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2285	.		
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2278	Restricted Proteolysis and LC-MS/MS To Evaluate the Orientation of Surface-Immobilized Antibodies.	
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2276	High-Throughput Targeted Quantitative Analysis of the Interaction between HSP90 and Kinases.	
2275	Proteomics Approach To Trace Site-Specific Damage in Aquatic Extracellular Enzymes During Photoinactivation.	
2274	.	
2273	Potential of temperature- and salinity-driven shifts in diatom compatible solute concentrations to impact biogeochemical cycling within sea ice. 2020 , 8,	
2272	Post-translation modification of proteins in tears. 2010 , 31, 1853-61	40
2271	Reconstructing the pipeline by introducing multiplexed multiple reaction monitoring mass spectrometry for cancer biomarker verification: an NCI-CPTC initiative perspective. 2010 , 4, 904-14	32
2270	Generating and navigating proteome maps using mass spectrometry. 2010 , 11, 789-801	139
2269	Effect of collision energy optimization on the measurement of peptides by selected reaction monitoring (SRM) mass spectrometry. 2010 , 82, 10116-24	176
2268	Quantitative improvements in peptide recovery at elevated chromatographic temperatures from microcapillary liquid chromatography-mass spectrometry analyses of brain using selected reaction monitoring. 2010 , 82, 3435-40	21
2267	Training, selection, and robust calibration of retention time models for targeted proteomics. 2010 , 9, 5209-16	69
2266	Protein quantitation using mass spectrometry. 2010 , 673, 211-22	40
2265	Quantifying attomole amounts of proteins from complex samples by nano-LC and selected reaction monitoring. 2011 , 790, 141-64	6
2264	A targeted proteomics-based pipeline for verification of biomarkers in plasma. 2011 , 29, 625-34	290
2263	Mass spectrometry mapping of epidermal growth factor receptor phosphorylation related to oncogenic mutations and tyrosine kinase inhibitor sensitivity. 2011 , 10, 305-19	52
2262	Mutant proteins as cancer-specific biomarkers. 2011 , 108, 2444-9	136

2261	Differential carbonylation of proteins as a function of in vivo oxidative stress. 2011 , 10, 3959-72	58
2260	Quantification of proteins using peptide immunoaffinity enrichment coupled with mass spectrometry. 2011 ,	16
2259	Applying selected reaction monitoring to targeted proteomics. 2011 , 8, 165-73	40
2258	Comprehensive quantitative analysis of central carbon and amino-acid metabolism in <i>Saccharomyces cerevisiae</i> under multiple conditions by targeted proteomics. 2011 , 7, 464	88
2257	Quantitative Mass Spectrometry-Based Proteomics. 2011 , 419-438	
2256	Nanoproteomics. 2011 ,	2
2255	Rapid empirical discovery of optimal peptides for targeted proteomics. 2011 , 8, 1041-3	93
2254	Serum levels of pregnancy zone protein are elevated in presymptomatic Alzheimer's disease. 2011 , 10, 4902-10	42
2253	Serum/Plasma Proteomics. 2011 ,	7
2252	SRMBuilder: a user-friendly tool for selected reaction monitoring data analysis. 2011 , 9 Suppl 1, 51-62	3
2251	Profiling for novel proteomics biomarkers in neurodevelopmental disorders. 2011 , 8, 127-36	14
2250	Confident identification of 3-nitrotyrosine modifications in mass spectral data across multiple mass spectrometry platforms. 2011 , 74, 2510-21	15
2249	Targeted mass spectrometry approaches for protein biomarker verification. 2011 , 74, 2650-9	86
2248	Building and searching tandem mass (MS/MS) spectral libraries for peptide identification in proteomics. 2011 , 54, 424-31	41
2247	Targeted proteomics by selected reaction monitoring mass spectrometry: applications to systems biology and biomarker discovery. 2011 , 7, 292-303	66
2246	Trends and Developments in Bioinformatics in 2010: Prospects and Perspectives. 2011 , 20, 146-155	
2245	Current Perspectives and Recommendations for the Development of Mass Spectrometry Methods for the Determination of Allergens in Foods. 2011 , 94, 1026-1033	93
2244	mProphet: automated data processing and statistical validation for large-scale SRM experiments. 2011 , 8, 430-5	357

2243	Absolute quantification of protein and post-translational modification abundance with stable isotope-labeled synthetic peptides. 2011 , 6, 175-86	121
2242	Monitoring protein expression in whole-cell extracts by targeted label- and standard-free LC-MS/MS. 2011 , 6, 859-69	50
2241	In-depth proteomics of ovarian cancer ascites: combining shotgun proteomics and selected reaction monitoring mass spectrometry. 2011 , 10, 2286-99	63
2240	Improving SRM assay development: a global comparison between triple quadrupole, ion trap, and higher energy CID peptide fragmentation spectra. 2011 , 10, 4334-41	77
2239	A general strategy for studying multisite protein phosphorylation using label-free selected reaction monitoring mass spectrometry. 2011 , 418, 267-75	10
2238	A large, consistent plasma proteomics data set from prospectively collected breast cancer patient and healthy volunteer samples. 2011 , 9, 80	11
2237	PChopper: high throughput peptide prediction for MRM/SRM transition design. 2011 , 12, 338	4
2236	ATAQS: A computational software tool for high throughput transition optimization and validation for selected reaction monitoring mass spectrometry. 2011 , 12, 78	60
2235	A database of reaction monitoring mass spectrometry assays for elucidating therapeutic response in cancer. 2011 , 5, 383-96	43
2234	Understanding the improved sensitivity of spectral library searching over sequence database searching in proteomics data analysis. 2011 , 11, 1075-85	48
2233	An improved method for the construction of decoy peptide MS/MS spectra suitable for the accurate estimation of false discovery rates. 2011 , 11, 4085-95	21
2232	The ABRF Proteomics Research Group studies: educational exercises for qualitative and quantitative proteomic analyses. 2011 , 11, 1371-81	14
2231	Quantification of proteins and their modifications using QconCAT technology. 2011 , 500, 113-31	7
2230	Evaluation of large scale quantitative proteomic assay development using peptide affinity-based mass spectrometry. 2011 , 10, M110.005645	118
2229	Methods for peptide and protein quantitation by liquid chromatography-multiple reaction monitoring mass spectrometry. 2011 , 10, M110.006593	88
2228	Building and searching tandem mass spectral libraries for peptide identification. 2011 , 10, R111.008565	49
2227	¹⁸ O-labeled proteome reference as global internal standards for targeted quantification by selected reaction monitoring-mass spectrometry. 2011 , 10, M110.007302	16
2226	Monitoring a nuclear factor- κ B signature of drug resistance in multiple myeloma. 2011 , 10, M110.005520	27

2225	Computational mass spectrometry-based proteomics. 2011 , 7, e1002277	47
2224	MRMaid: The SRM Assay Design Tool for Arabidopsis and Other Species. 2012 , 3, 164	14
2223	Platform-independent and label-free quantitation of proteomic data using MS1 extracted ion chromatograms in skyline: application to protein acetylation and phosphorylation. 2012 , 11, 202-14	328
2222	Measurement of fractional synthetic rates of multiple protein analytes by triple quadrupole mass spectrometry. 2012 , 58, 619-27	24
2221	Sequential multiplexed analyte quantification using peptide immunoaffinity enrichment coupled to mass spectrometry. 2012 , 11, M111.015347	48
2220	Development of a pharmaceutical hepatotoxicity biomarker panel using a discovery to targeted proteomics approach. 2012 , 11, 394-410	32
2219	File formats commonly used in mass spectrometry proteomics. 2012 , 11, 1612-21	66
2218	Functional proteomics establishes the interaction of SIRT7 with chromatin remodeling complexes and expands its role in regulation of RNA polymerase I transcription. 2012 , 11, 60-76	130
2217	Total kinetic analysis reveals how combinatorial methylation patterns are established on lysines 27 and 36 of histone H3. 2012 , 109, 13549-54	102
2216	Identification of differentially expressed proteins in direct expressed prostatic secretions of men with organ-confined versus extracapsular prostate cancer. 2012 , 11, 1870-84	62
2215	A computational tool to detect and avoid redundancy in selected reaction monitoring. 2012 , 11, 540-9	79
2214	Free and total biotherapeutic evaluation in chromatographic assays: interference from targets and immunogenicity. 2012 , 4, 2401-11	7
2213	Quantification of protein deposits on silicone hydrogel materials using stable-isotopic labeling and multiple reaction monitoring. 2012 , 28, 697-709	7
2212	MRMaid 2.0: mining PRIDE for evidence-based SRM transitions. 2012 , 16, 483-8	13
2211	Myeloperoxidase targets apolipoprotein A-I, the major high density lipoprotein protein, for site-specific oxidation in human atherosclerotic lesions. 2012 , 287, 6375-86	129
2210	Quantitative assessment of chromatin immunoprecipitation grade antibodies directed against histone modifications reveals patterns of co-occurring marks on histone protein molecules. 2012 , 11, 128-37	65
2209	Antibody-free, targeted mass-spectrometric approach for quantification of proteins at low picogram per milliliter levels in human plasma/serum. 2012 , 109, 15395-400	177
2208	Regulatory control or oxidative damage? Proteomic approaches to interrogate the role of cysteine oxidation status in biological processes. 2012 , 11, R111.013037	75

2207	Peptide production and decay rates affect the quantitative accuracy of protein cleavage isotope dilution mass spectrometry (PC-IDMS). 2012 , 11, 814-23	58
2206	Global stability of plasma proteomes for mass spectrometry-based analyses. 2012 , 11, M111.014340	50
2205	TraML--a standard format for exchange of selected reaction monitoring transition lists. 2012 , 11, R111.015040	58
2204	Protein expression signatures for inhibition of epidermal growth factor receptor-mediated signaling. 2012 , 11, M111.015222	17
2203	Proteomics in Drug Discovery and Development. 2012 , 1	
2202	Functional redundancy of the two 5-hydroxylases in monolignol biosynthesis of <i>Populus trichocarpa</i> : LC-MS/MS based protein quantification and metabolic flux analysis. 2012 , 236, 795-808	14
2201	Enhancing fatty acid production by the expression of the regulatory transcription factor FadR. 2012 , 14, 653-60	132
2200	Absolute quantification of prion protein (90-231) using stable isotope-labeled chymotryptic peptide standards in a LC-MRM AQUA workflow. 2012 , 23, 1522-33	28
2199	Accurate peptide fragment mass analysis: multiplexed peptide identification and quantification. 2012 , 11, 1621-32	78
2198	Effects of the miR-143/-145 microRNA cluster on the colon cancer proteome and transcriptome. 2012 , 11, 4744-54	38
2197	Protein significance analysis in selected reaction monitoring (SRM) measurements. 2012 , 11, M111.014662	116
2196	Chimeras taking shape: potential functions of proteins encoded by chimeric RNA transcripts. 2012 , 22, 1231-42	101
2195	The use of selected reaction monitoring in quantitative proteomics. 2012 , 4, 1763-86	62
2194	Development of a multiplex selected reaction monitoring assay for quantification of biochemical markers of down syndrome in amniotic fluid samples. 2012 , 11, 3880-7	20
2193	Relative quantification of serum proteins from pancreatic ductal adenocarcinoma patients by stable isotope dilution liquid chromatography-mass spectrometry. 2012 , 11, 1749-58	29
2192	MMSAT: automated quantification of metabolites in selected reaction monitoring experiments. 2012 , 84, 470-4	21
2191	A cross-platform toolkit for mass spectrometry and proteomics. 2012 , 30, 918-20	1583
2190	Precision of multiple reaction monitoring mass spectrometry analysis of formalin-fixed, paraffin-embedded tissue. 2012 , 11, 3498-505	47

2189	GeLC-MRM quantitation of mutant KRAS oncoprotein in complex biological samples. 2012 , 11, 3908-13	32
2188	Proteomic consequences of a single gene mutation in a colorectal cancer model. 2012 , 11, 1184-95	29
2187	Measuring H(2)(18)O tracer incorporation on a QQQ-MS platform provides a rapid, transferable screening tool for relative protein synthesis. 2012 , 11, 1591-7	2
2186	Lectin chromatography/mass spectrometry discovery workflow identifies putative biomarkers of aggressive breast cancers. 2012 , 11, 2508-20	45
2185	Bioinformatic challenges in targeted proteomics. 2012 , 11, 4393-402	15
2184	Multiplex targeted proteomic assay for biomarker detection in plasma: a pancreatic cancer biomarker case study. 2012 , 11, 1937-48	74
2183	An expansive human regulatory lexicon encoded in transcription factor footprints. 2012 , 489, 83-90	589
2182	Functional proteomics establishes the interaction of SIRT7 with chromatin remodeling complexes and expands its role in regulation of RNA polymerase I transcription. 2012 , 11, M111.015156	29
2181	Analysis of serum total and free PSA using immunoaffinity depletion coupled to SRM: correlation with clinical immunoassay tests. 2012 , 75, 4747-57	42
2180	Targeted proteome investigation via selected reaction monitoring mass spectrometry. 2012 , 75, 3495-513	52
2179	Label-free mass spectrometry-based proteomics for biomarker discovery and validation. 2012 , 12, 343-59	42
2178	MS/MS library facilitated MRM quantification of native peptides prepared by denaturing ultrafiltration. 2012 , 10, 7	3
2177	Development of protein biomarkers in cerebrospinal fluid for secondary progressive multiple sclerosis using selected reaction monitoring mass spectrometry (SRM-MS). 2012 , 9, 9	26
2176	The application of selective reaction monitoring confirms dysregulation of glycolysis in a preclinical model of schizophrenia. 2012 , 5, 146	26
2175	Homopteran Vector Biomarkers for Efficient Circulative Plant Virus Transmission are Conserved in Multiple Aphid Species and the Whitefly Bemisia tabaci. 2012 , 11, 249-262	5
2174	Mass spectrometry-based proteomics for systems biology. 2012 , 23, 591-7	78
2173	Urinary proteome analysis of irritable bowel syndrome (IBS) symptom subgroups. 2012 , 11, 5650-62	29
2172	Label-free quantitation of protein modifications by pseudo selected reaction monitoring with internal reference peptides. 2012 , 11, 3467-79	56

2171	Targeted proteomics for metabolic pathway optimization. 2012 , 944, 237-49	16
2170	Measurement of Protein Phosphorylation Stoichiometry by SRM-MS. 2012 , 4, 65-81	1
2169	Evaluation of direct infusion-multiple reaction monitoring mass spectrometry for quantification of heat shock proteins. 2012 , 84, 1981-6	8
2168	A critical appraisal of techniques, software packages, and standards for quantitative proteomic analysis. 2012 , 16, 431-42	46
2167	Comprehensive quantification of monolignol-pathway enzymes in <i>Populus trichocarpa</i> by protein cleavage isotope dilution mass spectrometry. 2012 , 11, 3390-404	38
2166	Proteomic analysis reveals drug accessible cell surface N-glycoproteins of primary and established glioblastoma cell lines. 2012 , 11, 4885-93	19
2165	Large-scale quantitative assessment of different in-solution protein digestion protocols reveals superior cleavage efficiency of tandem Lys-C/trypsin proteolysis over trypsin digestion. 2012 , 11, 5145-56	227
2164	Automated selected reaction monitoring software for accurate label-free protein quantification. 2012 , 11, 3766-73	25
2163	In silico design of targeted SRM-based experiments. 2012 , 13 Suppl 16, S8	9
2162	Statistical characterization of multiple-reaction monitoring mass spectrometry (MRM-MS) assays for quantitative proteomics. 2012 , 13 Suppl 16, S9	79
2161	Proteomic analysis identifies dysfunction in cellular transport, energy, and protein metabolism in different brain regions of atypical frontotemporal lobar degeneration. 2012 , 11, 2533-43	38
2160	Mass spectrometric tools for systematic analysis of protein phosphorylation. 2012 , 106, 3-32	11
2159	Proteomic analysis of the androgen receptor via MS-compatible purification of biotinylated protein on streptavidin resin. 2012 , 12, 43-53	5
2158	Mass spectrometry-based targeted quantitative proteomics: achieving sensitive and reproducible detection of proteins. 2012 , 12, 1093-110	126
2157	Using iRT, a normalized retention time for more targeted measurement of peptides. 2012 , 12, 1111-21	389
2156	Application of targeted proteomics to metabolically engineered <i>Escherichia coli</i> . 2012 , 12, 1289-99	20
2155	PASSEL: the PeptideAtlas SRMexperiment library. 2012 , 12, 1170-5	167
2154	Range of protein detection by selected/multiple reaction monitoring mass spectrometry in an unfractionated human cell culture lysate. 2012 , 12, 1185-93	35

2153	Sigpep: calculating unique peptide signature transition sets in a complete proteome background. 2012 , 12, 1142-6	8
2152	An assessment of current bioinformatic solutions for analyzing LC-MS data acquired by selected reaction monitoring technology. 2012 , 12, 1176-84	22
2151	Multiplexed quantification of estrogen receptor and HER2/Neu in tissue and cell lysates by peptide immunoaffinity enrichment mass spectrometry. 2012 , 12, 1253-60	41
2150	SRM targeted proteomics in search for biomarkers of HCV-induced progression of fibrosis to cirrhosis in HALT-C patients. 2012 , 12, 1244-52	25
2149	The development of selected reaction monitoring methods for targeted proteomics via empirical refinement. 2012 , 12, 1134-41	82
2148	Towards clinical applications of selected reaction monitoring for plasma protein biomarker studies. 2012 , 6, 42-59	13
2147	Targeted data extraction of the MS/MS spectra generated by data-independent acquisition: a new concept for consistent and accurate proteome analysis. 2012 , 11, O111.016717	1713
2146	Mass spectrometry-based proteomics and network biology. 2012 , 81, 379-405	326
2145	Identification of proteomic signatures associated with depression and psychotic depression in post-mortem brains from major depression patients. 2012 , 2, e87	132
2144	Selected reaction monitoring-based proteomics: workflows, potential, pitfalls and future directions. 2012 , 9, 555-66	997
2143	Replacing immunoassays with tryptic digestion-peptide immunoaffinity enrichment and LC-MS/MS. 2012 , 4, 281-90	75
2142	Automated workflow for large-scale selected reaction monitoring experiments. 2012 , 11, 1644-53	20
2141	Estimation of absolute protein quantities of unlabeled samples by selected reaction monitoring mass spectrometry. 2012 , 11, M111.013987	103
2140	A method to determine the kinetics of multiple proteins in human infants with respiratory distress syndrome. 2012 , 403, 2397-402	4
2139	Internal standards in the quantitative determination of protein biopharmaceuticals using liquid chromatography coupled to mass spectrometry. 2012 , 893-894, 1-14	100
2138	Quantification of proteome dynamics in <i>Corynebacterium glutamicum</i> by (15)N-labeling and selected reaction monitoring. 2012 , 75, 2660-9	22
2137	Evaluation of protein quantification using standard peptides containing single conservative amino acid replacements. 2012 , 47, 188-94	9
2136	Improved detection specificity for plasma proteins by targeting cysteine-containing peptides with photo-SRM. 2013 , 405, 2321-31	28

2135	Changes in atmospheric CO2 influence the allergenicity of <i>Aspergillus fumigatus</i> . 2013 , 19, 2381-8	15
2134	Proteomic analysis of nuclei dissected from fixed rat brain tissue using expression microdissection. 2013 , 85, 7139-45	9
2133	Measurement of acetylation turnover at distinct lysines in human histones identifies long-lived acetylation sites. 2013 , 4, 2203	76
2132	Automated selected reaction monitoring data analysis workflow for large-scale targeted proteomic studies. 2013 , 8, 1602-19	56
2131	Review of software tools for design and analysis of large scale MRM proteomic datasets. 2013 , 61, 287-98	66
2130	Analysis of protein expression in zebrafish during gonad differentiation by targeted proteomics. 2013 , 193, 210-20	27
2129	Proteome-wide detection and quantitative analysis of irreversible cysteine oxidation using long column UPLC-pSRM. 2013 , 12, 4302-15	19
2128	An acetylome peptide microarray reveals specificities and deacetylation substrates for all human sirtuin isoforms. 2013 , 4, 2327	145
2127	Proteomic and Mass Spectrometry Technologies for Biomarker Discovery. 2013 , 17-37	14
2126	Mass SpectrometryBased Approach for Protein Biomarker Verification. 2013 , 407-424	1
2125	Sirtuins. 2013 ,	1
2124	Crowdsourcing in proteomics: public resources lead to better experiments. 2013 , 44, 1129-37	24
2123	Quantitative Proteomics in Development of Disease Protein Biomarkers. 2013 , 259-278	2
2122	Trauma-associated human neutrophil alterations revealed by comparative proteomics profiling. 2013 , 7, 571-83	16
2121	Metabolic engineering of <i>Escherichia coli</i> for limonene and perillyl alcohol production. 2013 , 19, 33-41	281
2120	Long-gradient separations coupled with selected reaction monitoring for highly sensitive, large scale targeted protein quantification in a single analysis. 2013 , 85, 9196-203	37
2119	Unifying expression scale for peptide hydrophobicity in proteomic reversed phase high-pressure liquid chromatography experiments. 2013 , 85, 10878-86	8
2118	Antibody-free LC-MS/MS quantification of rhTRAIL in human and mouse serum. 2013 , 85, 10754-60	21

2117	S-nitrosoglutathione covalently modifies cysteine residues of human carbonyl reductase 1 and affects its activity. 2013 , 202, 136-45	9
2116	Quantifying protein interaction dynamics by SWATH mass spectrometry: application to the 14-3-3 system. 2013 , 10, 1246-53	249
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2114	Zinc finger nuclease knock-out of NADPH:cytochrome P450 oxidoreductase (POR) in human tumor cell lines demonstrates that hypoxia-activated prodrugs differ in POR dependence. 2013 , 288, 37138-53	20
2113	Alternative fusion protein strategies to express recalcitrant QconCAT proteins for quantitative proteomics of human drug metabolizing enzymes and transporters. 2013 , 12, 5934-42	47
2112	Quantitative proteomic analysis of microdissected breast cancer tissues: comparison of label-free and SILAC-based quantification with shotgun, directed, and targeted MS approaches. 2013 , 12, 4627-41	51
2111	Sirtuin 3 (SIRT3) protein regulates long-chain acyl-CoA dehydrogenase by deacetylating conserved lysines near the active site. 2013 , 288, 33837-33847	123
2110	Multi-peptide nLC-PC-IDMS-SRM-based assay for the quantification of biomarkers in the chicken ovarian cancer model. 2013 , 61, 323-30	12
2109	A proteomics approach to the identification of biomarkers for psoriasis utilising keratome biopsy. 2013 , 94, 176-85	23
2108	Engineering challenges for instrumenting and controlling integrated organ-on-chip systems. 2013 , 60, 682-90	130
2107	Identification of a seven glycopeptide signature for malignant pleural mesothelioma in human serum by selected reaction monitoring. 2013 , 10, 16	40
2106	The biology/disease-driven human proteome project (B/D-HPP): enabling protein research for the life sciences community. 2013 , 12, 23-7	87
2105	Global chromatin profiling reveals NSD2 mutations in pediatric acute lymphoblastic leukemia. 2013 , 45, 1386-91	192
2104	Capillary zone electrophoresis-multiple reaction monitoring from 100 pg of RAW 264.7 cell lysate digest. 2013 , 138, 3181-8	27
2103	Lysine 63-linked polyubiquitination is required for EGF receptor degradation. 2013 , 110, 15722-7	86
2102	Screening method using selected reaction monitoring for targeted proteomics studies of nasal lavage fluid. 2013 , 12, 234-47	15
2101	PROTEINCHALLENGE: crowd sourcing in proteomics analysis and software development. 2013 , 88, 41-6	16
2100	Method of the Year 2012. 2013 , 10, 1	98

