181	dia-PASEF data analysis using FragPipe and DIA-NN for deep proteomics of low sample amounts. 2022 , 13,	3
180	Pan-cancer proteomic map of 949 human cell lines. 2022 ,	5
179	Connecting aging biology and inflammation in the omics era. 2022 , 132,	1
178	Circulating proteins as predictive and prognostic biomarkers in breast cancer. 2022 , 19,	6
177	Optimized data-independent acquisition approach for proteomic analysis at single-cell level. 2022 , 19,	3
176	AlphaViz: Visualization and validation of critical proteomics data directly at the raw data level.	0
175	Inner membrane complex proteomics reveals a palmitoylation regulation critical for intraerythrocytic development of malaria parasite. 11,	0
174	Amphiregulin mediates non-cell-autonomous effect of senescence on reprogramming. 2022 , 40, 111074	1
173	Prioritize biologically relevant ions for data-independent acquisition (BRI-DIA) in LCMS/MS-based lipidomics analysis. 2022 , 18,	0
172	Dysregulated Protein Phosphorylation in a Mouse Model of FTLD-Tau.	

171	Global and precise identification of functional miRNA targets in mESCs by integrative analysis.	1
170	pH-Responsive Lipid Nanoparticles Achieve Efficient mRNA Transfection in Brain Capillary Endothelial Cells. 2022 , 14, 1560	0
169	Changes in the liver proteome in apoE knockout mice exposed to inhalation of silica nanoparticles indicate mitochondrial damage and impairment of ER stress responses associated with microvesicular steatosis.	
168	Improving Phosphoproteomics Profiling Using Data-Independent Mass Spectrometry. 2022 , 21, 1789-1799	3
167	A gas phase fractionation acquisition scheme integrating ion mobility for rapid diaPASEF library generation.	0
166	Prediction of peptide mass spectral libraries with machine learning.	0
165	In-depth Analysis of the Sirtuin 5-regulated Mouse Brain Acylome using Library-free Data-Independent Acquisitions.	
164	Data-Independent Acquisition and Quantification of Extracellular Matrix from Human Lung in Chronic Inflammation-Associated Carcinomas.	
163	Comprehensive chromatin proteomics resolves functional phases of pluripotency.	
162	Novel Diagnostic Biomarkers for High-Grade Serous Ovarian Cancer Uncovered by Data-Independent Acquisition Mass Spectrometry.	0
161	Rapid and in-depth coverage of the (phospho-)proteome with deep libraries and optimal window design for dia-PASEF. 2022 , 100279	3
160	HypDB: A functionally annotated web-based database of the proline hydroxylation proteome. 2022 , 20, e3001757	
159	Localization of Multiple O-Linked Glycans Exhibited in Isomeric Glycopeptides by Hot Electron Capture Dissociation.	0
158	Is DIA proteomics data FAIR? Current data sharing practices, available bioinformatics infrastructure and recommendations for the future. 2200014	1
157	Strategies for structure elucidation of small molecules based on LCMS/MS data from complex biological samples. 2022 , 20, 5085-5097	0
156	Proteomics and Schizophrenia: The Evolution of a Great Partnership. 2022 , 129-138	0
155	An Introduction to Mass Spectrometry-Based Proteomics. 2022 ,	0
154	Introduction to Mass Spectrometry Data. 2022 , 7-19	0

153	Analysis of the Human Pineal Proteome by Mass Spectrometry. 2022 , 123-132	0
152	Dear-DIAXMBD: deep autoencoder for data-independent acquisition proteomics.	0
151	Artificial intelligence defines protein-based classification of thyroid nodules. 2022 , 8,	0
150	Cellular Aging Secretes: a Comparison of Bone-Marrow-Derived and Induced Mesenchymal Stem Cells and Their Secretome Over Long-Term Culture.	1
149	More than a simple epithelial layer: multifunctional role of echinoderm coelomic epithelium.	1
148	Functional precision profiling reveals non-mutational rewiring of kinase signaling networks in colorectal cancer.	0