2099	Application of quantitative proteomics technologies to the biomarker discovery pipeline for multiple sclerosis. 2013 , 7, 91-108	12
2098	A novel spectral library workflow to enhance protein identifications. 2013 , 81, 173-84	9
2097	Recent advances in mass spectrometry: data independent analysis and hyper reaction monitoring. 2013 , 10, 551-66	104
2096	PfHPRT: a new biomarker candidate of acute Plasmodium falciparum infection. 2013 , 12, 1211-22	16
2095	Quantitative Proteomics in Genomic Medicine. 2013 , 155-165	
2094	Quantitative measurements of N-linked glycoproteins in human plasma by SWATH-MS. 2013 , 13, 1247-56	171
2093	Protein analysis by shotgun/bottom-up proteomics. 2013 , 113, 2343-94	902
2092	Quantitative analysis of chaperone network throughput in budding yeast. 2013 , 13, 1276-91	26
2091	Comparative study of targeted and label-free mass spectrometry methods for protein quantification. 2013 , 12, 2005-11	7
2090	A guide for integration of proteomic data standards into laboratory workflows. 2013 , 13, 480-92	7
2089	Proteomics and the analysis of proteomic data: 2013 overview of current protein-profiling technologies. 2013 , Chapter 13, Unit 13.21	11
2088	Cand1 promotes assembly of new SCF complexes through dynamic exchange of F box proteins. 2013 , 153, 206-15	169
2087	CaMKII regulates diacylglycerol lipase-1 and striatal endocannabinoid signaling. 2013 , 16, 456-63	52
2086	Targeted proteomics. 2013 , 10, 19-22	148
2085	Targeted quantitation of proteins by mass spectrometry. 2013 , 52, 3797-806	247
2084	Absolute quantification of transcription factors during cellular differentiation using multiplexed targeted proteomics. 2013 , 10, 570-6	72
2083	Label-free quantitative proteomics trends for protein-protein interactions. 2013 , 81, 91-101	47
2082	Quantitation of Met tyrosine phosphorylation using MRM-MS. 2013 , 1002, 181-93	2

2081	Label-free differential analysis of murine postsynaptic densities. 2013 , 1002, 295-309	1
2080	High performance computational analysis of large-scale proteome data sets to assess incremental contribution to coverage of the human genome. 2013 , 12, 2858-68	26
2079	Improved precision of proteomic measurements in immunoprecipitation based purifications using relative quantitation. 2013 , 85, 4301-6	11
2078	Development of a label-free LC-MS/MS strategy to approach the identification of candidate protein biomarkers of disease recurrence in prostate cancer patients in a clinical trial of combined hormone and radiation therapy. 2013 , 7, 316-26	18
2077	Targeted quantification of low ng/mL level proteins in human serum without immunoaffinity depletion. 2013 , 12, 3353-61	62
2076	Identification of multiple novel protein biomarkers shed by human serous ovarian tumors into the blood of immunocompromised mice and verified in patient sera. 2013 , 8, e60129	15
2075	The Mtb proteome library: a resource of assays to quantify the complete proteome of Mycobacterium tuberculosis. 2013 , 13, 602-612	139
2074	Dynamic methylation of Numb by Set8 regulates its binding to p53 and apoptosis. 2013 , 50, 565-76	68
2073	Quantitative cross-linking/mass spectrometry using isotope-labelled cross-linkers. 2013 , 88, 120-8	109
2072	MRMPROBS: a data assessment and metabolite identification tool for large-scale multiple reaction monitoring based widely targeted metabolomics. 2013 , 85, 5191-9	67
2071	Mass spectrometry-based proteomics: basic principles and emerging technologies and directions. 2013 , 990, 1-35	21
2070	Bioanalytical LC-MS/MS of protein-based biopharmaceuticals. 2013 , 929, 161-79	177
2069	Multiplexed MS/MS for improved data-independent acquisition. 2013 , 10, 744-6	215
2068	Oncogene-induced cellular senescence elicits an anti-Warburg effect. 2013 , 13, 2585-96	33
2067	Computational approaches to selected reaction monitoring assay design. 2013 , 1007, 219-35	0
2066	Mass Spectrometry Data Analysis in Proteomics. 2013 ,	7
2065	In-depth proteome analysis of the rubber particle of Hevea brasiliensis (para rubber tree). 2013 , 82, 155-68	50
2064	A method for systematic mapping of protein lysine methylation identifies functions for HP1 in DNA damage response. 2013 , 50, 723-35	77

2063	Rapid assessment of RNAi-mediated protein depletion by selected reaction monitoring mass spectrometry. 2013 , 12, 3246-54	5
2062	Characterization of reaction conditions providing rapid and specific cysteine alkylation for peptide-based mass spectrometry. 2013 , 1834, 372-9	42
2061	Mass spectrometry-based sequencing and SRM-based quantitation of two novel vitellogenin isoforms in the leatherback sea turtle (<i>Dermochelys coriacea</i>). 2013 , 12, 4122-35	9
2060	Design, implementation and multisite evaluation of a system suitability protocol for the quantitative assessment of instrument performance in liquid chromatography-multiple reaction monitoring-MS (LC-MRM-MS). 2013 , 12, 2623-39	87
2059	Comparison of protein immunoprecipitation-multiple reaction monitoring with ELISA for assay of biomarker candidates in plasma. 2013 , 12, 5996-6003	52
2058	Secretome of transmissible <i>Pseudomonas aeruginosa</i> AES-1R grown in a cystic fibrosis lung-like environment. 2013 , 12, 5357-69	14
2057	Proteomic analysis of exosomes from mutant KRAS colon cancer cells identifies intercellular transfer of mutant KRAS. 2013 , 12, 343-55	355
2056	Development and validation of MRM methods to quantify protein isoforms of polyphenol oxidase in loquat fruits. 2013 , 12, 5709-22	16
2055	Quantification of human kallikrein-2 in clinical samples by selected reaction monitoring. 2013 , 12, 4612-6	9
2054	Candidate serum biomarkers for early intestinal cancer using ¹⁵ N metabolic labeling and quantitative proteomics in the <i>ApcMin/+</i> mouse. 2013 , 12, 4152-66	19
2053	Understanding the role of proteolytic digestion on discovery and targeted proteomic measurements using liquid chromatography tandem mass spectrometry and design of experiments. 2013 , 12, 5820-9	39
2052	Automatic generation of predictive dynamic models reveals nuclear phosphorylation as the key <i>Msn2</i> control mechanism. 2013 , 6, ra41	41
2051	Grading breast cancer tissues using molecular portraits. 2013 , 12, 3612-23	25
2050	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
2049	Absolute quantification of selected proteins in the human osteoarthritic secretome. 2013 , 14, 20658-81	38
2048	Kinetics of antigen expression and epitope presentation during virus infection. 2013 , 9, e1003129	108
2047	Development and characterization of a novel plug and play liquid chromatography-mass spectrometry (LC-MS) source that automates connections between the capillary trap, column, and emitter. 2013 , 12, 1701-8	6
2046	Serum proteomics reveals systemic dysregulation of innate immunity in type 1 diabetes. 2013 , 210, 191-203	63

2045	A label-free selected reaction monitoring workflow identifies a subset of pregnancy specific glycoproteins as potential predictive markers of early-onset pre-eclampsia. 2013 , 12, 3148-59	39
2044	Investigations on collectin liver 1. 2013 , 288, 23407-20	56
2043	Temporal analysis of the magnaporthe oryzae proteome during conidial germination and cyclic AMP (cAMP)-mediated appressorium formation. 2013 , 12, 2249-65	34
2042	Rearrangements within human spliceosomes captured after exon ligation. 2013 , 19, 400-12	34
2041	The histone methyltransferase MMSET/WHSC1 activates TWIST1 to promote an epithelial-mesenchymal transition and invasive properties of prostate cancer. 2013 , 32, 2882-90	103
2040	Connecting genomic alterations to cancer biology with proteomics: the NCI Clinical Proteomic Tumor Analysis Consortium. 2013 , 3, 1108-12	162
2039	Current status and advances in quantitative proteomic mass spectrometry. 2013 , 2013, 180605	115
2038	Rapid detection and quantification of apolipoprotein L1 genetic variants and total levels in plasma by ultra-performance liquid chromatography/tandem mass spectrometry. 2013 , 27, 2639-47	15
2037	Serum proteomics in amnesic mild cognitive impairment. 2013 , 13, 2526-33	8
2036	Mass Informatics: From Mass Spectrometry Peaks to Biological Pathways. 2013 , 53, 157-165	1
2035	Quantitative measurement of phosphoproteome response to osmotic stress in arabidopsis based on Library-Assisted eXtracted Ion Chromatogram (LAXIC). 2013 , 12, 2354-69	55
2034	Phosphorylation of serine 1137/1138 of mouse insulin receptor substrate (IRS) 2 regulates cAMP-dependent binding to 14-3-3 proteins and IRS2 protein degradation. 2013 , 288, 16403-16415	19
2033	Systematic proteomic analysis identifies BACE2 and BACE1 substrates in pancreatic cells. 2013 , 288, 10536-47	64
2032	Functioning of a metabolic flux sensor in Escherichia coli. 2013 , 110, 1130-5	142
2031	Determination of an angiotensin II-regulated proteome in primary human kidney cells by stable isotope labeling of amino acids in cell culture (SILAC). 2013 , 288, 24834-47	24
2030	Quantitative Clinical Chemistry Proteomics (qCCP) using mass spectrometry: general characteristics and application. 2013 , 51, 919-35	43
2029	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
2028	A multiple reaction monitoring (MRM) method to detect Bcr-Abl kinase activity in CML using a peptide biosensor. 2013 , 8, e56627	10

2027	Odin (ANKS1A) modulates EGF receptor recycling and stability. 2013 , 8, e64817	15
2026	Genomic and proteomic analysis of Schizaphis graminum reveals cyclophilin proteins are involved in the transmission of cereal yellow dwarf virus. 2013 , 8, e71620	32
2025	Osteoprotegerin in exosome-like vesicles from human cultured tubular cells and urine. 2013 , 8, e72387	40
2024	Proteomic and mass spectrometry technologies for biomarker discovery. 2013 , 17-37	2
2023	Structural, kinetic and proteomic characterization of acetyl phosphate-dependent bacterial protein acetylation. 2014 , 9, e94816	178
2022	Development of a native Escherichia coli induction system for ionic liquid tolerance. 2014 , 9, e101115	30
2021	Detection of Mycobacterium tuberculosis peptides in the exosomes of patients with active and latent M. tuberculosis infection using MRM-MS. 2014 , 9, e103811	95
2020	Advances in Proteomic Technologies and Its Contribution to the Field of Cancer. 2014 , 2014, 238045	19
2019	Data Pre-Processing for Label-Free Multiple Reaction Monitoring (MRM) Experiments. 2014 , 3, 383-402	2
2018	Achroma Software-High-Quality Policy in (a-)Typical Mass Spectrometric Data Handling and Applied Functional Proteomics. 2014 , 07,	3
2017	Quantification of human mAbs in mouse tissues using generic affinity enrichment procedures and LC-MS detection. 2014 , 6, 1795-811	24
2016	Combining bioinformatics and MS-based proteomics: clinical implications. 2014 , 11, 269-84	6
2015	The use of targeted proteomics to determine the stoichiometry of large macromolecular assemblies. 2014 , 122, 117-46	21
2014	Maximizing peptide identification events in proteomic workflows using data-dependent acquisition (DDA). 2014 , 13, 329-38	68
2013	Functional interaction between ribosomal protein L6 and RbgA during ribosome assembly. 2014 , 10, e1004694	20
2012	PeptideManager: a peptide selection tool for targeted proteomic studies involving mixed samples from different species. 2014 , 5, 305	15
2011	Quantitative proteomics at different depths in human articular cartilage reveals unique patterns of protein distribution. 2014 , 40, 34-45	39
2010	Evaluating melanoma drug response and therapeutic escape with quantitative proteomics. 2014 , 13, 1844-54	44

2009	Selected reaction monitoring to determine protein abundance in Arabidopsis using the Arabidopsis proteotypic predictor. 2014 , 164, 525-36	28
2008	The concentrations of EGFR, LRG1, ITIH4, and F5 in serum correlate with the number of colonic adenomas in ApcPirc/+ rats. 2014 , 7, 1160-9	11
2007	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. 2014 , 13, 2042-55	55
2006	Hyaluronan enhances wound repair and increases collagen III in aged dermal wounds. 2014 , 22, 521-6	34
2005	Conserved peptide fragmentation as a benchmarking tool for mass spectrometers and a discriminating feature for targeted proteomics. 2014 , 13, 2056-71	65
2004	Protter: interactive protein feature visualization and integration with experimental proteomic data. <i>Bioinformatics</i> , 2014 , 30, 884-6	7.2 666
2003	Site-specific human histone H3 methylation stability: fast K4me3 turnover. 2014 , 14, 2190-9	20
2002	Kinetic analysis of BCL11B multisite phosphorylation-dephosphorylation and coupled sumoylation in primary thymocytes by multiple reaction monitoring mass spectroscopy. 2014 , 13, 5860-8	13
2001	Comprehensive quantitative comparison of the membrane proteome, phosphoproteome, and sialome of human embryonic and neural stem cells. 2014 , 13, 311-28	52
2000	Humans with atherosclerosis have impaired ABCA1 cholesterol efflux and enhanced high-density lipoprotein oxidation by myeloperoxidase. 2014 , 114, 1733-42	140
1999	Site-specific mapping and quantification of protein S-sulphenylation in cells. 2014 , 5, 4776	173
1998	High density and ligand affinity confer ultrasensitive signal detection by a guanylyl cyclase chemoreceptor. 2014 , 206, 541-57	29
1997	Checkpoint blockade cancer immunotherapy targets tumour-specific mutant antigens. 2014 , 515, 577-81	1331
1996	Integrated solid-phase extraction-capillary liquid chromatography (speLC) interfaced to ESI-MS/MS for fast characterization and quantification of protein and proteomes. 2014 , 13, 6169-75	18
1995	CPTAC Assay Portal: a repository of targeted proteomic assays. 2014 , 11, 703-4	113
1994	Comprehensive assessment of proteins regulated by dexamethasone reveals novel effects in primary human peripheral blood mononuclear cells. 2014 , 13, 5989-6000	41
1993	Selected reaction monitoring as an effective method for reliable quantification of disease-associated proteins in maple syrup urine disease. 2014 , 2, 383-92	11
1992	Development of a method for absolute quantification of equine acute phase proteins using concatenated peptide standards and selected reaction monitoring. 2014 , 13, 5635-47	11

1991	AFFIRM—a multiplexed immunoaffinity platform that combines recombinant antibody fragments and LC-SRM analysis. 2014 , 13, 5837-47	5
1990	A liquid chromatography-tandem mass spectrometry-based targeted proteomics approach for the assessment of transferrin receptor levels in breast cancer. 2014 , 8, 773-82	12
1989	Quantification of peptides from immunoglobulin constant and variable regions by LC-MRM MS for assessment of multiple myeloma patients. 2014 , 8, 783-95	22
1988	Proteomic identification of potential prognostic biomarkers in resectable pancreatic ductal adenocarcinoma. 2014 , 14, 945-55	33
1987	iReport: a generalised Galaxy solution for integrated experimental reporting. 2014 , 3, 19	4
1986	Comparative analyses of proteins from Haemophilus influenzae biofilm and planktonic populations using metabolic labeling and mass spectrometry. 2014 , 14, 329	21
1985	Validation of semaphorin 7A and ala-his-dipeptidase as biomarkers associated with the conversion from clinically isolated syndrome to multiple sclerosis. 2014 , 11, 181	22
1984	Phosphoprotein secretome of tumor cells as a source of candidates for breast cancer biomarkers in plasma. 2014 , 13, 1034-49	35
1983	Proteogenomic analysis reveals unanticipated adaptations of colorectal tumor cells to deficiencies in DNA mismatch repair. 2014 , 74, 387-97	42
1982	A targeted proteomics approach for profiling murine cytochrome P450 expression. 2014 , 349, 221-8	24
1981	Static and turnover kinetic measurement of protein biomarkers involved in triglyceride metabolism including apoB48 and apoA5 by LC/MS/MS. 2014 , 55, 1179-87	17
1980	Nonenzymatic domains of Kalirin7 contribute to spine morphogenesis through interactions with phosphoinositides and Abl. 2014 , 25, 1458-71	17
1979	Differential proteomic analysis of synovial fluid from rheumatoid arthritis and osteoarthritis patients. 2014 , 11, 1	82
1978	Targeted peptide measurements in biology and medicine: best practices for mass spectrometry-based assay development using a fit-for-purpose approach. 2014 , 13, 907-17	392
1977	Antibody-independent targeted quantification of TMPRSS2-ERG fusion protein products in prostate cancer. 2014 , 8, 1169-80	20
1976	Targeted proteomics for validation of biomarkers in early psychosis. 2014 , 76, e7-9	5
1975	Plasma proteome profiling of atherosclerotic disease manifestations reveals elevated levels of the cytoskeletal protein vinculin. 2014 , 101, 141-53	29
1974	Antigen 85 variation across lineages of Mycobacterium tuberculosis-implications for vaccine and biomarker success. 2014 , 97, 141-50	16

1973	Comparison of targeted peptide quantification assays for reductive dehalogenases by selective reaction monitoring (SRM) and precursor reaction monitoring (PRM). 2014 , 406, 283-91	38
1972	Accounting for population variation in targeted proteomics. 2014 , 13, 321-3	3
1971	Discovery of human sORF-encoded polypeptides (SEPs) in cell lines and tissue. 2014 , 13, 1757-65	111
1970	Development of proteomic technology of shotgun and label free combined with multiple reaction monitoring to simultaneously detect southern rice black-streaked dwarf virus and rice ragged stunt virus. 2014 , 25, 322-30	8
1969	Implementation of statistical process control for proteomic experiments via LC MS/MS. 2014 , 25, 581-7	33
1968	A bacterial tyrosine phosphatase inhibits plant pattern recognition receptor activation. 2014 , 343, 1509-12	107
1967	Adaptation of <i>Bacillus subtilis</i> carbon core metabolism to simultaneous nutrient limitation and osmotic challenge: a multi-omics perspective. 2014 , 16, 1898-917	61
1966	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. 2014 , 32, 223-6	2053
1965	A highly sensitive targeted mass spectrometric assay for quantification of AGR2 protein in human urine and serum. 2014 , 13, 875-82	51
1964	Shotgun Proteomics. 2014 ,	5
1963	PeptidePicker: a scientific workflow with web interface for selecting appropriate peptides for targeted proteomics experiments. 2014 , 106, 151-61	93
1962	Simultaneous quantification of the abundance of several cytochrome P450 and uridine 5'-diphospho-glucuronosyltransferase enzymes in human liver microsomes using multiplexed targeted proteomics. 2014 , 42, 500-10	121
1961	GlycoDelete engineering of mammalian cells simplifies N-glycosylation of recombinant proteins. 2014 , 32, 485-9	105
1960	A framework for installable external tools in Skyline. <i>Bioinformatics</i> , 2014 , 30, 2521-3	7.2 30
1959	Demonstrating the feasibility of large-scale development of standardized assays to quantify human proteins. 2014 , 11, 149-55	145
1958	Human protein aging: modification and crosslinking through dehydroalanine and dehydrobutyrine intermediates. 2014 , 13, 226-34	56
1957	Depletion of abundant plasma proteins by poly(N-isopropylacrylamide-acrylic acid) hydrogel particles. 2014 , 86, 1543-50	22
1956	Diabetic nephropathy induces changes in the proteome of human urinary exosomes as revealed by label-free comparative analysis. 2014 , 96, 92-102	101

1955	Tyrosine/cysteine cluster sensitizing human α -crystallin to ultraviolet radiation-induced photoaggregation in vitro. 2014 , 53, 979-90	22
1954	MS-GF+ makes progress towards a universal database search tool for proteomics. 2014 , 5, 5277	633
1953	Exploring intercellular signaling by proteomic approaches. 2014 , 14, 498-512	13
1952	Ovarian endometriosis signatures established through discovery and directed mass spectrometry analysis. 2014 , 13, 4983-94	14
1951	Differential cysteine labeling and global label-free proteomics reveals an altered metabolic state in skeletal muscle aging. 2014 , 13, 5008-21	73
1950	USP8 regulates mitophagy by removing K6-linked ubiquitin conjugates from parkin. 2014 , 33, 2473-91	222
1949	Discovery of novel disease-specific and membrane-associated candidate markers in a mouse model of multiple sclerosis. 2014 , 13, 679-700	7
1948	Using PeptideAtlas, SRMAtlas, and PASSEL: Comprehensive Resources for Discovery and Targeted Proteomics. 2014 , 46, 13.25.1-28	45
1947	Quantitative proteomic analysis reveals effects of epidermal growth factor receptor (EGFR) on invasion-promoting proteins secreted by glioblastoma cells. 2014 , 13, 2618-31	25
1946	Evaluation of data-dependent and -independent mass spectrometric workflows for sensitive quantification of proteins and phosphorylation sites. 2014 , 13, 5973-88	38
1945	Cell-specific labeling enzymes for analysis of cell-cell communication in continuous co-culture. 2014 , 13, 1866-76	26
1944	Establishing ion ratio thresholds based on absolute peak area for absolute protein quantification using protein cleavage isotope dilution mass spectrometry. 2014 , 139, 5439-50	7
1943	Application of adenosine triphosphate affinity probe and scheduled multiple-reaction monitoring analysis for profiling global kinome in human cells in response to arsenite treatment. 2014 , 86, 10700-7	10
1942	Protein kinase D2 is a digital amplifier of T cell receptor-stimulated diacylglycerol signaling in naive CD8+ T cells. 2014 , 7, 1999	25
1941	Expediting SRM assay development for large-scale targeted proteomics experiments. 2014 , 13, 4479-87	25
1940	Screening of missing proteins in the human liver proteome by improved MRM-approach-based targeted proteomics. 2014 , 13, 1969-78	22
1939	Assessment of peptide chemical modifications on the development of an accurate and precise multiplex selected reaction monitoring assay for apolipoprotein e isoforms. 2014 , 13, 1077-87	41
1938	Proteomics of Fuchs' endothelial corneal dystrophy support that the extracellular matrix of Descemet's membrane is disordered. 2014 , 13, 4659-67	31

1937	Development of a multipoint quantitation method to simultaneously measure enzymatic and structural components of the <i>Clostridium thermocellum</i> cellulosome protein complex. 2014 , 13, 692-701	11
1936	Targeted discovery and validation of plasma biomarkers of Parkinson's disease. 2014 , 13, 4535-45	25
1935	Targeted proteomics analysis of protein degradation in plant signaling on an LTQ-Orbitrap mass spectrometer. 2014 , 13, 4246-58	34
1934	Global analysis of protein structural changes in complex proteomes. 2014 , 32, 1036-44	187
1933	A targeted quantitative proteomics strategy for global kinome profiling of cancer cells and tissues. 2014 , 13, 1065-75	45
1932	Identification of novel biomarkers of brain damage in patients with hemorrhagic stroke by integrating bioinformatics and mass spectrometry-based proteomics. 2014 , 13, 969-81	25
1931	Exploring skyline for both MS(E) -based label-free proteomics and HRMS quantitation of small molecules. 2014 , 14, 169-80	11
1930	Modulation of the chromatin phosphoproteome by the Haspin protein kinase. 2014 , 13, 1724-40	25
1929	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
1928	Proteogenomic characterization of human colon and rectal cancer. 2014 , 513, 382-7	900
1927	Enzymatic protein digestion using a dissolvable polyacrylamide gel and its application to mass spectrometry-based proteomics. 2014 , 967, 36-40	9
1926	Differential localization of G protein β subunits. 2014 , 53, 2329-43	14
1925	Unconditioned commercial embryo culture media contain a large variety of non-declared proteins: a comprehensive proteomics analysis. 2014 , 29, 2421-30	55
1924	Integrating meta-analysis of microarray data and targeted proteomics for biomarker identification: application in breast cancer. 2014 , 13, 2897-909	16
1923	Quantitative analysis of UV-A shock and short term stress using iTRAQ, pseudo selective reaction monitoring (pSRM) and GC-MS based metabolite analysis of the cyanobacterium <i>Nostoc punctiforme</i> ATCC 29133. 2014 , 109, 332-55	11
1922	Quantitative proteomics in cardiovascular research: global and targeted strategies. 2014 , 8, 488-505	17
1921	A simple protocol to routinely assess the uniformity of proteomics analyses. 2014 , 13, 2688-95	22
1920	Determination of selected reaction monitoring peptide transitions via multiplexed product-ion scan modes. 2014 , 28, 773-80	2

1919	Numerical compression schemes for proteomics mass spectrometry data. 2014 , 13, 1537-42	37
1918	Multilayered genetic and omics dissection of mitochondrial activity in a mouse reference population. 2014 , 158, 1415-1430	161
1917	Panorama: a targeted proteomics knowledge base. 2014 , 13, 4205-10	149
1916	Proteogenomic convergence for understanding cancer pathways and networks. 2014 , 11, 22	28
1915	Identification of longitudinally dynamic biomarkers in Alzheimer's disease cerebrospinal fluid by targeted proteomics. 2014 , 9, 22	90
1914	Integrative proteomic analysis of the NMDA NR1 knockdown mouse model reveals effects on central and peripheral pathways associated with schizophrenia and autism spectrum disorders. 2014 , 5, 38	26
1913	Reduced catabolic protein expression in <i>Clostridium butyricum</i> DSM 10702 correlate with reduced 1,3-propanediol synthesis at high glycerol loading. 2014 , 4, 63	19
1912	Systematic evaluation of quantotypic peptides for targeted analysis of the human kinome. 2014 , 11, 1041-4	47
1911	Structural basis for phosphorylation and lysine acetylation cross-talk in a kinase motif associated with myocardial ischemia and cardioprotection. 2014 , 289, 25890-906	38
1910	Metabolic-stress-induced rearrangement of the 14-3-3 interactome promotes autophagy via a ULK1- and AMPK-regulated 14-3-3 interaction with phosphorylated Atg9. 2014 , 34, 4379-88	69
1909	A sentinel protein assay for simultaneously quantifying cellular processes. 2014 , 11, 1045-8	52
1908	Identification and Quantitation of Coding Variants and Isoforms of Pulmonary Surfactant Protein A. 2014 , 13, 3722-32	11
1907	Targeted proteomics of myofilament phosphorylation and other protein posttranslational modifications. 2014 , 8, 543-53	13
1906	OpenSWATH enables automated, targeted analysis of data-independent acquisition MS data. 2014 , 32, 219-23	508
1905	Plasma exosomal β synuclein is likely CNS-derived and increased in Parkinson's disease. 2014 , 128, 639-650	348
1904	Transcriptomics assisted proteomic analysis of <i>Nicotiana occidentalis</i> infected by <i>Candidatus Phytoplasma mali</i> strain AT. 2014 , 14, 1882-9	34
1903	Mass spectrometry-based workflow for accurate quantification of <i>Escherichia coli</i> enzymes: how proteomics can play a key role in metabolic engineering. 2014 , 13, 954-68	13
1902	Proteomic analysis of the epidermal growth factor receptor (EGFR) interactome and post-translational modifications associated with receptor endocytosis in response to EGF and stress. 2014 , 13, 1644-58	71

1901	The role of quantitative mass spectrometry in the discovery of pancreatic cancer biomarkers for translational science. 2014 , 12, 87	30
1900	Proteomic analysis of human osteoarthritis synovial fluid. 2014 , 11, 6	85
1899	Characterization of grain-specific peptide markers for the detection of gluten by mass spectrometry. 2014 , 62, 5835-44	61
1898	Verification of a Parkinson's disease protein signature in T-lymphocytes by multiple reaction monitoring. 2014 , 13, 3554-61	15
1897	Differential protein profile in sexed bovine semen: shotgun proteomics investigation. 2014 , 10, 1264-71	40
1896	Quantification of human growth hormone in serum with a labeled protein as an internal standard: essential considerations. 2014 , 86, 6525-32	27
1895	Confetti: a multiprotease map of the HeLa proteome for comprehensive proteomics. 2014 , 13, 1573-84	67
1894	Global analysis of cellular proteolysis by selective enzymatic labeling of protein N-termini. 2014 , 544, 327-58	32
1893	Functional characterization of the small regulatory subunit PetP from the cytochrome b6f complex in <i>Thermosynechococcus elongatus</i> . 2014 , 26, 3435-48	16
1892	A temporal examination of the planktonic and biofilm proteome of whole cell <i>Pseudomonas aeruginosa</i> PAO1 using quantitative mass spectrometry. 2014 , 13, 1095-105	50
1891	Quantitative multiple reaction monitoring analysis of synaptic proteins from human brain. 2014 , 227, 189-210	7
1890	Proteomic analysis of mitochondria from senescent <i>Podospora anserina</i> casts new light on ROS dependent aging mechanisms. 2014 , 56, 13-25	5
1889	Regulation of PPAR-alpha pathway by Dicer revealed through proteomic analysis. 2014 , 108, 306-15	15
1888	Mass++: A Visualization and Analysis Tool for Mass Spectrometry. 2014 , 13, 3846-3853	37
1887	p63 isoforms regulate metabolism of cancer stem cells. 2014 , 13, 2120-36	25
1886	Simplified and efficient quantification of low-abundance proteins at very high multiplex via targeted mass spectrometry. 2014 , 13, 1137-49	55
1885	Mass spectrometry-driven phosphoproteomics: patterning the systems biology mosaic. 2014 , 3, 83-112	56
1884	Probing phosphorylation-dependent protein interactions within functional domains of histone deacetylase 5 (HDAC5). 2014 , 14, 2156-66	12

1883	Drift time-specific collision energies enable deep-coverage data-independent acquisition proteomics. 2014 , 11, 167-70	284
1882	High-affinity recombinant antibody fragments (Fabs) can be applied in peptide enrichment immuno-MRM assays. 2014 , 13, 2187-96	30
1881	Adenovirus composition, proteolysis, and disassembly studied by in-depth qualitative and quantitative proteomics. 2014 , 289, 11421-11430	67
1880	Circulating proteolytic signatures of chemotherapy-induced cell death in humans discovered by N-terminal labeling. 2014 , 111, 7594-9	35
1879	Targeted quantitative analysis of synaptic proteins in Alzheimer's disease brain. 2014 , 75, 66-75	20
1878	An investigation of heat shock protein 27 and P-glycoprotein mediated multi-drug resistance in breast cancer using liquid chromatography-tandem mass spectrometry-based targeted proteomics. 2014 , 108, 188-97	25
1877	Data processing methods and quality control strategies for label-free LC-MS protein quantification. 2014 , 1844, 29-41	45
1876	Open source libraries and frameworks for mass spectrometry based proteomics: a developer's perspective. 2014 , 1844, 63-76	59
1875	New Insights from Proteomic Analysis of Wnt Signaling. 2014 , 125-135	
1874	A repository of assays to quantify 10,000 human proteins by SWATH-MS. 2014 , 1, 140031	266
1873	Phosphorylation of Parkin at Serine65 is essential for activation: elaboration of a Miro1 substrate-based assay of Parkin E3 ligase activity. 2014 , 4, 130213	92
1872	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
1871	Ariadne's Thread: A Robust Software Solution Leading to Automated Absolute and Relative Quantification of SRM Data. 2015 , 14, 3779-92	2
1870	Assessment of current mass spectrometric workflows for the quantification of low abundant proteins and phosphorylation sites. 2015 , 5, 297-304	4
1869	A standardized kit for automated quantitative assessment of candidate protein biomarkers in human plasma. 2015 , 7, 2991-3004	24
1868	An assessment of human gastric fluid composition as a function of PPI usage. 2015 , 3, e12269	20
1867	Representation of selected-reaction monitoring data in the mzQuantML data standard. 2015 , 15, 2592-6	6
1866	Autophagic degradation of aquaporin-2 is an early event in hypokalemia-induced nephrogenic diabetes insipidus. 2015 , 5, 18311	36

1865	Chronic acidosis in the tumour microenvironment selects for overexpression of LAMP2 in the plasma membrane. 2015 , 6, 8752	108
1864	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
1863	Isotope Dilution Analysis of Myelin Basic Protein Degradation After Brain Injury. 2015 , 221-242	
1862	Prediction of colorectal cancer diagnosis based on circulating plasma proteins. 2015 , 7, 1166-78	68
1861	Evaluation of Proteomic Data: From Profiling to Network Analysis by Way of Biomarker Discovery. 2015 , 163-182	
1860	Binding to serine 65-phosphorylated ubiquitin primes Parkin for optimal PINK1-dependent phosphorylation and activation. 2015 , 16, 939-54	135
1859	Selected Reaction Monitoring Mass Spectrometry for Absolute Protein Quantification. 2015 , e52959	6
1858	Histone H2AX Y142 phosphorylation is a low abundance modification. 2015 , 391, 139-145	7
1857	Influence of surface modification and static pressure on microdialysis protein extraction efficiency. 2015 , 17, 96	4
1856	A new dimethyl labeling-based SID-MRM-MS method and its application to three proteases involved in insulin maturation. 2015 , 1, 71-80	4
1855	Secretome profiling of <i>Cryptococcus neoformans</i> reveals regulation of a subset of virulence-associated proteins and potential biomarkers by protein kinase A. 2015 , 15, 206	33
1854	Middle-down electron capture dissociation and electron transfer dissociation for histone analysis. 2015 , 6,	3
1853	MRMPlus: an open source quality control and assessment tool for SRM/MRM assay development. 2015 , 16, 411	9
1852	Comprehensive identification of phosphorylation sites on the Numb endocytic adaptor protein. 2015 , 15, 434-46	2
1851	Dysregulated miRNA biogenesis downstream of cellular stress and ALS-causing mutations: a new mechanism for ALS. 2015 , 34, 2633-51	135
1850	Current controlled vocabularies are insufficient to uniquely map molecular entities to mass spectrometry signal. 2015 , 16 Suppl 7, S2	6
1849	Ceruloplasmin functional changes in Parkinson's disease-cerebrospinal fluid. 2015 , 10, 59	26
1848	Plasma preparation to measure FDA-approved protein markers by selected reaction monitoring. 2015 , 4, 32	7

1847	The use of ubiquitin lysine mutants to characterize E2-E3 linkage specificity: Mass spectrometry offers a cautionary "tail". 2015 , 15, 2910-5	10
1846	Protein acetylation dynamics in response to carbon overflow in <i>Escherichia coli</i> . 2015 , 98, 847-63	103
1845	Surfaceome of classical Hodgkin and non-Hodgkin lymphoma. 2015 , 9, 661-70	15
1844	Enhancing bottom-up and top-down proteomic measurements with ion mobility separations. 2015 , 15, 2766-76	45
1843	A laser ablation ICP-MS based method for multiplexed immunoblot analysis: applications to manganese-dependent protein dynamics of photosystem II in barley (<i>Hordeum vulgare</i> L.). 2015 , 83, 555-65	13
1842	Identification of Site-Specific Stroke Biomarker Candidates by Laser Capture Microdissection and Labeled Reference Peptide. 2015 , 16, 13427-41	15
1841	Parallel Reaction Monitoring: A Targeted Experiment Performed Using High Resolution and High Mass Accuracy Mass Spectrometry. 2015 , 16, 28566-81	157
1840	The effect of imipenem and diffusible signaling factors on the secretion of outer membrane vesicles and associated Ax21 proteins in <i>Stenotrophomonas maltophilia</i> . 2015 , 6, 298	54
1839	Developing Potential Candidates of Preclinical Preeclampsia. 2015 , 16, 27208-27	2
1838	Complete Removal of Extracellular IgG Antibodies in a Randomized Dose-Escalation Phase I Study with the Bacterial Enzyme IdeS--A Novel Therapeutic Opportunity. 2015 , 10, e0132011	52
1837	Trade-Off between Growth and Carbohydrate Accumulation in Nutrient-Limited <i>Arthrospira</i> sp. PCC 8005 Studied by Integrating Transcriptomic and Proteomic Approaches. 2015 , 10, e0132461	35
1836	Elucidation of Cross-Talk and Specificity of Early Response Mechanisms to Salt and PEG-Simulated Drought Stresses in <i>Brassica napus</i> Using Comparative Proteomic Analysis. 2015 , 10, e0138974	35
1835	Spaceflight Effects on Cytochrome P450 Content in Mouse Liver. 2015 , 10, e0142374	22
1834	Potential Peripartum Markers of Infectious-Inflammatory Complications in Spontaneous Preterm Birth. 2015 , 2015, 343501	7
1833	Targeted Proteomics in Translational and Clinical Studies. 2015 ,	
1832	Proteomic Analysis of Lipid Raft-Like Detergent-Resistant Membranes of Lens Fiber Cells. 2015 , 56, 8349-60	20
1831	Quantitative mass spectrometry measurements reveal stoichiometry of principal postsynaptic density proteins. 2015 , 14, 2528-38	47
1830	Signal Transduction Reaction Monitoring Deciphers Site-Specific PI3K-mTOR/MAPK Pathway Dynamics in Oncogene-Induced Senescence. 2015 , 14, 2906-14	27

1829	Multidimensional fractionation is a requirement for quantitation of Golgi-resident glycosylation enzymes from cultured human cells. 2015 , 14, 747-55	2
1828	Inflammatory remodeling of the HDL proteome impairs cholesterol efflux capacity. 2015 , 56, 1519-30	115
1827	From raw data to biological discoveries: a computational analysis pipeline for mass spectrometry-based proteomics. 2015 , 26, 1820-6	11
1826	Hippocampal Proteomic and Metabonomic Abnormalities in Neurotransmission, Oxidative Stress, and Apoptotic Pathways in a Chronic Phencyclidine Rat Model. 2015 , 14, 3174-87	13
1825	Simultaneous Identification and Susceptibility Determination to Multiple Antibiotics of <i>Staphylococcus aureus</i> by Bacteriophage Amplification Detection Combined with Mass Spectrometry. 2015 , 87, 6769-77	27
1824	Proteotranscriptomic Profiling of 231-BR Breast Cancer Cells: Identification of Potential Biomarkers and Therapeutic Targets for Brain Metastasis. 2015 , 14, 2316-30	50
1823	Studies of binding interactions between Dufulin and southern rice black-streaked dwarf virus P9-1. 2015 , 23, 3629-37	17
1822	Kidney tissue proteomics reveals regucalcin downregulation in response to diabetic nephropathy with reflection in urinary exosomes. 2015 , 166, 474-484.e4	43
1821	Scoring Large-Scale Affinity Purification Mass Spectrometry Datasets with MiST. 2015 , 49, 8.19.1-8.19.16	38
1820	Processing strategies and software solutions for data-independent acquisition in mass spectrometry. 2015 , 15, 964-80	105
1819	LC-MS/MS-based serum proteomics for identification of candidate biomarkers for hepatocellular carcinoma. 2015 , 15, 2369-81	52
1818	Mammary Stem Cells. Preface. 2015 , 1293, v-vi	6
1817	Detection of FGF15 in plasma by stable isotope standards and capture by anti-peptide antibodies and targeted mass spectrometry. 2015 , 21, 898-904	47
1816	Label free targeted detection and quantification of celiac disease immunogenic epitopes by mass spectrometry. 2015 , 1391, 60-71	41
1815	Functional Proteomic Analysis of Repressive Histone Methyltransferase Complexes Reveals ZNF518B as a G9A Regulator. 2015 , 14, 1435-46	27
1814	Multiplexed peptide analysis using data-independent acquisition and Skyline. 2015 , 10, 887-903	132
1813	Proteomic enrichment analysis of psychotic and affective disorders reveals common signatures in presynaptic glutamatergic signaling and energy metabolism. 2014 , 18,	41
1812	Targeted phosphoproteomics of insulin signaling using data-independent acquisition mass spectrometry. 2015 , 8, rs6	43

1811	Purification of LC/GC-MS based biomolecular expression profiles using a topic model. 2015,	0
1810	Reconstitution of Formylglycine-generating Enzyme with Copper(II) for Aldehyde Tag Conversion. 2015, 290, 15730-15745	48
1809	Analysis of Major Histocompatibility Complex (MHC) Immunopeptidomes Using Mass Spectrometry. 2015, 14, 3105-17	143
1808	Cell cycle-dependent changes in H3K56ac in human cells. 2015, 14, 3851-63	12
1807	Multi-allergen Quantitation and the Impact of Thermal Treatment in Industry-Processed Baked Goods by ELISA and Liquid Chromatography-Tandem Mass Spectrometry. 2015, 63, 10669-80	84
1806	Automated, Online Sample Preparation for LC-MS Analyses: Affinity Capture, Digestion, and Clean-Up. 2015, 335-356	1
1805	SWATH-MS in proteomics: current status. 2015, 8, 192	3
1804	Ten years of QconCATs: Application of multiplexed quantification to small medically relevant proteomes. 2015, 391, 93-104	13
1803	Proteomic investigation of embryonic rat heart-derived H9c2 cell line sheds new light on the molecular phenotype of the popular cell model. 2015, 339, 174-86	10
1802	Integrative analysis of LC-MS based glycomic and proteomic data. 2015, 2015, 8185-8	1
1801	In-depth evaluation of software tools for data-independent acquisition based label-free quantification. 2015, 15, 3140-51	40
1800	DIGESTIF: a universal quality standard for the control of bottom-up proteomics experiments. 2015, 14, 787-803	20
1799	SWATH enables precise label-free quantification on proteome scale. 2015, 15, 1215-23	103
1798	An enhanced in vivo stable isotope labeling by amino acids in cell culture (SILAC) model for quantification of drug metabolism enzymes. 2015, 14, 750-60	6
1797	Principal component analysis of proteomics (PCAP) as a tool to direct metabolic engineering. 2015, 28, 123-133	118
1796	Nano-scale liquid chromatography coupled to tandem mass spectrometry using the multiple reaction monitoring mode based quantitative platform for analyzing multiple enzymes associated with central metabolic pathways of <i>Saccharomyces cerevisiae</i> using ultra fast mass spectrometry. 2015, 119, 117-20	12
1795	Studying macromolecular complex stoichiometries by peptide-based mass spectrometry. 2015, 15, 862-79	15
1794	Important options available--from start to finish--for translating proteomics results to clinical chemistry. 2015, 9, 235-52	8

1793	A longitudinal proteomic assessment of peptide degradation and loss under acidic storage conditions. 2015 , 473, 11-3	1
1792	Toxicoproteomic analysis of pulmonary carbon nanotube exposure using LC-MS/MS. 2015 , 329, 80-7	12
1791	An integrated quantitative and targeted proteomics reveals fitness mechanisms of <i>Aeromonas hydrophila</i> under oxytetracycline stress. 2015 , 14, 1515-25	29
1790	Sensitive targeted quantification of ERK phosphorylation dynamics and stoichiometry in human cells without affinity enrichment. 2015 , 87, 1103-10	28
1789	Carboxyl-ester lipase maturity-onset diabetes of the young disease protein biomarkers in secretin-stimulated duodenal juice. 2015 , 14, 521-30	3
1788	Profiling global kinome signatures of the radioresistant MCF-7/C6 breast cancer cells using MRM-based targeted proteomics. 2015 , 14, 193-201	27
1787	Oxidation of p53 through DNA charge transport involves a network of disulfides within the DNA-binding domain. 2015 , 54, 932-41	6
1786	Data-independent MS/MS quantification of neuropeptides for determination of putative feeding-related neurohormones in microdialysate. 2015 , 6, 174-80	10
1785	Quantitative proteomic analysis of histone modifications. 2015 , 115, 2376-418	241
1784	Qualis-SIS: automated standard curve generation and quality assessment for multiplexed targeted quantitative proteomic experiments with labeled standards. 2015 , 14, 1137-46	34
1783	Development and application of a quantitative multiplexed small GTPase activity assay using targeted proteomics. 2015 , 14, 967-76	11
1782	Molecular investigation of the radiation resistance of edible cyanobacterium <i>Arthrospira</i> sp. PCC 8005. 2015 , 4, 187-207	30
1781	A mammalian transcription factor-specific peptide repository for targeted proteomics. 2015 , 15, 752-6	4
1780	Trans-Proteomic Pipeline, a standardized data processing pipeline for large-scale reproducible proteomics informatics. 2015 , 9, 745-54	222
1779	Anti-peptide monoclonal antibodies generated for immuno-multiple reaction monitoring-mass spectrometry assays have a high probability of supporting Western blot and ELISA. 2015 , 14, 382-98	29
1778	Verification of the biomarker candidates for non-small-cell lung cancer using a targeted proteomics approach. 2015 , 14, 1412-9	52
1777	Structural basis for assembly and function of the Nup82 complex in the nuclear pore scaffold. 2015 , 208, 283-97	52
1776	Using data-independent, high-resolution mass spectrometry in protein biomarker research: perspectives and clinical applications. 2015 , 9, 307-21	130

1775	Protein phosphatase 2A (PP2A) regulatory subunit B' interacts with cytoplasmic ACONITASE 3 and modulates the abundance of AOX1A and AOX1D in Arabidopsis thaliana. 2015 , 205, 1250-1263	42
1774	Targeted proteomic analyses of nasal lavage fluid in persulfate-challenged hairdressers with bleaching powder-associated rhinitis. 2015 , 14, 860-73	6
1773	Advances in high-resolution accurate mass spectrometry application to targeted proteomics. 2015 , 15, 880-90	78
1772	Quantitative proteomics of bronchoalveolar lavage fluid in idiopathic pulmonary fibrosis. 2015 , 14, 1238-49	59
1771	DIA-Umpire: comprehensive computational framework for data-independent acquisition proteomics. 2015 , 12, 258-64, 7 p following 264	371
1770	Characterization of a human pluripotent stem cell-derived model of neuronal development using multiplexed targeted proteomics. 2015 , 9, 684-94	14
1769	Building high-quality assay libraries for targeted analysis of SWATH MS data. 2015 , 10, 426-41	229
1768	KLK1 and ZG16B proteins and arginine-proline metabolism identified as novel targets to monitor atherosclerosis, acute coronary syndrome and recovery. 2015 , 11, 1056-1067	31
1767	Quantitative proteome analysis of temporally resolved phagosomes following uptake via key phagocytic receptors. 2015 , 14, 1334-49	36
1766	Revisiting the arthritogenic peptide theory: quantitative not qualitative changes in the peptide repertoire of HLA-B27 allotypes. 2015 , 67, 702-13	88
1765	Reproducible and consistent quantification of the Saccharomyces cerevisiae proteome by SWATH-mass spectrometry. 2015 , 14, 739-49	136
1764	Importance of ALDH1A enzymes in determining human testicular retinoic acid concentrations. 2015 , 56, 342-57	41
1763	A Cluster of Proteins Implicated in Kidney Disease Is Increased in High-Density Lipoprotein Isolated from Hemodialysis Subjects. 2015 , 14, 2792-806	31
1762	Absolute Proteome Composition and Dynamics during Dormancy and Resuscitation of Mycobacterium tuberculosis. 2015 , 18, 96-108	155
1761	An integrated targeted metabolomic platform for high-throughput metabolite profiling and automated data processing. 2015 , 11, 1575-1586	58
1760	Quantitative measurement of immunoglobulins and free light chains using mass spectrometry. 2015 , 87, 8268-74	19
1759	New CETP inhibitor K-312 reduces PCSK9 expression: a potential effect on LDL cholesterol metabolism. 2015 , 309, E177-90	35
1758	Biomarker Discovery and Verification of Esophageal Squamous Cell Carcinoma Using Integration of SWATH/MRM. 2015 , 14, 3793-803	35