147	Blood-based protein biomarkers for the diagnosis of acute stroke: A discovery-based SWATH-MS proteomic approach. 13,	0
146	Transcriptomic and proteomic analyses provide insights into the adaptive responses to the combined impact of salinity and alkalinity in <i>Gymnocypris przewalskii</i> . 2022 , 9,	0
145	Data-independent acquisition proteomics methods for analyzing post-translational modifications. 2200046	1
144	Metabolic dyshomeostasis induced by SARS-CoV-2 structural proteins reveals immunological insights into viral olfactory interactions. 13,	0
143	Proteotype coevolution and quantitative diversity across 11 mammalian species. 2022 , 8,	1
142	Lifetime development changes in rats tracked by urinary proteome.	0
141	Ketone body metabolism declines with age in mice in a sex-dependent manner.	0
140	Label-free quantitative SWATH-MS proteomic analysis of adult myocardial slices in vitro after biomimetic electromechanical stimulation. 2022 , 12,	0
139	nF-encyclopedia: A cloud-ready pipeline for chromatogram library data-independent acquisition proteomics workflows.	0
138	Temporal Extracellular Vesicle Protein Changes following Intraarticular Treatment with Integrin $\alpha 5 \beta 1$ -selected Mesenchymal Stem Cells in Equine Osteoarthritis.	0
137	Proteomics-based molecular and functional characteristic profiling of muscle tissue in Triploid crucian carp.	0
136	Chromatography High-Resolution Mass Spectrometry in Food and Environmental Chemistry. 2022 ,	0

- 135 Data-independent acquisition and quantification of extracellular matrix from human lung in chronic inflammation-associated carcinomas. 2200021 0
- 134 Population serum proteomics uncovers prognostic protein classifier and molecular mechanisms for metabolic syndrome. 0
- 133 Defective mitochondria-lysosomal axis enhances the release of extracellular vesicles containing mitochondrial DNA and proteins in Huntington's disease. **2022**, 1, 1
- 132 Proteomics Profiling of Stool Samples from Preterm Neonates with SWATH/DIA Mass Spectrometry for Predicting Necrotizing Enterocolitis. **2022**, 23, 11601 0
- 131 Proteomics coupled with in vitro model to study the early crosstalk occurring between newly excysted juveniles of *Fasciola hepatica* and host intestinal cells. **2022**, 16, e0010811 0
- 130 Is nontargeted data acquisition for target analysis (nDATA) in mass spectrometry a forward-thinking analytical approach?. 1
- 129 Multi-Omics Reveals Mechanisms of Partial Modulation of COVID-19 Dysregulation by Glucocorticoid Treatment. **2022**, 23, 12079 0
- 128 Proteomic response of early juvenile Pacific oysters (*Crassostrea gigas*) to temperature. 10, e14158 0
- 127 GLUT1 ablation in astrocytes paradoxically improves central and peripheral glucose metabolism via enhanced insulin-stimulated ATP release. 0
- 126 Automated Proteomics Sample Preparation of Phosphatidylserine-Positive Extracellular Vesicles from Human Body Fluids. 1
- 125 Recent advances in the field of single-cell proteomics. **2023**, 27, 101556 1
- 124 SWATH Mass Spectrometry-Based CSF Proteome Profile of GBA-Linked Parkinson's Disease Patients. **2022**, 23, 14166 0
- 123 Potential use of EGFR-targeted molecular therapies for tumor suppressor CYLD-negative and poor prognosis oral squamous cell carcinoma with chemoresistance. **2022**, 22, 0
- 122 A Peptide-Centric Quantitative Proteomics Dataset for the Phenotypic Assessment of Alzheimer's Disease. 0
- 121 The stallion sperm acrosome: Considerations from a research and clinical perspective. **2022**, 0
- 120 Strategies for increasing the depth and throughput of protein analysis by plexDIA. 0
- 119 LC-MS / MS -Based Proteomics Methods for Quantifying Drug-Metabolizing Enzymes and Transporters. **2022**, 143-176 0