1757	An extensive library of surrogate peptides for all human proteins. 2015 , 129, 93-97	9
1756	Peptide Immunoaffinity Enrichment and Targeted Mass Spectrometry Enables Multiplex, Quantitative Pharmacodynamic Studies of Phospho-Signaling. 2015 , 14, 2261-73	49
1755	Evaluating kinase ATP uptake and tyrosine phosphorylation using multiplexed quantification of chemically labeled and post-translationally modified peptides. 2015 , 81, 41-9	9
1754	The rice immune receptor XA21 recognizes a tyrosine-sulfated protein from a Gram-negative bacterium. 2015 , 1, e1500245	151
1753	Quantification of SAHA-Dependent Changes in Histone Modifications Using Data-Independent Acquisition Mass Spectrometry. 2015 , 14, 3252-62	36
1752	Cell Surface Proteomics Provides Insight into Stage-Specific Remodeling of the Host-Parasite Interface in <i>Trypanosoma brucei</i> . 2015 , 14, 1977-88	35
1751	Identification and Characterization of a Golgi-Localized UDP-Xylose Transporter Family from <i>Arabidopsis</i> . 2015 , 27, 1218-27	46
1750	Orthogonal Injection Ion Funnel Interface Providing Enhanced Performance for Selected Reaction Monitoring-Triple Quadrupole Mass Spectrometry. 2015 , 87, 7326-31	10
1749	Quantification of cytokines secreted by primary human cells using multiple reaction monitoring: evaluation of analytical parameters. 2015 , 407, 6525-36	14
1748	Characterization of histone post-translational modifications during virus infection using mass spectrometry-based proteomics. 2015 , 90, 8-20	17
1747	Endogenous Parkin Preserves Dopaminergic Substantia Nigral Neurons following Mitochondrial DNA Mutagenic Stress. 2015 , 87, 371-81	216
1746	Data-independent-acquisition mass spectrometry for identification of targeted-peptide site-specific modifications. 2015 , 407, 6627-35	15
1745	High resolution parallel reaction monitoring with electron transfer dissociation for middle-down proteomics. 2015 , 87, 8360-6	26
1744	Extending the limits of quantitative proteome profiling with data-independent acquisition and application to acetaminophen-treated three-dimensional liver microtissues. 2015 , 14, 1400-10	471
1743	MS1 Peptide Ion Intensity Chromatograms in MS2 (SWATH) Data Independent Acquisitions. Improving Post Acquisition Analysis of Proteomic Experiments. 2015 , 14, 2405-19	45
1742	Advances in high-resolution quantitative proteomics: implications for clinical applications. 2015 , 12, 489-98	28
1741	Mining Missing Membrane Proteins by High-pH Reverse-Phase StageTip Fractionation and Multiple Reaction Monitoring Mass Spectrometry. 2015 , 14, 3658-69	20
1740	Large-Scale Interlaboratory Study to Develop, Analytically Validate and Apply Highly Multiplexed, Quantitative Peptide Assays to Measure Cancer-Relevant Proteins in Plasma. 2015 , 14, 2357-74	135

1739	In vivo assessment of protease dynamics in cutaneous wound healing by degradomics analysis of porcine wound exudates. 2015 , 14, 354-70	37
1738	Dynamic Proteome Response of <i>Pseudomonas aeruginosa</i> to Tobramycin Antibiotic Treatment. 2015 , 14, 2126-37	29
1737	Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. 2015 , 14, 3415-31	50
1736	Global, in situ, site-specific analysis of protein S-sulfenylation. 2015 , 10, 1022-37	101
1735	Distributed and interactive visual analysis of omics data. 2015 , 129, 78-82	6
1734	Protein degradation corrects for imbalanced subunit stoichiometry in OST complex assembly. 2015 , 26, 2596-608	33
1733	Absolute and multiplex quantification of antibodies in serum using PSAQ standards and LC-MS/MS. 2015 , 7, 1237-51	17
1732	Label-free SRM-based relative quantification of antibiotic resistance mechanisms in <i>Pseudomonas aeruginosa</i> clinical isolates. 2015 , 6, 81	17
1731	SIRT1 deacetylates ROR α and enhances Th17 cell generation. 2015 , 212, 607-17	98
1730	mzDB: a file format using multiple indexing strategies for the efficient analysis of large LC-MS/MS and SWATH-MS data sets. 2015 , 14, 771-81	16
1729	The blue light-dependent phosphorylation of the CCE domain determines the photosensitivity of Arabidopsis CRY2. 2015 , 8, 631-43	33
1728	Automated Validation of Results and Removal of Fragment Ion Interferences in Targeted Analysis of Data-independent Acquisition Mass Spectrometry (MS) using SWATHProphet. 2015 , 14, 1411-8	26
1727	Novel liquid chromatography-mass spectrometry method for sensitive determination of the mustard allergen Sin a 1 in food. 2015 , 183, 58-63	16
1726	Simultaneous Quantification of Viral Antigen Expression Kinetics Using Data-Independent (DIA) Mass Spectrometry. 2015 , 14, 1361-72	18
1725	Analytical platform evaluation for quantification of ERG in prostate cancer using protein and mRNA detection methods. 2015 , 13, 54	21
1724	Using the canary genome to decipher the evolution of hormone-sensitive gene regulation in seasonal singing birds. 2015 , 16, 19	44
1723	Selective Sirt2 inhibition by ligand-induced rearrangement of the active site. 2015 , 6, 6263	169
1722	Proteomics characterization of exosome cargo. 2015 , 87, 75-82	109

1721	Defining roles of PARKIN and ubiquitin phosphorylation by PINK1 in mitochondrial quality control using a ubiquitin replacement strategy. 2015 , 112, 6637-42		182
1720	Identification of differentially expressed serum proteins in gastric adenocarcinoma. 2015 , 127, 80-8		43
1719	Potato leafroll virus structural proteins manipulate overlapping, yet distinct protein interaction networks during infection. 2015 , 15, 2098-112		20
1718	Cerebrospinal fluid peptides as potential Parkinson disease biomarkers: a staged pipeline for discovery and validation. 2015 , 14, 544-55		42
1717	Allergen relative abundance in several wheat varieties as revealed via a targeted quantitative approach using MS. 2015 , 15, 1736-45		23
1716	CHCHD2 Is Coamplified with EGFR in NSCLC and Regulates Mitochondrial Function and Cell Migration. 2015 , 13, 1119-29		30
1715	Multiplexed, Quantitative Workflow for Sensitive Biomarker Discovery in Plasma Yields Novel Candidates for Early Myocardial Injury. 2015 , 14, 2375-93		141
1714	Efficient visualization of high-throughput targeted proteomics experiments: TAPIR. <i>Bioinformatics</i> , 2015 , 31, 2415-7	7.2	11
1713	Quantitative analysis of low-abundance serological proteins with peptide affinity-based enrichment and pseudo-multiple reaction monitoring by hybrid quadrupole time-of-flight mass spectrometry. 2015 , 882, 38-48		13
1712	Plant mitochondrial proteomics. 2015 , 1305, 83-106		1
1711	Discovery and targeted proteomics on cutaneous biopsies infected by borrelia to investigate lyme disease. 2015 , 14, 1254-64		16
1710	specL--an R/Bioconductor package to prepare peptide spectrum matches for use in targeted proteomics. <i>Bioinformatics</i> , 2015 , 31, 2228-31	7.2	9
1709	AID expression in B-cell lymphomas causes accumulation of genomic uracil and a distinct AID mutational signature. 2015 , 25, 60-71		48
1708	Quantification of extracellular matrix proteins from a rat lung scaffold to provide a molecular readout for tissue engineering. 2015 , 14, 961-73		107
1707	Phosphorylation of synaptic GTPase-activating protein (synGAP) by Ca ²⁺ /calmodulin-dependent protein kinase II (CaMKII) and cyclin-dependent kinase 5 (CDK5) alters the ratio of its GAP activity toward Ras and Rap GTPases. 2015 , 290, 4908-4927		48
1706	Targeted label-free approach for quantification of epoxide hydrolase and glutathione transferases in microsomes. 2015 , 478, 8-13		11
1705	CaMKII Phosphorylation of Na(V)1.5: Novel in Vitro Sites Identified by Mass Spectrometry and Reduced S516 Phosphorylation in Human Heart Failure. 2015 , 14, 2298-311		32
1704	Multidimensional proteomics for cell biology. 2015 , 16, 269-80		288

1703	Quantitative variability of 342 plasma proteins in a human twin population. 2015 , 11, 786	222
1702	Detection and quantification of proteins in clinical samples using high resolution mass spectrometry. 2015 , 81, 15-23	45
1701	Sequential Window Acquisition of all Theoretical Mass Spectra (SWATH) Analysis for Characterization and Quantification of Histone Post-translational Modifications. 2015 , 14, 2420-8	76
1700	Global Phosphoproteomic Analysis of Human Skeletal Muscle Reveals a Network of Exercise-Regulated Kinases and AMPK Substrates. 2015 , 22, 922-35	233
1699	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
1698	Meat Authentication via Multiple Reaction Monitoring Mass Spectrometry of Myoglobin Peptides. 2015 , 87, 10315-22	57
1697	Ranking Fragment Ions Based on Outlier Detection for Improved Label-Free Quantification in Data-Independent Acquisition LC-MS/MS. 2015 , 14, 4581-93	18
1696	Quantification of HER2 by Targeted Mass Spectrometry in Formalin-Fixed Paraffin-Embedded (FFPE) Breast Cancer Tissues. 2015 , 14, 2786-99	24
1695	Quantitative profiling of protein tyrosine kinases in human cancer cell lines by multiplexed parallel reaction monitoring assays. 2015 , mcp.O115.051813	3
1694	Low Resolution Data-Independent Acquisition in an LTQ-Orbitrap Allows for Simplified and Fully Untargeted Analysis of Histone Modifications. 2015 , 87, 11448-54	43
1693	An MRM-based workflow for absolute quantitation of lysine-acetylated metabolic enzymes in mouse liver. 2015 , 140, 7868-75	7
1692	Development and Validation of a Liquid Chromatography-Tandem Mass Spectrometry Method for the Quantitation of Microcystins in Blue-Green Algal Dietary Supplements. 2015 , 63, 10303-12	23
1691	Reproducible quantitative proteotype data matrices for systems biology. 2015 , 26, 3926-31	33
1690	Targeted Proteomics-Driven Computational Modeling of Macrophage S1P Chemosensing. 2015 , 14, 2661-81	12
1689	In-depth characterization of trypsin-like serine peptidases in the midgut of the sugar fed <i>Culex quinquefasciatus</i> . 2015 , 8, 373	9
1688	CheY's acetylation sites responsible for generating clockwise flagellar rotation in <i>Escherichia coli</i> . 2015 , 95, 231-44	29
1687	A simple dual online ultra-high pressure liquid chromatography system (sDO-UHPLC) for high throughput proteome analysis. 2015 , 140, 5700-6	7
1686	Mass Spectrometry for Biomarker Development. 2015 , 17-48	1

1685	Detection and Quantitation of Circulating Human Irisin by Tandem Mass Spectrometry. 2015 , 22, 734-740	310
1684	SRM/MRM targeted proteomics as a tool for biomarker validation and absolute quantification in human urine. 2015 , 15, 1441-54	35
1683	Loss of BAP1 function leads to EZH2-dependent transformation. 2015 , 21, 1344-9	231
1682	mapDIA: Preprocessing and statistical analysis of quantitative proteomics data from data independent acquisition mass spectrometry. 2015 , 129, 108-120	101
1681	Multiplexed Targeted Mass Spectrometry-Based Assays for the Quantification of N-Linked Glycosite-Containing Peptides in Serum. 2015 , 87, 10830-8	25
1680	Serum Glycoprotein Biomarker Discovery and Qualification Pipeline Reveals Novel Diagnostic Biomarker Candidates for Esophageal Adenocarcinoma. 2015 , 14, 3023-39	26
1679	Targeted proteomics of solid cancers: from quantification of known biomarkers towards reading the digital proteome maps. 2015 , 12, 651-67	7
1678	Gene replacement and quantitative mass spectrometry approaches validate guanosine monophosphate synthetase as essential for growth. 2015 , 4, 277-282	4
1677	The Use of Variable Q1 Isolation Windows Improves Selectivity in LC-SWATH-MS Acquisition. 2015 , 14, 4359-71	114
1676	ETD Outperforms CID and HCD in the Analysis of the Ubiquitylated Proteome. 2015 , 26, 1580-7	16
1675	Loss of diphthamide pre-activates NF- κ B and death receptor pathways and renders MCF7 cells hypersensitive to tumor necrosis factor. 2015 , 112, 10732-7	27
1674	Peptide-Centric Proteome Analysis: An Alternative Strategy for the Analysis of Tandem Mass Spectrometry Data. 2015 , 14, 2301-7	104
1673	The cysteine dioxygenase homologue from <i>Pseudomonas aeruginosa</i> is a 3-mercaptopropionate dioxygenase. 2015 , 290, 24424-37	38
1672	Transformative Impact of Proteomics on Cardiovascular Health and Disease: A Scientific Statement From the American Heart Association. 2015 , 132, 852-72	112
1671	Using Data Independent Acquisition (DIA) to Model High-responding Peptides for Targeted Proteomics Experiments. 2015 , 14, 2331-40	32
1670	Computational and Mass-Spectrometry-Based Workflow for the Discovery and Validation of Missing Human Proteins: Application to Chromosomes 2 and 14. 2015 , 14, 3621-34	31
1669	Targeted multiplexed selected reaction monitoring analysis evaluates protein expression changes of molecular risk factors for major psychiatric disorders. 2014 , 18,	32
1668	Biochemical isolation of Argonaute protein complexes by Ago-APP. 2015 , 112, 11841-5	45

1667	Elucidation of Xylem-Specific Transcription Factors and Absolute Quantification of Enzymes Regulating Cellulose Biosynthesis in <i>Populus trichocarpa</i> . 2015 , 14, 4158-68	12
1666	Targeted Proteomics of Human Metapneumovirus in Clinical Samples and Viral Cultures. 2015 , 87, 10247-54	22
1665	Diet-induced neuropeptide expression: feasibility of quantifying extended and highly charged endogenous peptide sequences by selected reaction monitoring. 2015 , 87, 9966-73	4
1664	Antibody-Coupled Magnetic Beads Can Be Reused in Immuno-MRM Assays To Reduce Cost and Extend Antibody Supply. 2015 , 14, 4425-31	15
1663	Analysis of Major Histocompatibility Complex (MHC) Immunopeptidomes Using Mass Spectrometry. 2015 , 14, 3105-3117	76
1662	Quantitative ADME proteomics - CYP and UGT enzymes in the Beagle dog liver and intestine. 2015 , 32, 74-90	34
1661	Recent advances in targeted proteomics for clinical applications. 2015 , 9, 423-31	48
1660	Oxidative stress influences positive strand RNA virus genome synthesis and capping. 2015 , 475, 219-29	58
1659	Viewing the proteome: how to visualize proteomics data?. 2015 , 15, 1341-55	25
1658	Building the Connectivity Map of epigenetics: chromatin profiling by quantitative targeted mass spectrometry. 2015 , 72, 57-64	40
1657	Distinct proteomic profiles in post-mortem pituitary glands from bipolar disorder and major depressive disorder patients. 2015 , 60, 40-8	29
1656	Induction of complementary function reductase enzymes in colon cancer cells by dithiole-3-thione versus sodium selenite. 2015 , 29, 10-20	5
1655	A targeted multiplexed proteomic investigation identifies ketamine-induced changes in immune markers in rat serum and expression changes in protein kinases/phosphatases in rat brain. 2015 , 14, 411-21	24
1654	Tools for monitoring system suitability in LC MS/MS centric proteomic experiments. 2015 , 15, 891-902	28
1653	Parallel reaction monitoring (PRM) and selected reaction monitoring (SRM) exhibit comparable linearity, dynamic range and precision for targeted quantitative HDL proteomics. 2015 , 113, 388-99	132
1652	Absolute quantification of <i>Corynebacterium glutamicum</i> glycolytic and anaplerotic enzymes by QconCAT. 2015 , 113, 366-77	11
1651	Targeted mass spectrometry analysis of the proteins IGF1, IGF2, IBP2, IBP3 and A2GL by blood protein precipitation. 2015 , 113, 29-37	26
1650	A kinetic-based approach to understanding heterologous mevalonate pathway function in <i>E. coli</i> . 2015 , 112, 111-9	37

1649	Proteomics of apheresis platelet supernatants during routine storage: Gender-related differences. 2015 , 112, 190-209	19
1648	Systems Toxicology. 2016 , 1-39	1
1647	Spatially Directed Proteomics of the Human Lens Outer Cortex Reveals an Intermediate Filament Switch Associated With the Remodeling Zone. 2016 , 57, 4108-14	8
1646	Dynamic Proteomic Analysis of Pancreatic Mesenchyme Reveals Novel Factors That Enhance Human Embryonic Stem Cell to Pancreatic Cell Differentiation. 2016 , 2016, 6183562	18
1645	Development of Diagnostic Biomarkers for Detecting Diabetic Retinopathy at Early Stages Using Quantitative Proteomics. 2016 , 2016, 6571976	22
1644	Interleukin-6 Induced "Acute" Phenotypic Microenvironment Promotes Th1 Anti-Tumor Immunity in Cryo-Thermal Therapy Revealed By Shotgun and Parallel Reaction Monitoring Proteomics. 2016 , 6, 773-94	32
1643	Spatio-Temporal Detection of the Thiomonas Population and the Thiomonas Arsenite Oxidase Involved in Natural Arsenite Attenuation Processes in the Carnoulès Acid Mine Drainage. 2016 , 4, 3	9
1642	The Role of Proteomics in Biomarker Development for Improved Patient Diagnosis and Clinical Decision Making in Prostate Cancer. 2016 , 6,	15
1641	Apolipoprotein A1-Unique Peptide as a Diagnostic Biomarker for Acute Ischemic Stroke. 2016 , 17, 458	7
1640	LC-MS/MS Validation Analysis of Trastuzumab Using dSIL Approach for Evaluating Pharmacokinetics. 2016 , 21,	11
1639	Quantitative and Selective Analysis of Feline Growth Related Proteins Using Parallel Reaction Monitoring High Resolution Mass Spectrometry. 2016 , 11, e0167138	7
1638	SWATH2stats: An R/Bioconductor Package to Process and Convert Quantitative SWATH-MS Proteomics Data for Downstream Analysis Tools. 2016 , 11, e0153160	31
1637	iTRAQ-Based Quantitative Proteomic Comparison of Early- and Late-Passage Human Dermal Papilla Cell Secretome in Relation to Inducing Hair Follicle Regeneration. 2016 , 11, e0167474	14
1636	Proteomic Database Search and Analytical Quantification for Mass Spectrometry. 2016 , 193-210	
1635	Technical advances in proteomics: new developments in data-independent acquisition. 2016 , 5,	119
1634	Molecular serum signature of treatment resistant depression. 2016 , 233, 3051-9	13
1633	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
1632	Absolute protein quantification of the yeast chaperome under conditions of heat shock. 2016 , 16, 2128-40	12

1631	Detection of proteolytic signatures for Parkinson's disease. 2016 , 11, 15-32	
1630	A targeted proteomic strategy for the measurement of oral cancer candidate biomarkers in human saliva. 2016 , 16, 159-73	48
1629	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
1628	A clinically based protein discovery strategy to identify potential biomarkers of response to anti-TNF- α treatment of psoriatic arthritis. 2016 , 10, 645-62	17
1627	Dynamic reorganization of photosystem II supercomplexes in response to variations in light intensities. 2016 , 1857, 1651-60	40
1626	Attenuation of pattern recognition receptor signaling is mediated by a MAP kinase kinase kinase. 2016 , 17, 441-54	39
1625	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
1624	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
1623	Quantification of decellularized human myocardial matrix: A comparison of six patients. 2016 , 10, 75-83	67
1622	Serine and threonine residues of plant STN7 kinase are differentially phosphorylated upon changing light conditions and specifically influence the activity and stability of the kinase. 2016 , 87, 484-94	28
1621	Targeted proteomics coming of age - SRM, PRM and DIA performance evaluated from a core facility perspective. 2016 , 16, 2183-92	27
1620	Proteomic analysis of breast tumors confirms the mRNA intrinsic molecular subtypes using different classifiers: a large-scale analysis of fresh frozen tissue samples. 2016 , 18, 69	8
1619	Enhanced base excision repair capacity in carotid atherosclerosis may protect nuclear DNA but not mitochondrial DNA. 2016 , 97, 386-397	2
1618	Binding properties of YjeQ (RsgA), RbfA, RimM and Era to assembly intermediates of the 30S subunit. 2016 , 44, 9918-9932	26
1617	Advances in targeted proteomics and applications to biomedical research. 2016 , 16, 2160-82	134
1616	Untargeted, spectral library-free analysis of data-independent acquisition proteomics data generated using Orbitrap mass spectrometers. 2016 , 16, 2257-71	45
1615	Protein biomarker discovery and fast monitoring for the identification and detection of Anisakids by parallel reaction monitoring (PRM) mass spectrometry. 2016 , 142, 130-7	43
1614	Comparison of commercial nanoliquid chromatography columns for fast, targeted mass spectrometry-based proteomics. 2016 , 2, FSO119	11

1613	Discordant signaling and autophagy response to fasting in hearts of obese mice: Implications for ischemia tolerance. 2016 , 311, H219-28	26
1612	Versatile, sensitive liquid chromatography mass spectrometry - Implementation of 10 μ m OT columns suitable for small molecules, peptides and proteins. 2016 , 6, 37507	28
1611	Modular Assembly of the Bacterial Large Ribosomal Subunit. 2016 , 167, 1610-1622.e15	97
1610	Urinary Kininogen-1 and Retinol binding protein-4 respond to Acute Kidney Injury: predictors of patient prognosis?. 2016 , 6, 19667	14
1609	Gadd45a Protein Promotes Skeletal Muscle Atrophy by Forming a Complex with the Protein Kinase MEKK4. 2016 , 291, 17496-17509	25
1608	Gene-specific correlation of RNA and protein levels in human cells and tissues. 2016 , 12, 883	230
1607	Surface and Exoproteomes of Gram-Positive Pathogens for Vaccine Discovery. 2017 , 404, 309-337	
1606	The Advent of Mass Spectrometry-Based Proteomics in Systems Biology Research. 2016 , 166-176	0
1605	Quantitative analyses of the hepatic proteome of methylmercury-exposed Atlantic cod (<i>Gadus morhua</i>) suggest oxidative stress-mediated effects on cellular energy metabolism. 2016 , 17, 554	21
1604	An oxygen-sensitive toxin-antitoxin system. 2016 , 7, 13634	37
1603	Novel UCHL1 mutations reveal new insights into ubiquitin processing. 2017 , 26, 1031-1040	15
1602	Qualification and Verification of Protein Biomarker Candidates. 2016 , 919, 493-514	13
1601	Quantitative extracellular matrix proteomics to study mammary and liver tissue microenvironments. 2016 , 81, 223-232	66
1600	A proteogenomic approach for protein-level evidence of genomic variants in cancer cells. 2016 , 6, 35305	9
1599	Modern Proteomics Sample Preparation, Analysis and Practical Applications. 2016 ,	10
1598	Mass Spectrometry-Based Protein Quantification. 2016 , 919, 255-279	6
1597	Changes in Relative Thylakoid Protein Abundance Induced by Fluctuating Light in the Diatom <i>Thalassiosira pseudonana</i> . 2016 , 15, 1649-58	17
1596	Analysis of the sodium chloride-dependent respiratory kinetics of wheat mitochondria reveals differential effects on phosphorylating and non-phosphorylating electron transport pathways. 2016 , 39, 823-33	22