- 118 Transcription factors TEAD2 and E2A globally repress acetyl-CoA synthesis to promote tumorigenesis. **2022**, 82, 4246-4261.e11 0

117	The Origin and Implications of Artifact Ions in Bioanalytical LCMS. 2022 , 10-13	0
116	Proteomics in Inherited Metabolic Disorders. 2022 , 23, 14744	1
115	Proteomic overview of hepatocellular carcinoma cell lines and generation of the spectral library. 2022 , 9,	0
114	High-throughput proteomics of nanogram-scale samples with Zeno SWATH MS. 11,	0
113	The Biological Effects of Compound Microwave Exposure with 2.8 GHz and 9.3 GHz on Immune System: Transcriptomic and Proteomic Analysis. 2022 , 11, 3849	1
112	Robust and Highly Efficient Extractions of Proteins from Bones enable Deep, High-Throughput Proteomic Quantification to Gain Insights into Bone Biology.	0
111	Peptide-based LDH5 inhibitors enter cancer cells and impair proliferation. 2022 , 79,	0
110	Temporal extracellular vesicle protein changes following intraarticular treatment with integrin α 5 β 1-selected mesenchymal stem cells in equine osteoarthritis. 9,	0
109	Principles of gene regulation quantitatively connect DNA to RNA and proteins in bacteria. 2022 , 378,	0
108	Toxicoproteomics reveals an effect of clozapine on autophagy in human liver spheroids. 1-10	1
107	Filaggrin insufficiency renders keratinocyte-derived small extracellular vesicles capable of modulating CD1a-mediated T cell responses.	0
106	Dynamic Interactomics by Cross-Linking Mass Spectrometry: Mapping the Daily Cell Life in Postgenomic Era. 2022 , 26, 633-649	0
105	Transcriptome and proteome profiling of activated cardiac fibroblasts supports target prioritization in cardiac fibrosis. 9,	0
104	Sex-divergent effects on the NAD ⁺ -dependent deacetylase sirtuin signaling across the olfactory-entorhinal-amygdaloid axis in Alzheimer's and Parkinson's diseases.	0
103	Mass Spectrometric Methods for Non-Targeted Screening of Metabolites: A Future Perspective for the Identification of Unknown Compounds in Plant Extracts. 2022 , 9, 415	0
102	Synchro-PASEF allows precursor-specific fragment ion extraction and interference removal in data-independent acquisition. 2022 , 100489	0
101	In-depth analysis of the Sirtuin 5-regulated mouse brain malonylome and succinylome using library-free data-independent acquisitions. 2100371	1
100	High-quality and robust protein quantification in large clinical/pharmaceutical cohorts with IonStar proteomics investigation.	0

99	Toward a hypothesis-free understanding of how phosphorylation dynamically impacts protein turnover. 2100387	1
98	Meiotic nuclear pore complex remodeling provides key insights into nuclear basket organization. 2023 , 222,	0
97	Modular UBE2H-CTLH E2-E3 complexes regulate erythroid maturation. 11,	0
96	Proteomic profiling of cerebrospinal fluid in pediatric myelin oligodendrocyte glycoprotein antibody-associated disease.	0
95	MS-DAP Platform for Downstream Data Analysis of Label-Free Proteomics Uncovers Optimal Workflows in Benchmark Data Sets and Increased Sensitivity in Analysis of Alzheimer's Biomarker Data.	0
94	Prophage excision switches the primary ribosome rescue pathway and rescue-associated gene regulations in Escherichia coli.	0
93	Interrogation of an ovine serum peptide spectral library to annotate ambiguous clinicopathological biomarkers using data-independent acquisition. 11, 1433	0
92	Proteomic Portrait of Human Lymphoma Reveals Protein Molecular Fingerprint of Disease Specific Subtypes and Progression.	0
91	The Impact of Peri-implantitis on the Proteome Biology of Crevicular Fluid: A pilot study.	0
90	DPHL v2: An updated and comprehensive DIA pan-human assay library for quantifying more than 14,000 proteins.	0