1595	Mass Spectrometry Applied to Bottom-Up Proteomics: Entering the High-Throughput Era for Hypothesis Testing. 2016 , 9, 449-72	202
1594	Absolute quantification of proteins in the fatty acid biosynthetic pathway using protein standard absolute quantification. 2016 , 1, 150-157	9
1593	Data Independent Acquisition analysis in ProHits 4.0. 2016 , 149, 64-68	37
1592	A proteomic signature of ovarian cancer tumor fluid identified by highthroughput and verified by targeted proteomics. 2016 , 145, 226-236	29
1591	Autocrine and Paracrine Regulation of Keratinocyte Proliferation through a Novel Nrf2-IL-36 β Pathway. 2016 , 196, 4663-70	11
1590	An inhibitor of KDM5 demethylases reduces survival of drug-tolerant cancer cells. 2016 , 12, 531-8	188
1589	Bacterial Interactomes: Interacting Protein Partners Share Similar Function and Are Validated in Independent Assays More Frequently Than Previously Reported. 2016 , 15, 1539-55	12
1588	Clinical peptide and protein quantification by mass spectrometry (MS). 2016 , 84, 131-143	19
1587	Site-Specific N-Glycosylation of Recombinant Pentameric and Hexameric Human IgM. 2016 , 27, 1143-55	27
1586	Methods for the Analysis of Protein Phosphorylation-Mediated Cellular Signaling Networks. 2016 , 9, 295-315	20
1585	High-Throughput LC-MS/MS Proteomic Analysis of a Mouse Model of Mesiotemporal Lobe Epilepsy Predicts Microglial Activation Underlying Disease Development. 2016 , 15, 1546-62	24
1584	Discovery of serum protein biomarkers in drug-free patients with major depressive disorder. 2016 , 69, 60-8	43
1583	Reduced-representation Phosphosignatures Measured by Quantitative Targeted MS Capture Cellular States and Enable Large-scale Comparison of Drug-induced Phenotypes. 2016 , 15, 1622-41	69
1582	The effect of thermal processing on the behaviour of peanut allergen peptide targets used in multiple reaction monitoring mass spectrometry experiments. 2016 , 141, 4130-41	30
1581	Capillary Electrophoresis-Nanoelectrospray Ionization-Selected Reaction Monitoring Mass Spectrometry via a True Sheathless Metal-Coated Emitter Interface for Robust and High-Sensitivity Sample Quantification. 2016 , 88, 4418-25	37
1580	Targeted proteomics: Current status and future perspectives for quantification of food allergens. 2016 , 143, 15-23	48
1579	Targeting Carcinoembryonic Antigen with DNA Vaccination: On-Target Adverse Events Link with Immunologic and Clinical Outcomes. 2016 , 22, 4827-4836	20
1578	Application of nano-surface and molecular-orientation limited proteolysis to LC-MS bioanalysis of cetuximab. 2016 , 8, 1009-20	10

1577	A Multiplexed Cytokeratin Analysis Using Targeted Mass Spectrometry Reveals Specific Profiles in Cancer-Related Pleural Effusions. 2016 , 18, 399-412	7
1576	Novel IEF Peptide Fractionation Method Reveals a Detailed Profile of N-Terminal Acetylation in Chemotherapy-Responsive and -Resistant Ovarian Cancer Cells. 2016 , 15, 4073-4081	6
1575	Stable nuclear expression of ATP8 and ATP6 genes rescues a mtDNA Complex V null mutant. 2016 , 44, 9342-9357	19
1574	A novel microflow LC-MS method for the quantitation of endocannabinoids in serum. 2016 , 1033-1034, 271-277	18
1573	Quantification of Lysine Acetylation and Succinylation Stoichiometry in Proteins Using Mass Spectrometric Data-Independent Acquisitions (SWATH). 2016 , 27, 1758-1771	50
1572	Dataset of target mass spectromic proteome profiling for human chromosome 18. 2016 , 8, 1365-9	1
1571	An Automated Pipeline to Monitor System Performance in Liquid Chromatography-Tandem Mass Spectrometry Proteomic Experiments. 2016 , 15, 4763-4769	36
1570	Strategies for large-scale targeted metabolomics quantification by liquid chromatography-mass spectrometry. 2016 , 141, 6362-6373	114
1569	Quantitative Cross-linking/Mass Spectrometry Using Isotope-labeled Cross-linkers and MaxQuant. 2016 , 15, 2769-78	26
1568	Simultaneous Proteomic Discovery and Targeted Monitoring using Liquid Chromatography, Ion Mobility Spectrometry, and Mass Spectrometry. 2016 , 15, 3694-3705	20
1567	Quantification of antibody coupled to magnetic particles by targeted mass spectrometry. 2016 , 408, 8325-8332	10
1566	The Tyrosine Sulfate Domain of Fibromodulin Binds Collagen and Enhances Fibril Formation. 2016 , 291, 23744-23755	16
1565	Selected reaction monitoring mass spectrometry for relative quantification of proteins involved in cellular life and death processes. 2016 , 1035, 49-56	3
1564	Alpha-, Beta-, and Gamma-synuclein Quantification in Cerebrospinal Fluid by Multiple Reaction Monitoring Reveals Increased Concentrations in Alzheimer's and Creutzfeldt-Jakob Disease but No Alteration in Synucleinopathies. 2016 , 15, 3126-3138	63
1563	A multicenter study benchmarks software tools for label-free proteome quantification. 2016 , 34, 1130-1136	202
1562	Basics of Mass Spectrometry and Its Applications in Biomarker Discovery. 2016 , 41-63	
1561	Determining the Mitochondrial Methyl Proteome in <i>Saccharomyces cerevisiae</i> using Heavy Methyl SILAC. 2016 , 15, 4436-4451	13
1560	Focus on Bioinformatics, Software, and MS-Based "Omics," Honoring Dr. Michael J. MacCoss, Recipient of the 2015 ASMS Biemann Medal. 2016 , 27, 1715-1718	1

1559	Targeted Proteomics (MRM) in Cardiovascular Research. 2016 , 213-226	
1558	Quantification of allergenic plant traces in baked products by targeted proteomics using isotope marked peptides. 2016 , 74, 286-293	19
1557	LFQProfiler and RNP(xl): Open-Source Tools for Label-Free Quantification and Protein-RNA Cross-Linking Integrated into Proteome Discoverer. 2016 , 15, 3441-8	19
1556	TRIC: an automated alignment strategy for reproducible protein quantification in targeted proteomics. 2016 , 13, 777-83	122
1555	An Open Data Format for Visualization and Analysis of Cross-Linked Mass Spectrometry Results. 2016 , 27, 1728-1734	5
1554	Hierarchical RNA Processing Is Required for Mitochondrial Ribosome Assembly. 2016 , 16, 1874-90	80
1553	Impact of genetic deletion of platform apolipoproteins on the size distribution of the murine lipoproteome. 2016 , 146, 184-94	6
1552	Optimized Protocol for Quantitative Multiple Reaction Monitoring-Based Proteomic Analysis of Formalin-Fixed, Paraffin-Embedded Tissues. 2016 , 15, 2717-28	35
1551	Protein Z: A putative novel biomarker for early detection of ovarian cancer. 2016 , 138, 2984-92	35
1550	Molecular and proteome analyses highlight the importance of the Cpx envelope stress system for acid stress and cell wall stability in Escherichia coli. 2016 , 5, 582-96	22
1549	Clinical applications of MS-based protein quantification. 2016 , 10, 323-45	27
1548	Age modifies respiratory complex I and protein homeostasis in a muscle type-specific manner. 2016 , 15, 89-99	43
1547	Proteome rearrangements after auditory learning: high-resolution profiling of synapse-enriched protein fractions from mouse brain. 2016 , 138, 124-38	11
1546	Targeted Quantitative Screening of Chromosome 18 Encoded Proteome in Plasma Samples of Astronaut Candidates. 2016 , 15, 4039-4046	24
1545	Translational Targeted Proteomics Profiling of Mitochondrial Energy Metabolic Pathways in Mouse and Human Samples. 2016 , 15, 3204-13	24
1544	CEP5 and XIP1/CEPR1 regulate lateral root initiation in Arabidopsis. 2016 , 67, 4889-99	54
1543	Transitioning from Targeted to Comprehensive Mass Spectrometry Using Genetic Algorithms. 2016 , 27, 1745-1751	2
1542	Dynamic phosphorylation of RelA on Ser42 and Ser45 in response to TNF β stimulation regulates DNA binding and transcription. 2016 , 6,	15

1541	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. 2016 , 13, 741-8	337
1540	Identification of Organ-Enriched Protein Biomarkers of Acute Liver Injury by Targeted Quantitative Proteomics of Blood in Acetaminophen- and Carbon-Tetrachloride-Treated Mouse Models and Acetaminophen Overdose Patients. 2016 , 15, 3724-3740	18
1539	A Skyline Plugin for Pathway-Centric Data Browsing. 2016 , 27, 1752-1757	5
1538	Adipocyte-secreted chemerin is processed to a variety of isoforms and influences MMP3 and chemokine secretion through an NFkB-dependent mechanism. 2016 , 436, 114-29	17
1537	State of the Art of Chromosome 18-Centric HPP in 2016: Transcriptome and Proteome Profiling of Liver Tissue and HepG2 Cells. 2016 , 15, 4030-4038	16
1536	Codon Optimization to Enhance Expression Yields Insights into Chloroplast Translation. 2016 , 172, 62-77	37
1535	aPKC Inhibition by Par3 CR3 Flanking Regions Controls Substrate Access and Underpins Apical-Junctional Polarization. 2016 , 38, 384-98	32
1534	Quantitative analysis of wild-type and V600E mutant BRAF proteins in colorectal carcinoma using immunoenrichment and targeted mass spectrometry. 2016 , 933, 144-55	6
1533	Specificity of Protein Covalent Modification by the Electrophilic Proteasome Inhibitor Carfilzomib in Human Cells. 2016 , 15, 3233-3242	19
1532	Identification and Quantification of Histone PTMs Using High-Resolution Mass Spectrometry. 2016 , 574, 3-29	24
1531	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
1530	Combined Quantification of the Global Proteome, Phosphoproteome, and Proteolytic Cleavage to Characterize Altered Platelet Functions in the Human Scott Syndrome. 2016 , 15, 3154-3169	31
1529	Dynamic Phosphorylation of Apoptosis Signal Regulating Kinase 1 (ASK1) in Response to Oxidative and Electrophilic Stress. 2016 , 29, 2175-2183	8
1528	Diet-Microbiota Interactions Mediate Global Epigenetic Programming in Multiple Host Tissues. 2016 , 64, 982-992	280
1527	Current Trends and Future Perspectives of State-of-the-Art Proteomics Technologies Applied to Cardiovascular Disease Research. 2016 , 80, 1674-83	7
1526	A comparative proteomic analysis of Salmonella typhimurium under the regulation of the RstA/RstB and PhoP/PhoQ systems. 2016 , 1864, 1686-1695	16
1525	Mass-spectrometric exploration of proteome structure and function. 2016 , 537, 347-55	1070
1524	A High-Throughput Targeted Proteomic Approach for Comprehensive Profiling of Methylglyoxal-Induced Perturbations of the Human Kinome. 2016 , 88, 9773-9779	19

1523	Quantitative Mass Spectrometry To Study Inflammatory Cartilage Degradation and Resulting Interactions with the Complement System. 2016 , 197, 3415-3424	11
1522	Manual of Cardiovascular Proteomics. 2016 ,	2
1521	Basic Concepts in Mass Spectrometry and Protein Quantitation. 2016 , 15-32	
1520	Direct glycan structure determination of intact N-linked glycopeptides by low-energy collision-induced dissociation tandem mass spectrometry and predicted spectral library searching. 2016 , 934, 152-62	12
1519	Epiproteomics: quantitative analysis of histone marks and codes by mass spectrometry. 2016 , 33, 142-50	49
1518	The unique peptidome: Taxon-specific tryptic peptides as biomarkers for targeted metaproteomics. 2016 , 16, 2313-8	20
1517	Effect of Intestinal Flora on Protein Expression of Drug-Metabolizing Enzymes and Transporters in the Liver and Kidney of Germ-Free and Antibiotics-Treated Mice. 2016 , 13, 2691-701	54
1516	Predictive chromatography of peptides and proteins as a complementary tool for proteomics. 2016 , 141, 4816-4832	24
1515	Coffee consumption modulates inflammatory processes in an individual fashion. 2016 , 60, 2529-2541	15
1514	Targeted proteomics identifies liquid-biopsy signatures for extracapsular prostate cancer. 2016 , 7, 11906	59
1513	Robust Label-free, Quantitative Profiling of Circulating Plasma Microparticle (MP) Associated Proteins. 2016 , 15, 3640-3652	17
1512	Conservation of protein abundance patterns reveals the regulatory architecture of the EGFR-MAPK pathway. 2016 , 9, rs6	78
1511	Chemical Glycoproteomics. 2016 , 116, 14277-14306	161
1510	Unconventional endosome-like compartment and retromer complex in <i>Toxoplasma gondii</i> govern parasite integrity and host infection. 2016 , 7, 11191	37
1509	Essential structural elements in tRNA(Pro) for EF-P-mediated alleviation of translation stalling. 2016 , 7, 11657	48
1508	Hybrid mass spectrometry approaches in glycoprotein analysis and their usage in scoring biosimilarity. 2016 , 7, 13397	105
1507	tRNA-mediated codon-biased translation in mycobacterial hypoxic persistence. 2016 , 7, 13302	79
1506	Comparative proteomics reveals that central metabolism changes are associated with resistance against <i>Sporisorium scitamineum</i> in sugarcane. 2016 , 17, 800	37

1505	The MaxQuant computational platform for mass spectrometry-based shotgun proteomics. 2016 , 11, 2301-2319	1656
1504	Food allergen detection by mass spectrometry: the role of systems biology. 2016 , 2, 16022	49
1503	PARP3 is a sensor of nicked nucleosomes and monoribosylates histone H2B(Glu2). 2016 , 7, 12404	50
1502	The Arabidopsis Golgi-localized GDP-L-fucose transporter is required for plant development. 2016 , 7, 12119	38
1501	New insights into the molecular mechanisms of chemical carcinogenesis: In vivo adduction of histone H2B by a reactive metabolite of the chemical carcinogen furan. 2016 , 264, 106-113	16
1500	Introduction. 2016 , 1-15	1
1499	Comparative proteomics of cucurbit phloem indicates both unique and shared sets of proteins. 2016 , 88, 633-647	11
1498	Mass spectrometric analysis of synaptosomal membrane preparations for the determination of brain receptors, transporters and channels. 2016 , 16, 2911-2920	14
1497	Study of O-Phosphorylation Sites in Proteins Involved in Photosynthesis-Related Processes in Synechocystis sp. Strain PCC 6803: Application of the SRM Approach. 2016 , 15, 4638-4652	22
1496	Glycosylation site occupancy in health, congenital disorder of glycosylation and fatty liver disease. 2016 , 6, 33927	14
1495	Computational Methods in Mass Spectrometry-Based Proteomics. 2016 , 939, 63-89	7
1494	The BANK1 SLE-risk variants are associated with alterations in peripheral B cell signaling and development in humans. 2016 , 173, 171-180	25
1493	Topic model-based mass spectrometric data analysis in cancer biomarker discovery studies. 2016 , 17 Suppl 4, 545	0
1492	Astrocyte-mediated regulation of multidrug resistance p-glycoprotein in fetal and neonatal brain endothelial cells: age-dependent effects. 2016 , 4, e12853	10
1491	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
1490	Complete Workflow for Analysis of Histone Post-translational Modifications Using Bottom-up Mass Spectrometry: From Histone Extraction to Data Analysis. 2016 ,	90
1489	Protein turnover measurement using selected reaction monitoring-mass spectrometry (SRM-MS). 2016 , 374,	8
1488	Quantitative analysis of human centrosome architecture by targeted proteomics and fluorescence imaging. 2016 , 35, 2152-2166	57

1487	Species Determination and Quantitation in Mixtures Using MRM Mass Spectrometry of Peptides Applied to Meat Authentication. 2016 ,	3
1486	Saliva-Induced Clotting Captures Streptococci: Novel Roles for Coagulation and Fibrinolysis in Host Defense and Immune Evasion. 2016 , 84, 2813-23	11
1485	Quantification of angiotensin II-regulated proteins in urine of patients with polycystic and other chronic kidney diseases by selected reaction monitoring. 2016 , 13, 16	13
1484	Analysis of <i>Drosophila melanogaster</i> proteome dynamics during embryonic development by a combination of label-free proteomics approaches. 2016 , 16, 2068-80	17
1483	Advances in quadrupole and time-of-flight mass spectrometry for peptide MRM based translational research analysis. 2016 , 16, 2206-20	12
1482	Riboflavin-Responsive and -Non-responsive Mutations in FAD Synthase Cause Multiple Acyl-CoA Dehydrogenase and Combined Respiratory-Chain Deficiency. 2016 , 98, 1130-1145	97
1481	Generating aldehyde-tagged antibodies with high titers and high formylglycine yields by supplementing culture media with copper(II). 2016 , 16, 23	32
1480	Use of chemical modification and mass spectrometry to identify substrate-contacting sites in proteinaceous RNase P, a tRNA processing enzyme. 2016 , 44, 5344-55	13
1479	Statins increase hepatic cholesterol synthesis and stimulate fecal cholesterol elimination in mice. 2016 , 57, 1455-64	74
1478	Automated Microchromatography Enables Multiplexing of Immunoaffinity Enrichment of Peptides to Greater than 150 for Targeted MS-Based Assays. 2016 , 88, 7548-55	28
1477	Impact of Serum and Plasma Matrices on the Titration of Human Inflammatory Biomarkers Using Analytically Validated SRM Assays. 2016 , 15, 2366-78	8
1476	Differential quantification of isobaric phosphopeptides using data-independent acquisition mass spectrometry. 2016 , 12, 2385-8	7
1475	Automated DBS microsampling, microscale automation and microflow LC-MS for therapeutic protein PK. 2016 , 8, 649-59	9
1474	Assembly Dynamics and Stoichiometry of the Apoptosis Signal-regulating Kinase (ASK) Signalosome in Response to Electrophile Stress. 2016 , 15, 1947-61	23
1473	Oncogenic KRAS and BRAF Drive Metabolic Reprogramming in Colorectal Cancer. 2016 , 15, 2924-38	58
1472	RNAi induced knockdown of a cadherin-like protein (EF531715) does not affect toxicity of Cry34/35Ab1 or Cry3Aa to <i>Diabrotica virgifera virgifera</i> larvae (Coleoptera: Chrysomelidae). 2016 , 75, 117-24	12
1471	Clinical translation of MS-based, quantitative plasma proteomics: status, challenges, requirements, and potential. 2016 , 13, 673-84	31
1470	Efficient Microscale Basic Reverse Phase Peptide Fractionation for Global and Targeted Proteomics. 2016 , 15, 2346-54	12

1469	Glyco-centric lectin magnetic bead array (LeMBA) - proteomics dataset of human serum samples from healthy, Barrett's esophagus and esophageal adenocarcinoma individuals. 2016 , 7, 1058-62	5
1468	Validation, optimisation, and application data in support of the development of a targeted selected ion monitoring assay for degraded cardiac troponin T. 2016 , 7, 397-405	4
1467	Metabolic engineering of <i>Clostridium cellulolyticum</i> for the production of n-butanol from crystalline cellulose. 2016 , 15, 6	79
1466	Mismatch in epitope specificities between IFN γ inflamed and uninfamed conditions leads to escape from T lymphocyte killing in melanoma. 2016 , 4, 10	17
1465	Nuclear Phosphoproteomic Screen Uncovers ACLY as Mediator of IL-2-induced Proliferation of CD4+ T lymphocytes. 2016 , 15, 2076-92	29
1464	Multiple apolipoprotein kinetics measured in human HDL by high-resolution/accurate mass parallel reaction monitoring. 2016 , 57, 714-28	28
1463	BatMass: a Java Software Platform for LC-MS Data Visualization in Proteomics and Metabolomics. 2016 , 15, 2500-9	28
1462	Integrative Analysis of Proteomic, Glycomic, and Metabolomic Data for Biomarker Discovery. 2016 , 20, 1225-1231	9
1461	Bacterial Electron Transfer Chains Primed by Proteomics. 2016 , 68, 219-352	2
1460	Identification of Novel N-Glycosylation Sites at Noncanonical Protein Consensus Motifs. 2016 , 15, 2087-101	27
1459	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
1458	High-precision iRT prediction in the targeted analysis of data-independent acquisition and its impact on identification and quantitation. 2016 , 16, 2246-56	80
1457	Parallel reaction monitoring using quadrupole-Orbitrap mass spectrometer: Principle and applications. 2016 , 16, 2146-59	165
1456	MASP1, THBS1, GPLD1 and ApoA-IV are novel biomarkers associated with prediabetes: the KORA F4 study. 2016 , 59, 1882-92	40
1455	Auxin/AID versus conventional knockouts: distinguishing the roles of CENP-T/W in mitotic kinetochore assembly and stability. 2016 , 6, 150230	17
1454	In silico verification and parallel reaction monitoring prevalidation of potential prostate cancer biomarkers. 2016 , 12, 43-57	9
1453	Development of a targeted selected ion monitoring assay for the elucidation of protease induced structural changes in cardiac troponin T. 2016 , 136, 123-32	23
1452	Utilizing enzymatic digestion procedures in the bioanalytical laboratory. 2016 , 8, 29-36	2