89	Characterization and implications of host-cell protein aggregates in biopharmaceutical processing.	0
88	Advancements in Oncoproteomics Technologies: Treading toward Translation into Clinical Practice. 2023 , 11, 2	1
87	Profiling mouse brown and white adipocytes to identify metabolically relevant small ORFs and functional microproteins. 2023 , 35, 166-183.e11	0
86	Developing quantitative assays for six urinary glycoproteins using parallel reaction monitoring, data-independent acquisition, and TMT-based data-dependent acquisition. 2200072	0
85	Current progress and critical challenges to overcome in the bioinformatics of mass spectrometry-based metaproteomics. 2023 ,	0
84	Benchmarking commonly used software suites and analysis workflows for DIA proteomics and phosphoproteomics. 2023 , 14,	0
83	NeuroLINCS Proteomics: Defining human-derived iPSC proteomes and protein signatures of pluripotency. 2023 , 10,	0
82	Degradation Kinetics of Lignocellulolytic Enzymes in a Biogas Reactor Using Quantitative Mass Spectrometry. 2023 , 9, 67	0

81	Next-generation interaction proteomics for quantitative Jumbophage-bacteria interaction mapping.	0
80	DIA mass spectrometry characterizes urinary proteomics in neonatal and adult donkeys. 2022 , 12,	0
79	The Impact of Peri-implantitis on the Proteome Biology of Crevicular Fluid: A pilot study.	0
78	Fiber-Type Shifting in Sarcopenia of Old Age: Proteomic Profiling of the Contractile Apparatus of Skeletal Muscles. 2023 , 24, 2415	1
77	The proteomic landscape of synaptic diversity across brain regions and cell types.	0
76	Data-independent acquisition boosts quantitative metaproteomics for deep characterization of gut microbiota. 2023 , 9,	1
75	Targeted Quantification of Protein Phosphorylation and Its Contributions towards Mathematical Modeling of Signaling Pathways. 2023 , 28, 1143	0
74	Fructose Induced KHK-C Increases ER Stress and Modulates Hepatic Transcriptome to Drive Liver Disease in Diet-Induced and Genetic Models of NAFLD.	0
73	Proteomics of Animal Viruses. 2023 , 89-199	0
72	Deletion of genes linked to the C1-fixing gene cluster affects growth, by-products, and proteome of <i>Clostridium autoethanogenum</i> .	0
71	Reconstruction of Glutathione Metabolism in the Neuronal Model of Rotenone-Induced Neurodegeneration Using Mass Isotopologue Analysis with Hydrophilic Interaction Liquid Chromatography-Zeno High-Resolution Multiple Reaction Monitoring.	0
70	Automating the design-build-test-learn cycle towards next-generation bacterial cell factories. 2023 , 74, 1-15	0
69	Strategies for Increasing the Depth and Throughput of Protein Analysis by plexDIA.	0
68	Data-Driven Optimization of DIA Mass-Spectrometry by DO-MS.	0
67	Phosphoproteomic analysis of metformin signaling in colorectal cancer cells elucidates mechanism of action and potential therapeutic opportunities. 2023 , 13,	1
66	Quantitative Chemoproteomic Methods for Reactive Cysteine Profiling.	0
65	Sequence distribution determination by SWAMP-MS a systematic way of analyzing multiple fragmented polymers with mass spectrometry. 2023 , 140,	0
64	A Streamlined High-Throughput Plasma Proteomics Platform for Clinical Proteomics with Improved Proteome Coverage, Reproducibility, and Robustness. 2023 , 34, 754-762	0

- 63 The Proteome of Large or Small Extracellular Vesicles in Pig Seminal Plasma Differs, Defining Sources and Biological Functions. **2023**, 22, 100514 ○
- 62 Rapid Profiling of Protein Complex Reorganization in Perturbed Systems. ○
- 61 Single-day protein LCMS bioanalysis: can next-generation trypsin cut it?. ○
- 60 A highly sensitive and robust LC-MS platform for host cell protein characterization in biotherapeutics. **2023**, 82, 101675 ○