1451	Discovery of potential colorectal cancer serum biomarkers through quantitative proteomics on the colonic tissue interstitial fluids from the AOM-DSS mouse model. 2016 , 132, 31-40	22
1450	Cytoskeleton deregulation and impairment in amino acids and energy metabolism in early atherosclerosis at aortic tissue with reflection in plasma. 2016 , 1862, 725-732	20
1449	Transgelin is upregulated in stromal cells of lymph node positive breast cancer. 2016 , 132, 103-11	16
1448	Development of a Quantitative SRM-Based Proteomics Method to Study Iron Metabolism of <i>Synechocystis</i> sp. PCC 6803. 2016 , 15, 266-79	20
1447	The Proteomic Profile of Deleted in Breast Cancer 1 (DBC1) Interactions Points to a Multifaceted Regulation of Gene Expression. 2016 , 15, 791-809	10
1446	Integrated analysis of shotgun proteomic data with PatternLab for proteomics 4.0. 2016 , 11, 102-17	156
1445	Low Mass Blood Peptides Discriminative of Inflammatory Bowel Disease (IBD) Severity: A Quantitative Proteomic Perspective. 2016 , 15, 256-65	22
1444	Quantitative Profiling of Protein Tyrosine Kinases in Human Cancer Cell Lines by Multiplexed Parallel Reaction Monitoring Assays. 2016 , 15, 682-91	33
1443	The Flavodiiron Protein Flv3 Functions as a Homo-Oligomer During Stress Acclimation and is Distinct from the Flv1/Flv3 Hetero-Oligomer Specific to the O ₂ Photoreduction Pathway. 2016 , 57, 1468-1483	25
1442	Label-free quantification in ion mobility-enhanced data-independent acquisition proteomics. 2016 , 11, 795-812	160
1441	Quantitative MS-based enzymology of caspases reveals distinct protein substrate specificities, hierarchies, and cellular roles. 2016 , 113, E2001-10	72
1440	Improved Identification and Analysis of Small Open Reading Frame Encoded Polypeptides. 2016 , 88, 3967-75	73
1439	Development and Evaluation of a Parallel Reaction Monitoring Strategy for Large-Scale Targeted Metabolomics Quantification. 2016 , 88, 4478-86	76
1438	Plug-and-play analysis of the human phosphoproteome by targeted high-resolution mass spectrometry. 2016 , 13, 431-4	77
1437	Isolating and Quantifying Plasma HDL Proteins by Sequential Density Gradient Ultracentrifugation and Targeted Proteomics. 2016 , 1410, 105-20	10
1436	Ageing-induced changes in the redox status of peripheral motor nerves imply an effect on redox signalling rather than oxidative damage. 2016 , 94, 27-35	18
1435	Proteome analysis of <i>Bordetella pertussis</i> isolated from human macrophages. 2016 , 136, 55-67	14
1434	Relative sensitivity of immunohistochemistry, multiple reaction monitoring mass spectrometry, in situ hybridization and PCR to detect Coxsackievirus B1 in A549 cells. 2016 , 77, 21-8	18

1433	Qualitative and Quantitative Proteomics Methods for the Analysis of the Anopheles gambiae Mosquito Proteome. 2016 , 37-62	1
1432	Population-specific renal proteomes of marine and freshwater three-spined sticklebacks. 2016 , 135, 112-131	10
1431	Phosphoproteomic analysis of interacting tumor and endothelial cells identifies regulatory mechanisms of transendothelial migration. 2016 , 9, ra15	27
1430	Hypoxia Increases IGFBP-1 Phosphorylation Mediated by mTOR Inhibition. 2016 , 30, 201-16	19
1429	Preface. 2016 , 1410, v	1
1428	Proteomic approaches to uncovering virus-host protein interactions during the progression of viral infection. 2016 , 13, 325-40	57
1427	Multiplexed Immunoaffinity Enrichment of Peptides with Anti-peptide Antibodies and Quantification by Stable Isotope Dilution Multiple Reaction Monitoring Mass Spectrometry. 2016 , 1410, 135-67	9
1426	Global Protein Oxidation Profiling Suggests Efficient Mitochondrial Proteome Homeostasis During Aging. 2016 , 15, 1692-709	8
1425	Mass Spectrometry in Plant-omics. 2016 , 88, 3422-34	50
1424	Targeted Proteomics Identifies Paraoxonase/Arylesterase 1 (PON1) and Apolipoprotein Cs as Potential Risk Factors for Hypoalphalipoproteinemia in Diabetic Subjects Treated with Fenofibrate and Rosiglitazone. 2016 , 15, 1083-93	17
1423	Proteomic profiling predicts drug response to novel targeted anticancer therapeutics. 2016 , 13, 411-20	5
1422	Differential proteomics analysis to identify proteins and pathways associated with male sterility of soybean using iTRAQ-based strategy. 2016 , 138, 72-82	40
1421	Mining the human urine proteome for monitoring renal transplant injury. 2016 , 89, 1244-52	55
1420	Natural Genetic Variation Differentially Affects the Proteome and Transcriptome in Caenorhabditis elegans. 2016 , 15, 1670-80	15
1419	Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. 2016 , 6, 286-94	23
1418	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. 2016 , 15, 1867-76	26
1417	Targeted MS Assay Predicting Tamoxifen Resistance in Estrogen-Receptor-Positive Breast Cancer Tissues and Sera. 2016 , 15, 1230-42	16
1416	Mechanistic investigation of the on-surface enzymatic digestion (oSED) protein adsorption detection method using targeted mass spectrometry. 2016 , 141, 1714-20	1

1415	Targeted Proteomics Approach for Precision Plant Breeding. 2016 , 15, 638-46	30
1414	Recommendations for the Generation, Quantification, Storage, and Handling of Peptides Used for Mass Spectrometry-Based Assays. 2016 , 62, 48-69	135
1413	Immobilized Metal Affinity Chromatography Coupled to Multiple Reaction Monitoring Enables Reproducible Quantification of Phospho-signaling. 2016 , 15, 726-39	40
1412	Selected Reaction Monitoring to Measure Proteins of Interest in Complex Samples: A Practical Guide. 2016 , 1394, 43-56	11
1411	A Targeted MRM Approach for Tempo-Spatial Proteomics Analyses. 2016 , 1394, 75-85	4
1410	The Compact and Biologically Relevant Structure of Inter- β -inhibitor Is Maintained by the Chondroitin Sulfate Chain and Divalent Cations. 2016 , 291, 4658-70	5
1409	Adaptation of Skyline for Targeted Lipidomics. 2016 , 15, 291-301	33
1408	The spider hemolymph clot proteome reveals high concentrations of hemocyanin and von Willebrand factor-like proteins. 2016 , 1864, 233-41	10
1407	Benchmarking quantitative label-free LC-MS data processing workflows using a complex spiked proteomic standard dataset. 2016 , 132, 51-62	53
1406	Alterations in the phosphoproteomic profile of cells expressing a non-functional form of the SHP2 phosphatase. 2016 , 33, 524-36	5
1405	Impact of Sample Matrix on Accuracy of Peptide Quantification: Assessment of Calibrator and Internal Standard Selection and Method Validation. 2016 , 88, 746-53	17
1404	Physiological responses of a Southern Ocean diatom to complex future ocean conditions. 2016 , 6, 207-213	104
1403	Preprocessing and Analysis of LC-MS-Based Proteomic Data. 2016 , 1362, 63-76	16
1402	Longitudinal Urinary Protein Variability in Participants of the Space Flight Simulation Program. 2016 , 15, 114-24	21
1401	Impact of a synthetic cannabinoid (CP-47,497-C8) on protein expression in human cells: evidence for induction of inflammation and DNA damage. 2016 , 90, 1369-82	13
1400	Protein profiles distinguish stable and progressive chronic lymphocytic leukemia. 2016 , 57, 1033-43	6
1399	RNA Sequencing Identifies Novel Translational Biomarkers of Kidney Fibrosis. 2016 , 27, 1702-13	45
1398	Measurement by a Novel LC-MS/MS Methodology Reveals Similar Serum Concentrations of Vitamin D-Binding Protein in Blacks and Whites. 2016 , 62, 179-87	91

1397	Activation of the Endogenous Renin-Angiotensin-Aldosterone System or Aldosterone Administration Increases Urinary Exosomal Sodium Channel Excretion. 2016 , 27, 646-56	38
1396	Discovery and confirmation of a protein biomarker panel with potential to predict response to biological therapy in psoriatic arthritis. 2016 , 75, 234-41	37
1395	System-based proteomic and metabonomic analysis of the Df(16)A mouse identifies potential miR-185 targets and molecular pathway alterations. 2017 , 22, 384-395	15
1394	Proteome analysis of mast cell releasates reveals a role for chymase in the regulation of coagulation factor XIIIa levels via proteolytic degradation. 2017 , 139, 323-334	20
1393	Development of soybeans with low P34 allergen protein concentration for reduced allergenicity of soy foods. 2017 , 97, 1010-1017	5
1392	Psychiatric disorders biochemical pathways unraveled by human brain proteomics. 2017 , 267, 3-17	26
1391	Proteomic analysis of ovarian cancer cells during epithelial-mesenchymal transition (EMT) induced by epidermal growth factor (EGF) reveals mechanisms of cell cycle control. 2017 , 151, 2-11	31
1390	Algorithms and design strategies towards automated glycoproteomics analysis. 2017 , 36, 475-498	68
1389	Absolute quantification of myosin heavy chain isoforms by selected reaction monitoring can underscore skeletal muscle changes in a mouse model of amyotrophic lateral sclerosis. 2017 , 409, 2143-2153	13
1388	Communication between viruses guides lysis-lysogeny decisions. 2017 , 541, 488-493	298
1387	Characterization of human and Staphylococcus aureus proteins in respiratory mucosa by in vivo- and immunoproteomics. 2017 , 155, 31-39	26
1386	Quantification by nano liquid chromatography parallel reaction monitoring mass spectrometry of human apolipoprotein A-I, apolipoprotein B, and hemoglobin A1c in dried blood spots. 2017 , 11, 1600103	19
1385	Intestinal Farnesoid X Receptor Controls Transintestinal Cholesterol Excretion in Mice. 2017 , 152, 1126-1138.e69	69
1384	Targeted Proteomics for Multiplexed Verification of Markers of Colorectal Tumorigenesis. 2017 , 16, 407-427	29
1383	High-Titer Rheumatoid Arthritis Antibodies Preferentially Bind Fibrinogen Citrullinated by Peptidylarginine Deiminase 4. 2017 , 69, 986-995	29
1382	Multimiomics reveal non-alcoholic fatty liver disease in rats following chronic exposure to an ultra-low dose of Roundup herbicide. 2017 , 7, 39328	98
1381	Comprehensive mass spectrometry based biomarker discovery and validation platform as applied to diabetic kidney disease. 2017 , 14, 1-10	22
1380	A review on mass spectrometry-based quantitative proteomics: Targeted and data independent acquisition. 2017 , 964, 7-23	190

1379	SILAC-Based Quantitative Proteomic Analysis Unveils Arsenite-Induced Perturbation of Multiple Pathways in Human Skin Fibroblast Cells. 2017 , 30, 1006-1014	11
1378	Combined Proteome and Eicosanoid Profiling Approach for Revealing Implications of Human Fibroblasts in Chronic Inflammation. 2017 , 89, 1945-1954	17
1377	Murine Cytomegalovirus Deubiquitinase Regulates Viral Chemokine Levels To Control Inflammation and Pathogenesis. 2017 , 8,	11
1376	Quantitative glycomics using liquid phase separations coupled to mass spectrometry. 2017 , 142, 700-720	12
1375	Proteomic analysis of human follicular fluid in poor ovarian responders during in vitro fertilization. 2017 , 17, 1600333	10
1374	Quantitative proteomics of breast tumors: Tissue quality assessment to clinical biomarkers. 2017 , 17, 1600335	6
1373	Determination of wheat, rye and spelt authenticity in bread by targeted peptide biomarkers. 2017 , 58, 82-91	24
1372	Metabolomic Identification of Subtypes of Nonalcoholic Steatohepatitis. 2017 , 152, 1449-1461.e7	139
1371	Identification and Characterization of Cardiac Troponin T Fragments in Serum of Patients Suffering from Acute Myocardial Infarction. 2017 , 63, 563-572	23
1370	SWATH-MS as a tool for biomarker discovery: From basic research to clinical applications. 2017 , 17, 1600278	97
1369	Assessment of Label-Free Quantification in Discovery Proteomics and Impact of Technological Factors and Natural Variability of Protein Abundance. 2017 , 16, 1410-1424	60
1368	Optimization by infusion of multiple reaction monitoring transitions for sensitive quantification of peptides by liquid chromatography/mass spectrometry. 2017 , 31, 753-761	6
1367	Proteoform Profile Mapping of the Human Serum Complement Component C9 Revealing Unexpected New Features of N-, O-, and C-Glycosylation. 2017 , 89, 3483-3491	33
1366	Fumarase Deficiency Causes Protein and Metabolite Succination and Intoxicates Mycobacterium tuberculosis. 2017 , 24, 306-315	28
1365	Integrating phosphoproteomics into the clinical management of prostate cancer. 2017 , 6, 9	6
1364	Targeted proteomics driven verification of biomarker candidates associated with breast cancer aggressiveness. 2017 , 1865, 488-498	16
1363	The TRAIL-Induced Cancer Secretome Promotes a Tumor-Supportive Immune Microenvironment via CCR2. 2017 , 65, 730-742.e5	122
1362	ProteoModLR for functional proteomic analysis. 2017 , 18, 153	3

1361	Missing Value Monitoring Enhances the Robustness in Proteomics Quantitation. 2017 , 16, 1719-1727	8
1360	Inactivation of iron-sulfur cluster biogenesis regulator SufR in <i>Synechocystis</i> sp. PCC 6803 induces unique iron-dependent protein-level responses. 2017 , 1861, 1085-1098	13
1359	TIRR regulates 53BP1 by masking its histone methyl-lysine binding function. 2017 , 543, 211-216	61
1358	Quantification of small GTPase glucosylation by clostridial glucosylating toxins using multiplexed MRM analysis. 2017 , 17, 1700016	6
1357	Lipoic acid treatment prevents cystine urolithiasis in a mouse model of cystinuria. 2017 , 23, 288-290	34
1356	Correlation of pre-operative plasma protein concentrations in cardiac surgery patients with bleeding outcomes using a targeted quantitative proteomics approach. 2017 , 11, 1600175	3
1355	Mass Spectrometry-Based Analysis for the Discovery and Validation of Potential Colorectal Cancer Stool Biomarkers. 2017 , 586, 247-274	11
1354	Parallel changes in serum proteins and diffusion tensor imaging in methamphetamine-associated psychosis. 2017 , 7, 43777	7
1353	Maternal nutrition modulates fetal development by inducing placental efficiency changes in gilts. 2017 , 18, 213	22
1352	Identification of a direct Aquaporin-0 binding site in the lens-specific cytoskeletal protein filensin. 2017 , 159, 23-29	10
1351	Phosphoproteins in extracellular vesicles as candidate markers for breast cancer. 2017 , 114, 3175-3180	201
1350	Clustered, Regularly Interspaced Short Palindromic Repeats (CRISPR)/Cas9-coupled Affinity Purification/Mass Spectrometry Analysis Revealed a Novel Role of Neurofibromin in mTOR Signaling. 2017 , 16, 594-607	6
1349	Automated SWATH Data Analysis Using Targeted Extraction of Ion Chromatograms. 2017 , 1550, 289-307	23
1348	Super-SILAC mix coupled with SIM/AIMS assays for targeted verification of phosphopeptides discovered in a large-scale phosphoproteome analysis of hepatocellular carcinoma. 2017 , 157, 40-51	5
1347	Generation of High-Quality SWATH Acquisition Data for Label-free Quantitative Proteomics Studies Using TripleTOF Mass Spectrometers. 2017 , 1550, 223-233	39
1346	Customized Consensus Spectral Library Building for Untargeted Quantitative Metabolomics Analysis with Data Independent Acquisition Mass Spectrometry and MetaboDIA Workflow. 2017 , 89, 4897-4906	27
1345	Clinical perspectives of dried blood spot protein quantification using mass spectrometry methods. 2017 , 54, 173-184	14
1344	Quantitative proteomic analysis of Parkin substrates in <i>Drosophila</i> neurons. 2017 , 12, 29	40

1343	mTORC1 Promotes T-bet Phosphorylation To Regulate Th1 Differentiation. 2017 , 198, 3939-3948	28
1342	Targeted mass spectrometry: An emerging powerful approach to unblock the bottleneck in phosphoproteomics. 2017 , 1055-1056, 29-38	21
1341	Body Fluid Degradomics and Characterization of Basic N-Terminome. 2017 , 585, 177-199	6
1340	Analysis of the Proteome of Hair-Cell Stereocilia by Mass Spectrometry. 2017 , 585, 329-354	2
1339	Proteomics Analysis Identifies Orthologs of Human Chitinase-Like Proteins as Inducers of Tube Morphogenesis Defects in. 2017 , 206, 973-984	6
1338	WITHDRAWN: Quantitative mass spectrometry analysis of PD-L1 protein expression, N-glycosylation and expression stoichiometry with PD-1 and PD-L2 in human melanoma. 2017 ,	
1337	Current trends in quantitative proteomics - an update. 2017 , 52, 319-341	51
1336	Peptide Immunoaffinity Enrichment with Targeted Mass Spectrometry: Application to Quantification of ATM Kinase Phospho-Signaling. 2017 , 1599, 197-213	8
1335	Molecular Profiling. 2017 ,	3
1334	Transposon-driven transcription is a conserved feature of vertebrate spermatogenesis and transcript evolution. 2017 , 18, 1231-1247	26
1333	Quantitative Mass Spectrometry by Isotope Dilution and Multiple Reaction Monitoring (MRM). 2017 , 1606, 313-332	10
1332	The mitochondrial respiratory chain is essential for haematopoietic stem cell function. 2017 , 19, 614-625	151
1331	Effects of insulin and the glucagon-like peptide 1 receptor agonist liraglutide on the kidney proteome in db/db mice. 2017 , 5, e13187	6
1330	From data to knowledge: The future of multi-omics data analysis for the rhizosphere. 2017 , 3, 222-229	19
1329	A survey of proteomic biomarkers for heterotopic ossification in blood serum. 2017 , 12, 69	8
1328	Characterisation of extracellular vesicle-subsets derived from brain endothelial cells and analysis of their protein cargo modulation after TNF exposure. 2017 , 6, 1302705	61
1327	SMYD2-Mediated Histone Methylation Contributes to HIV-1 Latency. 2017 , 21, 569-579.e6	54
1326	TRAF2 and OTUD7B govern a ubiquitin-dependent switch that regulates mTORC2 signalling. 2017 , 545, 365-369	90

1325	Molecular basis for blue light-dependent phosphorylation of Arabidopsis cryptochrome 2. 2017 , 8, 15234	56
1324	Chemical and pathogen-induced inflammation disrupt the murine intestinal microbiome. 2017 , 5, 47	64
1323	Protein and Sugar Export and Assembly in Gram-positive Bacteria. 2017 ,	2
1322	Acclimation of Oxygenic Photosynthesis to Iron Starvation Is Controlled by the sRNA IsaR1. 2017 , 27, 1425-1436.e7	56
1321	Clinical applications of quantitative proteomics using targeted and untargeted data-independent acquisition techniques. 2017 , 14, 419-429	74
1320	InvS Coordinates Expression of PrgH and FimZ and Is Required for Invasion of Epithelial Cells by Salmonella enterica serovar Typhimurium. 2017 , 199,	10
1319	Introducing plasma/serum glycodepletion for the targeted proteomics analysis of cytolysis biomarkers. 2017 , 170, 473-480	6
1318	Quantification of ATP7B Protein in Dried Blood Spots by Peptide Immuno-SRM as a Potential Screen for Wilson's Disease. 2017 , 16, 862-871	31
1317	Heterogeneous Ribosomes Preferentially Translate Distinct Subpools of mRNAs Genome-wide. 2017 , 67, 71-83.e7	308
1316	Biotechnological production of recombinant tissue plasminogen activator protein (reteplase) from transplastomic tobacco cell cultures. 2017 , 118, 130-137	12
1315	Targeted unlabeled multiple reaction monitoring analysis of cell markers for the study of sample heterogeneity in isolated rat brain cortical microvessels. 2017 , 142, 597-609	10
1314	Colorectal Cancer Cell Line Proteomes Are Representative of Primary Tumors and Predict Drug Sensitivity. 2017 , 153, 1082-1095	40
1313	Targeted quantification of functional enzyme dynamics in environmental samples for microbially mediated biogeochemical processes. 2017 , 9, 512-521	12
1312	Conditional Switch between Frameshifting Regimes upon Translation of dnaX mRNA. 2017 , 66, 558-567.e4	29
1311	Multiplexed MRM-Based Protein Quantitation Using Two Different Stable Isotope-Labeled Peptide Isotopologues for Calibration. 2017 , 16, 2527-2536	19
1310	Second generation multiple reaction monitoring assays for enhanced detection of ultra-low abundance peptides in human serum. 2017 , 14, 21	29
1309	Spectral library-based glycopeptide analysis-detection of circulating galectin-3 binding protein in pancreatic cancer. 2017 , 11, 1700064	13
1308	MsViz: A Graphical Software Tool for In-Depth Manual Validation and Quantitation of Post-translational Modifications. 2017 , 16, 3092-3101	7

1307	Intestinal Muc2 mucin O-glycosylation is affected by microbiota and regulated by differential expression of glycosyltransferases. 2017 , 27, 318-328	72
1306	A comprehensive evaluation of popular proteomics software workflows for label-free proteome quantification and imputation. 2018 , 19, 1344-1355	60
1305	LCMS/MS Bioanalytical Method Development Strategy for Therapeutic Monoclonal Antibodies in Preclinical Studies. 2017 , 145-159	2
1304	Strategies of Drug Transporter Quantitation by LC-MS: Importance of Peptide Selection and Digestion Efficiency. 2017 , 19, 1469-1478	10
1303	Copper-zinc superoxide dismutase is activated through a sulfenic acid intermediate at a copper ion entry site. 2017 , 292, 12025-12040	39
1302	The cellular ceramide transport protein CERT promotes Chlamydia psittaci infection and controls bacterial sphingolipid uptake. 2017 , 19, e12752	19
1301	MSstatsQC: Longitudinal System Suitability Monitoring and Quality Control for Targeted Proteomic Experiments. 2017 , 16, 1335-1347	15
1300	Heme-thiolate sulfenylation of human cytochrome P450 4A11 functions as a redox switch for catalytic inhibition. 2017 , 292, 11230-11242	16
1299	Quantitative Phospho-proteomic Analysis of TNF/ κ B Signaling Reveals a Role for RIPK1 Phosphorylation in Suppressing Necrotic Cell Death. 2017 , 16, 1200-1216	13
1298	Quantitative Mass Spectrometry Analysis of PD-L1 Protein Expression, -glycosylation and Expression Stoichiometry with PD-1 and PD-L2 in Human Melanoma. 2017 , 16, 1705-1717	36
1297	A qualitative and quantitative evaluation of the peptide characteristics of microwave- and ultrasound-assisted digestion in discovery and targeted proteomic analyses. 2017 , 31, 1353-1362	10
1296	Time-Resolved Proteomics Extends Ribosome Profiling-Based Measurements of Protein Synthesis Dynamics. 2017 , 4, 636-644.e9	39
1295	Role of Type 2 NAD(P)H Dehydrogenase NdbC in Redox Regulation of Carbon Allocation in. 2017 , 174, 1863-1880	15
1294	Cylindromatosis Tumor Suppressor Protein (CYLD) Deubiquitinase is Necessary for Proper Ubiquitination and Degradation of the Epidermal Growth Factor Receptor. 2017 , 16, 1433-1446	11
1293	Absolute Protein Quantification by Mass Spectrometry: Not as Simple as Advertised. 2017 , 89, 7406-7415	46
1292	Towards reproducible MRM based biomarker discovery using dried blood spots. 2017 , 7, 45178	19
1291	Proteomic Methods in Neuropsychiatric Research. 2017 ,	2
1290	Loss of Cln3 impacts protein secretion in the social amoeba Dictyostelium. 2017 , 35, 61-72	21