- 59 Enzyme expression kinetics by Escherichia coli during transition from rich to minimal media depends on proteome reserves. **2023**, 8, 347-359 ○
- 58 Environment Modulates Protein Heterogeneity Through Transcriptional and Translational Stop Codon Miscoding. ○
- 57 Data-Independent Acquisition Mass Spectrometry of EPS-Urine Coupled to Machine Learning: A Predictive Model for Prostate Cancer. **2023**, 8, 6244-6252 ○
- 56 Data acquisition methods for non-targeted screening in environmental analysis. **2023**, 160, 116966 ○
- 55 A Novel Blood Proteomic Signature for Prostate Cancer. **2023**, 15, 1051 ○
- 54 Sex-divergent effects on the NAD⁺-dependent deacetylase sirtuin signaling across the olfactoryBntorhinalBmygdaloid axis in AlzheimerB and ParkinsonB diseases. **2023**, 14, 1
- 53 Mutation-class dependent signatures outweigh disease-associated processes in cystic fibrosis cells. **2023**, 13, 1
- 52 Recent methodological developments in data-dependent analysis and data-independent analysis workflows for exhaustive lipidome coverage. 3, ○
- 51 Deep learning baseline correction method via multi-scale analysis and regression. **2023**, 235, 104779 ○
- 50 HNRNPA2B1 as a potential therapeutic target for thymic epithelial tumor recurrence: An integrative network analysis. **2023**, 155, 106665 ○
- 49 Profiling Serum Intact N-Glycopeptides Using Data-Independent Acquisition Mass Spectrometry. **2023**, 365-391 ○
- 48 Early Cancer Biomarker Discovery Using DIA-MS Proteomic Analysis of EVs from Peripheral Blood. **2023**, 127-152 ○
- 47 Histone malonylation is regulated by SIRT5 and KAT2A. **2023**, 26, 106193 ○
- 46 Benchmarking Bioinformatics Pipelines in Data-Independent Acquisition Mass Spectrometry for Immunopeptidomics. **2023**, 22, 100515 ○

- 45 Network-based elucidation of colon cancer drug resistance by phosphoproteomic time-series analysis. ○
- 44 Genome-wide genotype-serum proteome mapping provides insights into the cross-ancestry differences in cardiometabolic disease susceptibility. **2023**, 14, ○
- 43 Speedy-PASEF: Analytical flow rate chromatography and trapped ion mobility for deep high-throughput proteomics. ○
- 42 Quantitative proteomics reveals reduction in central carbon and energy metabolisms contributes to gentamicin resistance in *Staphylococcus aureus*. **2023**, 277, 104849 ○
- 41 Anemonefishes: A model system for evolutionary genomics. 12, 204 ○
- 40 Optimizing linear ion trap data independent acquisition towards single cell proteomics. ○
- 39 Ketohexokinase-C regulates global protein acetylation to decrease carnitine palmitoyltransferase 1a-mediated fatty acid oxidation. **2023**, ○
- 38 Substantial Downregulation of Mitochondrial and Peroxisomal Proteins during Acute Kidney Injury revealed by Data-Independent Acquisition Proteomics. ○
- 37 SWATH-MS-Based Proteomics Reveals the Regulatory Metabolism of Amaryllidaceae Alkaloids in Three *Lycoris* Species. **2023**, 24, 4495 1
- 36 Proteomics as a Tool for the Study of Mitochondrial Proteome, Its Dysfunctionality and Pathological Consequences in Cardiovascular Diseases. **2023**, 24, 4692 ○
- 35 Using the Proteomics Toolbox to Resolve Topology and Dynamics of Compartmentalized cAMP Signaling. **2023**, 24, 4667 ○
- 34 Proteomic analysis identifies dysregulated proteins and associated molecular pathways in a cohort of gallbladder cancer patients of African ancestry. **2023**, 20, ○
- 33 Data Independent Acquisition Reveals In-Depth Serum Proteome Changes in Canine Leishmaniosis. **2023**, 13, 365 ○
- 32 Resistance prediction in high-grade serous ovarian carcinoma with neoadjuvant chemotherapy using data-independent acquisition proteomics and an ovary-specific spectral library. ○
- 31 Advances in Mass Spectrometry-Based Single Cell Analysis. **2023**, 12, 395 ○