1289	The elaborate route for UDP-arabinose delivery into the Golgi of plants. 2017 , 114, 4261-4266	31
1288	An Approach to Spatiotemporally Resolve Protein Interaction Networks in Living Cells. 2017 , 169, 350-360.e12209	
1287	SRM dataset of the proteome of inactivated iron-sulfur cluster biogenesis regulator SufR in sp. PCC 6803. 2017 , 11, 572-575	3
1286	Identification of candidate protein markers of Bovine Parainfluenza Virus Type 3 infection using an in vitro model. 2017 , 203, 257-266	2
1285	One-Pot Two-Nanoprobe Assay Uncovers Targeted Glycoprotein Biosignature. 2017 , 89, 3973-3980	18
1284	Analysis of 17 β -estradiol, estriol and estrone in American eel (<i>Anguilla rostrata</i>) tissue samples using liquid chromatography coupled to electrospray differential ion mobility tandem mass spectrometry. 2017 , 31, 842-850	14
1283	Matrix metalloproteinase processing of PTHrP yields a selective regulator of osteogenesis, PTHrP. 2017 , 36, 4498-4507	9
1282	SWATH-ID: An instrument method which combines identification and quantification in a single analysis. 2017 , 17, e1500522	16
1281	DOSCATs: Double standards for protein quantification. 2017 , 7, 45570	6
1280	Mediator lipidomics by liquid chromatography-tandem mass spectrometry. 2017 , 1862, 777-781	4
1279	Measurement of In Vivo Protein Binding Affinities in a Signaling Network with Mass Spectrometry. 2017 , 6, 1305-1314	6
1278	Selective Reaction Monitoring Mass Spectrometry for Quantitation of Glycolytic Enzymes in Postmortem Brain Samples. 2017 , 974, 205-212	0
1277	Precise Temporal Profiling of Signaling Complexes in Primary Cells Using SWATH Mass Spectrometry. 2017 , 18, 3219-3226	23
1276	Adapting Data-Independent Acquisition for Mass Spectrometry-Based Protein Site-Specific N-Glycosylation Analysis. 2017 , 89, 4532-4539	25
1275	Large-Scale SRM Screen of Urothelial Bladder Cancer Candidate Biomarkers in Urine. 2017 , 16, 1617-1631	16
1274	Coupling Front-End Separations, Ion Mobility Spectrometry, and Mass Spectrometry For Enhanced Multidimensional Biological and Environmental Analyses. 2017 , 10, 71-92	63
1273	Deciphering the Acute Cellular Phosphoproteome Response to Irradiation with X-rays, Protons and Carbon Ions. 2017 , 16, 855-872	18
1272	Profiling of antioxidative enzyme expression induced by various food components using targeted proteome analysis. 2017 , 61, 1600655	4

1271	An alpha-synuclein MRM assay with diagnostic potential for Parkinson's disease and monitoring disease progression. 2017 , 11, 1700045	5
1270	An Optimized Chromatographic Strategy for Multiplexing In Parallel Reaction Monitoring Mass Spectrometry: Insights from Quantitation of Activated Kinases. 2017 , 16, 265-277	28
1269	Quantitative proteomics analysis of cartilage response to mechanical injury and cytokine treatment. 2017 , 63, 11-22	29
1268	Proteomic Analysis of Primary Human Airway Epithelial Cells Exposed to the Respiratory Toxicant Diacetyl. 2017 , 16, 538-549	18
1267	A large-scale targeted proteomics assay resource based on an in vitro human proteome. 2017 , 14, 251-258	61
1266	Myofibrillar Z-discs Are a Protein Phosphorylation Hot Spot with Protein Kinase C (PKC β) Modulating Protein Dynamics. 2017 , 16, 346-367	22
1265	Building proteomic tool boxes to monitor MHC class I and class II peptides. 2017 , 17, 1600061	20
1264	Knockout of a difficult-to-remove CHO host cell protein, lipoprotein lipase, for improved polysorbate stability in monoclonal antibody formulations. 2017 , 114, 1006-1015	97
1263	Host Plants Indirectly Influence Plant Virus Transmission by Altering Gut Cysteine Protease Activity of Aphid Vectors. 2017 , 16, S230-S243	28
1262	A Strategy to Combine Sample Multiplexing with Targeted Proteomics Assays for High-Throughput Protein Signature Characterization. 2017 , 65, 361-370	87
1261	A Multi-network Approach Identifies Protein-Specific Co-expression in Asymptomatic and Symptomatic Alzheimer's Disease. 2017 , 4, 60-72.e4	219
1260	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
1259	ABRF Proteome Informatics Research Group (iPRG) 2015 Study: Detection of Differentially Abundant Proteins in Label-Free Quantitative LC-MS/MS Experiments. 2017 , 16, 945-957	35
1258	Model-Based Analysis of Quantitative Proteomics Data with Data Independent Acquisition Mass Spectrometry. 2017 , 125-140	
1257	Biomonitoring Human Albumin Adducts: The Past, the Present, and the Future. 2017 , 30, 332-366	63
1256	Lipoprotein profiling methodology based on determination of apolipoprotein concentration. 2017 , 9, 9-19	2
1255	Statistical Analysis of Proteomics, Metabolomics, and Lipidomics Data Using Mass Spectrometry. 2017 ,	4
1254	Mass Spectrometry Analysis of Lysine Posttranslational Modifications of Tau Protein from Alzheimer's Disease Brain. 2017 , 1523, 161-177	10

1253	The Rodent Liver Undergoes Weaning-Induced Involution and Supports Breast Cancer Metastasis. 2017 , 7, 177-187	30
1252	Measuring protein structural changes on a proteome-wide scale using limited proteolysis-coupled mass spectrometry. 2017 , 12, 2391-2410	83
1251	The PRMT5/WDR77 complex regulates alternative splicing through ZNF326 in breast cancer. 2017 , 45, 11106-11120	34
1250	A cryptic Tudor domain links BRWD2/PHIP to COMPASS-mediated histone H3K4 methylation. 2017 , 31, 2003-2014	29
1249	Proteomic footprint of myocardial ischemia/reperfusion injury: Longitudinal study of the at-risk and remote regions in the pig model. 2017 , 7, 12343	19
1248	Digging More Missing Proteins Using an Enrichment Approach with ProteoMiner. 2017 , 16, 4330-4339	18
1247	Ubiquitin Linkage-Specific Affimers Reveal Insights into K6-Linked Ubiquitin Signaling. 2017 , 68, 233-246.e5	95
1246	Hydroxylamine Chemical Digestion for Insoluble Extracellular Matrix Characterization. 2017 , 16, 4177-4184	34
1245	Sample Preparation for Mass Spectrometry-based Identification of RNA-binding Regions. 2017 ,	1
1244	Composition and Regulation of the Cellular Repertoire of SCF Ubiquitin Ligases. 2017 , 171, 1326-1339.e14	74
1243	Systematic proteome and proteostasis profiling in human Trisomy 21 fibroblast cells. 2017 , 8, 1212	59
1242	An inhibitor of the proteasomal deubiquitinating enzyme USP14 induces tau elimination in cultured neurons. 2017 , 292, 19209-19225	73
1241	Dynamic changes of urine proteome in a Walker 256 tumor-bearing rat model. 2017 , 6, 2713-2722	29
1240	Model of Chronic Equine Endometritis Involving a Pseudomonas aeruginosa Biofilm. 2017 , 85,	17
1239	Polypharmacology-based ceritinib repurposing using integrated functional proteomics. 2017 , 13, 1222-1231	39
1238	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
1237	Functional proteomics outlines the complexity of breast cancer molecular subtypes. 2017 , 7, 10100	27
1236	Revisiting biomarker discovery by plasma proteomics. 2017 , 13, 942	361

1235	Ricin-like proteins from the castor plant do not influence liquid chromatography-mass spectrometry detection of ricin in forensically relevant samples. 2017 , 140, 18-31	16
1234	Proteomic analysis of human lacrimal and tear fluid in dry eye disease. 2017 , 7, 13363	33
1233	Analysis of substrate specificity of oligosaccharyltransferases (OSTs) by functional expression of domain-swapped chimeras in yeast. 2017 , 292, 20342-20352	4
1232	Aurora Kinase B, a novel regulator of TERF1 binding and telomeric integrity. 2017 , 45, 12340-12353	11
1231	Statistical control of peptide and protein error rates in large-scale targeted data-independent acquisition analyses. 2017 , 14, 921-927	129
1230	iTRAQ-based comparative proteomic analysis reveals tissue-specific and novel early-stage molecular mechanisms of salt stress response in <i>Carex rigescens</i> . 2017 , 143, 99-114	26
1229	Proteomics for Drug Discovery. 2017 ,	0
1228	High Sensitivity Quantitative Proteomics Using Automated Multidimensional Nano-flow Chromatography and Accumulated Ion Monitoring on Quadrupole-Orbitrap-Linear Ion Trap Mass Spectrometer. 2017 , 16, 2006-2016	29
1227	High-Resolution Parallel Reaction Monitoring with Electron Transfer Dissociation for Middle-Down Proteomics: An Application to Study the Quantitative Changes Induced by Histone Modifying Enzyme Inhibitors and Activators. 2017 , 1647, 61-69	4
1226	A human APOC3 missense variant and monoclonal antibody accelerate apoC-III clearance and lower triglyceride-rich lipoprotein levels. 2017 , 23, 1086-1094	63
1225	Lipidomics informatics for life-science. 2017 , 261, 131-136	18
1224	Development of a Multiplexed Assay for Oral Cancer Candidate Biomarkers Using Peptide Immunoaffinity Enrichment and Targeted Mass Spectrometry. 2017 , 16, 1829-1849	18
1223	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. 2017 , 16, 4288-4298	61
1222	Targeted degradomics in protein terminomics and protease substrate discovery. 2017 , 399, 47-54	16
1221	Progress on the HUPO Draft Human Proteome: 2017 Metrics of the Human Proteome Project. 2017 , 16, 4281-4287	46
1220	Differential regulation of vaginal lipocalins (OBP, MUP) during the estrous cycle of the house mouse. 2017 , 7, 11674	17
1219	Heterodimeric capping protein is required for stereocilia length and width regulation. 2017 , 216, 3861-3881	26
1218	Proteomic Response of Human Umbilical Vein Endothelial Cells to Histamine Stimulation. 2017 , 17, 1700116	4

1217	Quantitative Multiple-Reaction Monitoring Proteomic Analysis of G α and G β Subunits in C57Bl6/J Brain Synaptosomes. 2017 , 56, 5405-5416	12
1216	Statistical characterization of therapeutic protein modifications. 2017 , 7, 7896	2
1215	The TLR2 Antagonist Staphylococcal Superantigen-Like Protein 3 Acts as a Virulence Factor to Promote Bacterial Pathogenicity in vivo. 2017 , 9, 561-573	13
1214	Proteome-wide acetylation dynamics in human cells. 2017 , 7, 10296	34
1213	Targeted Proteomic Analyses of Histone H4 Acetylation Changes Associated with Homologous-Recombination-Deficient High-Grade Serous Ovarian Carcinomas. 2017 , 16, 3704-3710	6
1212	MdFDIA: A Mass Defect Based Four-Plex Data-Independent Acquisition Strategy for Proteome Quantification. 2017 , 89, 10248-10255	17
1211	Targeted Quantification of Peptide Biomarkers. 2017 , 211-225	
1210	Large-Scale Quantitative Proteomics Identifies the Ubiquitin Ligase Nedd4-1 as an Essential Regulator of Liver Regeneration. 2017 , 42, 616-625.e8	10
1209	Deep-Dive Targeted Quantification for Ultrasensitive Analysis of Proteins in Nondepleted Human Blood Plasma/Serum and Tissues. 2017 , 89, 9139-9146	17
1208	Targeted Mass Spectrometry Approach Enabled Discovery of O-Glycosylated Insulin and Related Signaling Peptides in Mouse and Human Pancreatic Islets. 2017 , 89, 9184-9191	29
1207	Targeted proteomic assays for quantitation of proteins identified by proteogenomic analysis of ovarian cancer. 2017 , 4, 170091	18
1206	Identification of Proteomic Features To Distinguish Benign Pulmonary Nodules from Lung Adenocarcinoma. 2017 , 16, 3266-3276	18
1205	Human mitochondrial cytochrome P450 27C1 is localized in skin and preferentially desaturates -retinol to 3,4-dehydroretinol. 2017 , 292, 13672-13687	16
1204	pyQms enables universal and accurate quantification of mass spectrometry data. 2017 , 16, 1736-1745	13
1203	Integrating Discovery-driven Proteomics and Selected Reaction Monitoring To Develop a Noninvasive Assay for Geoduck Reproductive Maturation. 2017 , 16, 3298-3309	11
1202	Integrating Next-Generation Genomic Sequencing and Mass Spectrometry To Estimate Allele-Specific Protein Abundance in Human Brain. 2017 , 16, 3336-3347	28
1201	Centriolar Satellites Control GABARAP Ubiquitination and GABARAP-Mediated Autophagy. 2017 , 27, 2123-2136.e7	59
1200	Importance of N- and C-terminal residues of substance P 1-7 for alleviating allodynia in mice after peripheral administration. 2017 , 106, 345-351	8

1199	multiplierz v2.0: A Python-based ecosystem for shared access and analysis of native mass spectrometry data. 2017 , 17, 1700091	33
1198	Lipid profiling of complex biological mixtures by liquid chromatography/mass spectrometry using a novel scanning quadrupole data-independent acquisition strategy. 2017 , 31, 1599-1606	14
1197	Absolute Quantification of Toxicological Biomarkers via Mass Spectrometry. 2017 , 1641, 337-348	1
1196	Quantitation of 87 Proteins by nLC-MRM/MS in Human Plasma: Workflow for Large-Scale Analysis of Biobank Samples. 2017 , 16, 3242-3254	8
1195	FD5180, a Novel Protein Kinase Affinity Probe, and the Effect of Bead Loading on Protein Kinase Identification. 2017 , 2, 3828-3838	2
1194	Synthesis of the compatible solute proline by <i>Bacillus subtilis</i> : point mutations rendering the osmotically controlled proHJ promoter hyperactive. 2017 , 19, 3700-3720	9
1193	Accurate quantification of 5 German cockroach (GCr) allergens in complex extracts using multiple reaction monitoring mass spectrometry (MRM MS). 2017 , 47, 1661-1670	12
1192	LpxK Is Essential for Growth of ATCC 19606: Relationship to Toxic Accumulation of Lipid A Pathway Intermediates. 2017 , 2,	15
1191	Immunoaffinity techniques coupled to mass spectrometry for the analysis of human peptide hormones: advances and applications. 2017 , 14, 799-807	16
1190	Repression of Stress-Induced LINE-1 Expression Protects Cancer Cell Subpopulations from Lethal Drug Exposure. 2017 , 32, 221-237.e13	104
1189	The use of LC predicted retention times to extend metabolites identification with SWATH data acquisition. 2017 , 1071, 3-10	29
1188	An online 2D-reversed-phase - Reversed-phase chromatographic method for sensitive and robust plasma protein quantitation. 2017 , 168, 28-36	15
1187	Quantitative Proteomics Reveals Temporal Proteomic Changes in Signaling Pathways during BV2 Mouse Microglial Cell Activation. 2017 , 16, 3419-3432	14
1186	PECAN: library-free peptide detection for data-independent acquisition tandem mass spectrometry data. 2017 , 14, 903-908	92
1185	Molecular signatures that can be transferred across different omics platforms. <i>Bioinformatics</i> , 2017 , 33, i333-i340	7.2 9
1184	An Engineered orco Mutation Produces Aberrant Social Behavior and Defective Neural Development in Ants. 2017 , 170, 736-747.e9	126
1183	Multiplexed Liquid Chromatography-Multiple Reaction Monitoring Mass Spectrometry Quantification of Cancer Signaling Proteins. 2017 , 1647, 19-45	5
1182	Bioinformatics Resources for Interpreting Proteomics Mass Spectrometry Data. 2017 , 1647, 267-295	1

1181	UBE2O remodels the proteome during terminal erythroid differentiation. 2017 , 357,	77
1180	A wellness study of 108 individuals using personal, dense, dynamic data clouds. 2017 , 35, 747-756	235
1179	Systems Pharmacology Dissection of Cholesterol Regulation Reveals Determinants of Large Pharmacodynamic Variability between Cell Lines. 2017 , 5, 604-619.e7	13
1178	Quantification of Breast Cancer Protein Biomarkers at Different Expression Levels in Human Tumors. 2018 , 1788, 251-268	0
1177	Targeted Proteomics Driven Verification of Biomarker Candidates Associated with Breast Cancer Aggressiveness. 2018 , 1788, 177-184	
1176	Selected reaction monitoring approach for validating peptide biomarkers. 2017 , 114, 13519-13524	15
1175	A semi-synthetic organism that stores and retrieves increased genetic information. 2017 , 551, 644-647	183
1174	The target landscape of clinical kinase drugs. 2017 , 358,	389
1173	Combination Strategy of Quantitative Proteomics Uncovers the Related Proteins of Colorectal Cancer in the Interstitial Fluid of Colonic Tissue from the AOM-DSS Mouse Model. 2018 , 1788, 185-192	2
1172	A Peptide Signaling System that Rapidly Enforces Paternity in the <i>Aedes aegypti</i> Mosquito. 2017 , 27, 3734-3742.e5	21
1171	The genetic basis for the adaptation of <i>E. coli</i> to sugar synthesis from CO. 2017 , 8, 1705	26
1170	LC-SRM-Based Targeted Quantification of Urinary Protein Biomarkers. 2018 , 1788, 145-156	3
1169	Mass Spectrometry-Based Serum Proteomics for Biomarker Discovery and Validation. 2017 , 1619, 451-466	7
1168	Blood and Plasma Proteomics: Targeted Quantitation and Posttranslational Redox Modifications. 2017 , 1619, 353-371	4
1167	Challenges and perspectives of metaproteomic data analysis. 2017 , 261, 24-36	116
1166	Computational proteomics tools for identification and quality control. 2017 , 261, 126-130	9
1165	Proteomic analysis by iTRAQ-MRM of soybean resistance to <i>Lamprosema Indicate</i> . 2017 , 18, 444	16
1164	Brain Region and Isoform-Specific Phosphorylation Alters Kalirin SH2 Domain Interaction Sites and Calpain Sensitivity. 2017 , 8, 1554-1569	7

1163	The Use of Multiple Reaction Monitoring on QQQ-MS for the Analysis of Protein- and Site-Specific Glycosylation Patterns in Serum. 2017 , 1503, 63-82	5
1162	Transcription factor proteomics-Tools, applications, and challenges. 2017 , 17, 1600317	17
1161	In-tip nanoreactors for cancer cells proteome profiling. 2017 , 949, 43-52	7
1160	Quantitative Proteomics Reveals Fundamental Regulatory Differences in Oncogenic HRAS and Isocitrate Dehydrogenase (IDH1) Driven Astrocytoma. 2017 , 16, 39-56	20
1159	Multiplexed MRM-based assays for the quantitation of proteins in mouse plasma and heart tissue. 2017 , 17, 1600097	16
1158	Towards comprehensive and quantitative proteomics for diagnosis and therapy of human disease. 2017 , 17, 1600079	34
1157	SILAC-based quantitative proteomic analysis reveals widespread molecular alterations in human skin keratinocytes upon chronic arsenic exposure. 2017 , 17, 1600257	15
1156	Resource: Mapping the Triticum aestivum proteome. 2017 , 89, 601-616	37
1155	Annexin A2 and alpha actinin 4 expression correlates with metastatic potential of primary endometrial cancer. 2017 , 1865, 846-857	18
1154	Peptide serum markers in islet autoantibody-positive children. 2017 , 60, 287-295	13
1153	Characterization of Receptor-Associated Protein Complex Assembly in Interleukin (IL)-2- and IL-15-Activated T-Cell Lines. 2017 , 16, 106-121	3
1152	N-linked glycosite profiling and use of Skyline as a platform for characterization and relative quantification of glycans in differentiating xylem of Populus trichocarpa. 2017 , 409, 487-497	18
1151	Computational quality control tools for mass spectrometry proteomics. 2017 , 17, 1600159	23
1150	Multiplexed panel of precisely quantified salivary proteins for biomarker assessment. 2017 , 17, 1600230	10
1149	Parallel reaction monitoring of clinical Mycobacterium tuberculosis lineages reveals pre-existent markers of rifampicin tolerance in the emerging Beijing lineage. 2017 , 150, 9-17	8
1148	Multicentric study of the effect of pre-analytical variables in the quality of plasma samples stored in biobanks using different complementary proteomic methods. 2017 , 150, 109-120	22
1147	PeptideTracker: A knowledge base for collecting and storing information on protein concentrations in biological tissues. 2017 , 17, 1600210	14
1146	Tandem mass spectral libraries of peptides and their roles in proteomics research. 2017 , 36, 634-648	31

1145	Supporting metabolomics with adaptable software: design architectures for the end-user. 2017 , 43, 110-117	8
1144	Multiplex Biomarker Techniques. 2017 ,	4
1143	Multi-omics Analysis of Serum Samples Demonstrates Reprogramming of Organ Functions Via Systemic Calcium Mobilization and Platelet Activation in Metastatic Melanoma. 2017 , 16, 86-99	27
1142	Multiplexed mass spectrometry monitoring of biomarker candidates for osteoarthritis. 2017 , 152, 216-225	23
1141	DAPAR & ProStaR: software to perform statistical analyses in quantitative discovery proteomics. <i>Bioinformatics</i> , 2017 , 33, 135-136	7.2 116
1140	Proteomic discovery and verification of serum amyloid A as a predictor marker of patients at risk of post-stroke infection: a pilot study. 2017 , 14, 27	18
1139	Identification of an enterovirus recombinant with a torovirus-like gene insertion during a diarrhea outbreak in fattening pigs. 2017 , 3, vex024	20
1138	A Comprehensive Assessment of the Genetic Determinants in Salmonella Typhimurium for Resistance to Hydrogen Peroxide Using Proteogenomics. 2017 , 7, 17073	18
1137	Monitoring of the spatial and temporal dynamics of BER/SSBR pathway proteins, including MYH, UNG2, MPG, NTH1 and NEIL1-3, during DNA replication. 2017 , 45, 8291-8301	18
1136	Minimum-noise production of translation factor eIF4G maps to a mechanistically determined optimal rate control window for protein synthesis. 2017 , 45, 1015-1025	14
1135	Prediction of Hopeless Peptides Unlikely to be Selected for Targeted Proteome Analysis. 2017 , 6, A0056	6
1134	Csk-homologous kinase (Chk) is an efficient inhibitor of Src-family kinases but a poor catalyst of phosphorylation of their C-terminal regulatory tyrosine. 2017 , 15, 29	5
1133	Performing Quantitative Determination of Low-Abundant Proteins by Targeted Mass Spectrometry Liquid Chromatography. 2017 ,	0
1132	$\beta\beta$ binding to a fibrinogen fragment lacking the α -chain dodecapeptide is activation dependent and EDTA inducible. 2017 , 1, 417-428	8
1131	Quantitative Proteomic Profiling of Tachyplesin I Targets in U251 Gliomaspheres. 2017 , 15,	11
1130	mzStudio: A Dynamic Digital Canvas for User-Driven Interrogation of Mass Spectrometry Data. 2017 , 5,	15
1129	Quantification of Cardiovascular Disease Biomarkers in Human Platelets by Targeted Mass Spectrometry. 2017 , 5,	8
1128	Characterization of Two Historic Smallpox Specimens from a Czech Museum. 2017 , 9,	18