- 30 Differential Effects of Cocaine and Morphine on the Diurnal Regulation of the Mouse Nucleus Accumbens Proteome. ○
- 29 A gas phase fractionation acquisition scheme integrating ion mobility for rapid diaPASEF library generation. **2023**, 23, 1
- 28 Simulated-to-real benchmarking of acquisition methods in untargeted metabolomics. 10, ○

- 27 Characterization of proteome profile data of chemicals based on data-independent acquisition MS with SWATH method. **2023**, 5, ○
- 26 DeepDetect: Deep Learning of Peptide Detectability Enhanced by Peptide Digestibility and Its Application to DIA Library Reduction. **2023**, 95, 6235-6243 ○
- 25 PROSE: phenotype-specific network signatures from individual proteomic samples. **2023**, 24, ○
- 24 Molecular and Cellular Crosstalk between Bone and Brain: Accessing Bidirectional Neural and Musculoskeletal Signaling during Aging and Disease. **2023**, 30, 1-29 ○
- 23 Mass spectrometry DDA parameters and global coverage of the metabolome: Spectral molecular networks of momordica cardiospermoides plants. **2023**, 19, ○
- 22 Measurement and utilization of the proteomic reactivity by mass spectrometry. ○
- 21 Evolution of Mass Spectrometry Instruments and Techniques for Blood Proteomics. **2023**, 22, 1009-1023 ○
- 20 PatternLab V Handles Multiplex Spectra in Shotgun Proteomic Searches and Increases Identification. **2023**, 34, 794-796 ○
- 19 Proteomic Analysis of Huntington's Disease Medium Spiny Neurons Identifies Alterations in Lipid Droplets. **2023**, 100534 ○
- 18 DIP-MS: A novel ultra-deep interaction proteomics for the deconvolution of protein complexes. ○
- 17 Highlighting In Vitro the Role of Brain-like Endothelial Cells on the Maturation and Metabolism of Brain Pericytes by SWATH Proteomics. **2023**, 12, 1010 ○
- 16 Glial-Restricted Precursors stimulate endogenous cytotgenesis and effectively recover emotional deficits in a model of cytotgenesis ablation. ○
- 15 Deregulated Transcription and Proteostasis in Adult mapt Knockout Mouse. **2023**, 24, 6559 ○
- 14 Age-Modulated Immuno-Metabolic Proteome Profiles of Deceased Donor Kidneys Predict 12-Month Posttransplant Outcome. ○
- 13 Changes of development from childhood to late adulthood in rats tracked by urinary proteome. **2023**, 100539 ○
- 12 Analytical characterization of host-cell-protein-rich aggregates in monoclonal antibody solutions. ○
- 11 Data-independent acquisition mass spectrometry reveals comprehensive plasma protein profiles in the natural history of patients with hereditary transthyretin amyloidosis (ATTRv). 1-13 ○
- 10 Panomics's Fingerprinting Approaches for Food Fraud Detection. **2023**, ○

- 9 Recent advances of data-independent acquisition mass spectrometry-based proteomics. **2023**, 23, ○
- 8 An automated proximity proteomics pipeline for subcellular proteome and protein interaction mapping. ○
- 7 In Vitro Models and Proteomics in Osteoarthritis Research. **2023**, 57-68 ○
- 6 A peptide-centric quantitative proteomics dataset for the phenotypic assessment of Alzheimer's disease. **2023**, 10, ○
- 5 The proteomic landscape of genome-wide genetic perturbations. **2023**, ○
- 4 Mslmpute: Estimation of missing peptide intensity data in label-free quantitative mass spectrometry. **2023**, 100558 ○
- 3 Advanced mass spectrometry workflows for accurate quantification of trace-level host cell proteins in drug products: Benefits of FAIMS separation and gas-phase fractionation DIA. ○
- 2 vCSF Danger-associated Molecular Patterns After Traumatic and Nontraumatic Acute Brain Injury: A Prospective Study. Publish Ahead of Print, ○
- 1 Functional proteomics based on protein microarray technology for biomedical research. **2023**, ○