1127	Impact of fibrinogen carbamylation on fibrin clot formation and stability. 2017 , 117, 899-910	31
1126	RNA polymerase II stalling at pre-mRNA splice sites is enforced by ubiquitination of the catalytic subunit. 2017 , 6,	11
1125	A Timely Shift from Shotgun to Targeted Proteomics and How It Can Be Groundbreaking for Cancer Research. 2017 , 7, 13	32
1124	Systematic proteomic analysis of LRRK2-mediated Rab GTPase phosphorylation establishes a connection to ciliogenesis. 2017 , 6,	211
1123	Cervical Cancer Cell Line Secretome Highlights the Roles of Transforming Growth Factor-Beta-Induced Protein ig-h3, Peroxiredoxin-2, and NRF2 on Cervical Carcinogenesis. 2017 , 2017, 4180703	27
1122	Evaluation of a Bead-Free Coimmunoprecipitation Technique for Identification of Virus-Host Protein Interactions Using High-Resolution Mass Spectrometry. 2017 , 28, 111-121	4
1121	Determining bacteriophage endopeptidase activity using either fluorophore-quencher labeled peptides combined with liquid chromatography-mass spectrometry (LC-MS) or Förster resonance energy transfer (FRET) assays. 2017 , 12, e0173919	12
1120	The cytoprotective protein clusterin is overexpressed in hypergastrinemic rodent models of oxyntic preneoplasia and promotes gastric cancer cell survival. 2017 , 12, e0184514	6
1119	Characterization of host proteins interacting with the lymphocytic choriomeningitis virus L protein. 2017 , 13, e1006758	12
1118	Proteomics investigation of OSCC-specific salivary biomarkers in a Hungarian population highlights the importance of identification of population-tailored biomarkers. 2017 , 12, e0177282	39
1117	The role of the two-component systems Cpx and Arc in protein alterations upon gentamicin treatment in Escherichia coli. 2017 , 17, 197	7
1116	Quantification of mutant SPOP proteins in prostate cancer using mass spectrometry-based targeted proteomics. 2017 , 15, 175	5
1115	Targeted proteomics reveals promising biomarkers of disease activity and organ involvement in antineutrophil cytoplasmic antibody-associated vasculitis. 2017 , 19, 218	29
1114	Human iPSC Models in Drug Discovery: Opportunities and Challenges. 2017 , 48-73	4
1113	Clinical Validation of a Serum Protein Panel (FLNA, FLNB and KRT19) for Diagnosis of Prostate Cancer. 2017 , 8,	11
1112	Characterisation of iunH gene knockout strain from Mycobacterium tuberculosis. 2017 , 112, 203-208	5
1111	Food Allergen Analysis: Detection, Quantification and Validation by Mass Spectrometry. 2017 ,	5
1110	Proteomic Adaptation of Australian Epidemic Bordetella pertussis. 2018 , 18, e1700237	12

1109	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
1108	Proteomic Identification of Interferon-Induced Proteins with Tetratricopeptide Repeats as Markers of M1 Macrophage Polarization. 2018 , 17, 1485-1499	19
1107	Infection and the Human Proteome with a Special Focus on the Immunoglobulin G-cleaving Enzyme IdeS. 2018 , 17, 1097-1111	9
1106	On the Reproducibility of Label-Free Quantitative Cross-Linking/Mass Spectrometry. 2018 , 29, 405-412	27
1105	Picky: a simple online PRM and SRM method designer for targeted proteomics. 2018 , 15, 156-157	25
1104	HU protein is involved in intracellular growth and full virulence of <i>Francisella tularensis</i> . 2018 , 9, 754-770	9
1103	Advancing translational research and precision medicine with targeted proteomics. 2018 , 189, 1-10	44
1102	A fully validated liquid chromatography-mass spectrometry method for the quantification of the soluble receptor of advanced glycation end-products (sRAGE) in serum using immunopurification in a 96-well plate format. 2018 , 182, 414-421	20
1101	An Internal Standard for Assessing Phosphopeptide Recovery from Metal Ion/Oxide Enrichment Strategies. 2018 , 29, 1505-1511	20
1100	Combined BRAF and HSP90 Inhibition in Patients with Unresectable -Mutant Melanoma. 2018 , 24, 5516-5524	37
1099	Thermal proteome profiling of breast cancer cells reveals proteasomal activation by CDK4/6 inhibitor palbociclib. 2018 , 37,	52
1098	Improving wood properties for wood utilization through multi-omics integration in lignin biosynthesis. 2018 , 9, 1579	96
1097	Selected reaction monitoring mass spectrometry of mastitis milk reveals pathogen-specific regulation of bovine host response proteins. 2018 , 101, 6532-6541	18
1096	Quantification of Site-specific Protein Lysine Acetylation and Succinylation Stoichiometry Using Data-independent Acquisition Mass Spectrometry. 2018 ,	6
1095	Pseudotargeted MS Method for the Sensitive Analysis of Protein Phosphorylation in Protein Complexes. 2018 , 90, 6214-6221	8
1094	Analysis of Histone Modifications by Mass Spectrometry. 2018 , 92, e54	10
1093	Rapid Assessment of Contaminants and Interferences in Mass Spectrometry Data Using Skyline. 2018 , 29, 1327-1330	15
1092	Revolutionizing Precision Oncology through Collaborative Proteogenomics and Data Sharing. 2018 , 173, 535-539	44

1091	Quantification of Urinary Protein Biomarkers of Autosomal Dominant Polycystic Kidney Disease by Parallel Reaction Monitoring. 2018 , 12, e1700157	3
1090	Multiple reaction monitoring targeted LC-MS analysis of potential cell death marker proteins for increased bioprocess control. 2018 , 410, 3197-3207	6
1089	Loss of histone H3K27me3 identifies a subset of meningiomas with increased risk of recurrence. 2018 , 135, 955-963	61
1088	A Library of Phosphoproteomic and Chromatin Signatures for Characterizing Cellular Responses to Drug Perturbations. 2018 , 6, 424-443.e7	47
1087	Nrf2 deficiency exacerbates age-related contractile dysfunction and loss of skeletal muscle mass. 2018 , 17, 47-58	38
1086	Dynamics of PARKIN-Dependent Mitochondrial Ubiquitylation in Induced Neurons and Model Systems Revealed by Digital Snapshot Proteomics. 2018 , 70, 211-227.e8	95
1085	Parallel reaction monitoring on a Q Exactive mass spectrometer increases reproducibility of phosphopeptide detection in bacterial phosphoproteomics measurements. 2018 , 189, 60-66	6
1084	Accurate Measurement of Formaldehyde-Induced DNA-Protein Cross-Links by High-Resolution Orbitrap Mass Spectrometry. 2018 , 31, 350-357	11
1083	Protein Turnover in Aging and Longevity. 2018 , 18, e1700108	44
1082	A protease cascade regulates release of the human malaria parasite Plasmodium falciparum from host red blood cells. 2018 , 3, 447-455	55
1081	Targeting KRAS Mutant Cancers with a Covalent G12C-Specific Inhibitor. 2018 , 172, 578-589.e17	507
1080	Prediction of the Hydrogen Peroxide-Induced Methionine Oxidation Propensity in Monoclonal Antibodies. 2018 , 107, 1282-1289	13
1079	Deficient Follistatin-like 3 Secretion by Asthmatic Airway Epithelium Impairs Fibroblast Regulation and Fibroblast-to-Myofibroblast Transition. 2018 , 59, 104-113	11
1078	UFD-2 is an adaptor-assisted E3 ligase targeting unfolded proteins. 2018 , 9, 484	12
1077	Quantitative proteomics and SWATH-MS to elucidate peri-receptor mechanisms in human salt taste sensitivity. 2018 , 254, 95-102	9
1076	Manual method of visually identifying candidate signals for a targeted peptide. 2018 , 1083, 258-270	0
1075	Leveraging Formylglycine-Generating Enzyme for Production of Site-Specifically Modified Bioconjugates. 2018 , 1728, 3-16	6
1074	Redox responses are preserved across muscle fibres with differential susceptibility to aging. 2018 , 177, 112-123	16

1073	Nonlinear Regression Improves Accuracy of Characterization of Multiplexed Mass Spectrometric Assays. 2018 , 17, 913-924	14
1072	Establishment of Dimethyl Labeling-based Quantitative Acetylproteomics in Arabidopsis. 2018 , 17, 1010-1027	19
1071	Differential Proteomics for Distinguishing Ischemic Stroke from Controls: a Pilot Study of the SpecTRA Project. 2018 , 9, 590-599	10
1070	Characterizing disease-associated changes in post-translational modifications by mass spectrometry. 2018 , 15, 245-258	28
1069	Asb2/Filamin A Axis Is Essential for Actin Cytoskeleton Remodeling During Heart Development. 2018 , 122, e34-e48	18
1068	Proteomics in Domestic Animals: from Farm to Systems Biology. 2018 ,	2
1067	Bioinformatics Support for Farm Animal Proteomics. 2018 , 361-386	
1066	Gel-Free Proteomics. 2018 , 55-101	
1065	Microfluidics-based LC-MS MRM approach for the relative quantification of Burkholderia cenocepacia secreted virulence factors. 2018 , 32, 469	4
1064	Structures of human PRC2 with its cofactors AEBP2 and JARID2. 2018 , 359, 940-944	109
1063	Variability Assessment of 90 Salivary Proteins in Intraday and Interday Samples from Healthy Donors by Multiple Reaction Monitoring-Mass Spectrometry. 2018 , 12, 1700039	11
1062	Updates on resources, software tools, and databases for plant proteomics in 2016-2017. 2018 , 39, 1543-1557	11
1061	Discovery and Validation of Novel Protein Biomarkers in Ovarian Cancer Patient Urine. 2018 , 12, e1700135	24
1060	Development of a Targeted Mass-Spectrometry Serum Assay To Quantify M-Protein in the Presence of Therapeutic Monoclonal Antibodies. 2018 , 17, 1326-1333	25
1059	Cellular Concentrations of the Transporters DctA and DcuB and the Sensor DcuS of Escherichia coli and the Contributions of Free and Complexed DcuS to Transcriptional Regulation by DcuR. 2018 , 200,	5
1058	Quantitative proteomics identifies redox switches for global translation modulation by mitochondrially produced reactive oxygen species. 2018 , 9, 324	100
1057	Mitochondrial translation requires folate-dependent tRNA methylation. 2018 , 554, 128-132	119
1056	Glutathione S-Transferase Protein Expression in Different Life Stages of Zebrafish (Danio rerio). 2018 , 162, 702-712	22

1055	Recent advances in mass spectrometry-based approaches for proteomics and biologics: Great contribution for developing therapeutic antibodies. 2018 , 185, 147-154	39
1054	The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. 2018 , 6, 13-24	199
1053	Is cupping blister harmful?-A proteomical analysis of blister fluid induced by cupping therapy and scald. 2018 , 36, 25-29	4
1052	Authentication of leguminous-based products by targeted biomarkers using high resolution time of flight mass spectrometry. 2018 , 90, 164-171	11
1051	Determining Linear Free Energy Relationships in Peptide Fragmentation Using Derivatization and Targeted Mass Spectrometry. 2018 , 90, 1587-1594	4
1050	Human disease glycomics: technology advances enabling protein glycosylation analysis - part 1. 2018 , 15, 165-182	21
1049	-Glycoproteomic Characterization of Mannosidase and Xylosyltransferase Mutant Strains of. 2018 , 176, 1952-1964	14
1048	Lactobacillus casei asp23 gene contributes to gentamycin resistance via regulating specific membrane-associated proteins. 2018 , 101, 1915-1920	7
1047	Specific TCell Responses against Minor Histocompatibility Antigens Cannot Generally Be Explained by Absence of Their Allelic Counterparts on the Cell Surface. 2018 , 18, e1700250	13
1046	Large Scale Identification of Variant Proteins in Glioma Stem Cells. 2018 , 9, 73-79	8
1045	Deciphering Multifactorial Resistance Phenotypes in by Genomics and Targeted Label-free Proteomics. 2018 , 17, 442-456	17
1044	Mass Spectrometry-Based Identification of Extracellular Domains of Cell Surface N-Glycoproteins: Defining the Accessible Surfaceome for Immunophenotyping Stem Cells and Their Derivatives. 2018 , 1722, 57-78	6
1043	Liquid Chromatography-High Resolution Mass Spectrometry Analysis of Platelet Frataxin as a Protein Biomarker for the Rare Disease Friedreich's Ataxia. 2018 , 90, 2216-2223	28
1042	Quantitative mass spectrometry imaging of glutathione in healthy and cancerous hen ovarian tissue sections by infrared matrix-assisted laser desorption electrospray ionization (IR-MALDESI). 2018 , 143, 654-661	25
1041	A functional link between NAD homeostasis and N-terminal protein acetylation in. 2018 , 293, 2927-2938	13
1040	Interplay of SpkG kinase and the Slr0151 protein in the phosphorylation of ferredoxin 5 in Synechocystis sp. strain PCC 6803. 2018 , 592, 411-421	11
1039	Membranal and Blood-Soluble HLA Class II Peptidome Analyses Using Data-Dependent and Independent Acquisition. 2018 , 18, e1700246	17
1038	CHCHD10 mutations p.R15L and p.G66V cause motoneuron disease by haploinsufficiency. 2018 , 27, 706-715	21

1037	Perturbing the acetylation status of the Type IV pilus retraction motor, PilT, reduces <i>Neisseria gonorrhoeae</i> viability. 2018 , 110, 677-688	2
1036	Activation peptide of the coagulation factor XIII (AP-F13A1) as a new biomarker for the screening of colorectal cancer. 2018 , 15, 15	6
1035	Molecular architecture of mouse and human pancreatic zymogen granules: protein components and their copy numbers. 2018 , 4, 94-103	3
1034	Quantitative targeted proteomic analysis of potential markers of tyrosine kinase inhibitor (TKI) sensitivity in EGFR mutated lung adenocarcinoma. 2018 , 189, 48-59	7
1033	A Targeted Proteomic Approach for Heat Shock Proteins Reveals DNAJB4 as a Suppressor for Melanoma Metastasis. 2018 , 90, 6835-6842	21
1032	Newt cells secrete extracellular vesicles with therapeutic bioactivity in mammalian cardiomyocytes. 2018 , 7, 1456888	19
1031	Detection and quantitation of immunogenic epitopes related to celiac disease in historical and modern hard red spring wheat cultivars. 2018 , 264, 101-107	26
1030	A Multiplexed Mass Spectrometry-Based Assay for Robust Quantification of Phosphosignaling in Response to DNA Damage. 2018 , 189, 505-518	15
1029	Discrimination of Isomers of Released N- and O-Glycans Using Diagnostic Product Ions in Negative Ion PGC-LC-ESI-MS/MS. 2018 , 29, 1194-1209	56
1028	Does fluoxetine exposure affect hypoxia tolerance in the Gulf toadfish, <i>Opsanus beta</i> ?. 2018 , 199, 55-64	7
1027	Specter: linear deconvolution for targeted analysis of data-independent acquisition mass spectrometry proteomics. 2018 , 15, 371-378	35
1026	The promise of targeted proteomics for quantitative network biology. 2018 , 54, 88-97	13
1025	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
1024	Single-nephron proteomes connect morphology and function in proteinuric kidney disease. 2018 , 93, 1308-1319	32
1023	Cost-effective generation of precise label-free quantitative proteomes in high-throughput by microLC and data-independent acquisition. 2018 , 8, 4346	38
1022	In Vivo Quantitative Monitoring of Subunit Stoichiometry for Metabolic Complexes. 2018 , 17, 1773-1783	3
1021	Targeted Quantification of Phosphorylation Dynamics in the Context of EGFR-MAPK Pathway. 2018 , 90, 5256-5263	27
1020	Conventional-Flow Liquid Chromatography-Mass Spectrometry for Exploratory Bottom-Up Proteomic Analyses. 2018 , 90, 5381-5389	20

1019	Circulating Sphingolipids, Insulin, HOMA-IR, and HOMA-B: The Strong Heart Family Study. 2018 , 67, 1663-1672	85
1018	Integrated SWATH-based and targeted-based proteomics provide insights into the retinal emmetropization process in guinea pig. 2018 , 181, 1-15	16
1017	Industrial brewing yeast engineered for the production of primary flavor determinants in hopped beer. 2018 , 9, 965	99
1016	Quantitation of myosin regulatory light chain phosphorylation in biological samples with multiple reaction monitoring mass spectrometry. 2018 , 1866, 608-616	2
1015	Locally translated mTOR controls axonal local translation in nerve injury. 2018 , 359, 1416-1421	130
1014	Detection and quantitation of irisin in human cerebrospinal fluid by tandem mass spectrometry. 2018 , 103, 60-64	28
1013	N-Terminomics identifies HtrA1 cleavage of thrombospondin-1 with generation of a proangiogenic fragment in the polarized retinal pigment epithelial cell model of age-related macular degeneration. 2018 , 70, 84-101	16
1012	Conversations with 100 Scientists in the Field Reveal a Bifurcated Perception of the State of Mass Spectrometry Software. 2018 , 17, 1335-1339	4
1011	The COMMD Family Regulates Plasma LDL Levels and Attenuates Atherosclerosis Through Stabilizing the CCC Complex in Endosomal LDLR Trafficking. 2018 , 122, 1648-1660	53
1010	Evaluation of microcystin contamination in blue-green algal dietary supplements using a protein phosphatase inhibition-based test kit. 2018 , 4, e00573	21
1009	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
1008	Panorama Public: A Public Repository for Quantitative Data Sets Processed in Skyline. 2018 , 17, 1239-1244	91
1007	Apical-to-basolateral transepithelial transport of cow's milk caseins by intestinal Caco-2 cell monolayers: MS-based quantitation of cellularly degraded β -casein fragments. 2018 , 164, 113-125	7
1006	Protein Turnover Measurements in Human Serum by Serial Immunoaffinity LC-MS/MS. 2018 , 64, 279-288	13
1005	Proteomics in plasma of ovariectomized rats and those exposed to estradiol valerate. 2018 , 178, 1-12	8
1004	Comparative Degradomics of Porcine and Human Wound Exudates Unravels Biomarker Candidates for Assessment of Wound Healing Progression in Trauma Patients. 2018 , 138, 413-422	16
1003	Comparison of Whole Body SOD1 Knockout with Muscle-Specific SOD1 Knockout Mice Reveals a Role for Nerve Redox Signaling in Regulation of Degenerative Pathways in Skeletal Muscle. 2018 , 28, 275-295	31
1002	Plant Membrane Proteomics. 2018 ,	

1001	Comparison of Targeted Mass Spectrometry Techniques with an Immunoassay: A Case Study for HSP90 α . 2018 , 12, 1700107	12
1000	Evidence of microglial activation following exposure to serum from first-onset drug-naïve schizophrenia patients. 2018 , 67, 364-373	10
999	Evaluation of a SPLUNC1-derived peptide for the treatment of cystic fibrosis lung disease. 2018 , 314, L192-L205	21
998	Quantitative Profiling of N-linked Glycosylation Machinery in Yeast. 2018 , 17, 18-30	18
997	Disulfide Mapping PLanner Software Tool. 2018 , 25, 430-434	
996	Global quantification of phosphoproteins combining metabolic labeling and gel-based proteomics in <i>B. pumilus</i> . 2018 , 39, 334-343	5
995	Mutant JAK3 phosphoproteomic profiling predicts synergism between JAK3 inhibitors and MEK/BCL2 inhibitors for the treatment of T-cell acute lymphoblastic leukemia. 2018 , 32, 788-800	50
994	Nitric oxide prevents Aft1 activation and metabolic remodeling in frataxin-deficient yeast. 2018 , 14, 131-141	7
993	Quantification of Coagulation Factor VIII by Selective Reaction Monitoring. 2018 , 1674, 275-282	
992	Development of a data independent acquisition mass spectrometry workflow to enable glycopeptide analysis without predefined glycan compositional knowledge. 2018 , 172, 68-75	30
991	Microfluidic Separation Coupled to Mass Spectrometry for Quantification of Peanut Allergens in a Complex Food Matrix. 2018 , 17, 647-655	21
990	Simultaneous quantification of succinylacetone and nitisinone for therapeutic drug monitoring in the treatment of Tyrosinemia type 1. 2018 , 1072, 259-266	4
989	Photoreceptor glucose metabolism determines normal retinal vascular growth. 2018 , 10, 76-90	27
988	A 14-Protein Signature for Rapid Identification of Poor Prognosis Stage III Metastatic Melanoma. 2018 , 12, e1700094	
987	Study of a novel agent for TCA precipitated proteins washing - comprehensive insights into the role of ethanol/HCl on molten globule state by multi-spectroscopic analyses. 2018 , 173, 77-88	6
986	Dual Data-Independent Acquisition Approach Combining Global HCP Profiling and Absolute Quantification of Key Impurities during Bioprocess Development. 2018 , 90, 1241-1247	12
985	Best-Matched Internal Standard Normalization in Liquid Chromatography-Mass Spectrometry Metabolomics Applied to Environmental Samples. 2018 , 90, 1363-1369	47
984	Phosphoprotein DIGE profiles reflect blast differentiation, cytogenetic risk stratification, FLT3/NPM1 mutations and therapy response in acute myeloid leukaemia. 2018 , 173, 32-41	8

983	Differential impacts of individual and combined exposures of deoxynivalenol and zearalenone on the HepaRG human hepatic cell proteome. 2018 , 173, 89-98	9
982	Effects of Alanyl-Glutamine Treatment on the Peritoneal Dialysis Effluent Proteome Reveal Pathomechanism-Associated Molecular Signatures. 2018 , 17, 516-532	14
981	Genetic Variants in ERAP1 and ERAP2 Associated With Immune-Mediated Diseases Influence Protein Expression and the Isoform Profile. 2018 , 70, 255-265	34
980	Targeted Quantification of Isoforms of a Thylakoid-Bound Protein: MRM Method Development. 2018 , 1696, 147-162	1
979	Development of a LC-MS method for the discrimination between trace level Prunus contaminants of spices. 2018 , 245, 289-296	7
978	Characterization of the Molecular Mechanisms Underlying Glucose Stimulated Insulin Secretion from Isolated Pancreatic β cells Using Post-translational Modification Specific Proteomics (PTMomics). 2018 , 17, 95-110	20
977	Comparison of Quantitative Mass Spectrometry Platforms for Monitoring Kinase ATP Probe Uptake in Lung Cancer. 2018 , 17, 63-75	13
976	The sweet spot for biologics: recent advances in characterization of biotherapeutic glycoproteins. 2018 , 15, 13-29	42
975	Proteomic profiling of TGFBI-null mouse corneas reveals only minor changes in matrix composition supportive of TGFBI knockdown as therapy against TGFBI-linked corneal dystrophies. 2018 , 285, 101-114	18
974	Towards a one-stop solution for large-scale proteomics data analysis. 2018 , 61, 351-354	2
973	Parallel comparative proteomics and phosphoproteomics reveal that cattle regulates phosphorylation of key enzymes in glycogen metabolism and glycolysis pathway. 2018 , 9, 11352-11370	23
972	Systematic verification of bladder cancer-associated tissue protein biomarker candidates in clinical urine specimens. 2018 , 9, 30731-30747	10
971	Difference in Mono-O-Glucosylation of Ras Subtype GTPases Between Toxin A and Toxin B From Strain 10463 and Lethal Toxin From Strain 6018. 2018 , 9, 3078	8
970	Attached stratified mucus separates bacteria from the epithelial cells in COPD lungs. 2018 , 3,	25
969	Phosphorylation-Dependent Inhibition of Akt1. 2018 , 9,	19
968	Impact of biological matrix on inflammatory protein biomarker quantification based on targeted mass spectrometry. 2018 , 10, 1383-1399	4
967	From Synapse to Function: A Perspective on the Role of Neuroproteomics in Elucidating Mechanisms of Drug Addiction. 2018 , 6,	4
966	SEPROGADIC - serum protein-based gastric cancer prediction model for prognosis and selection of proper adjuvant therapy. 2018 , 8, 16892	4

965	The Interaction Dynamics of Two Potato Leafroll Virus Movement Proteins Affects Their Localization to the Outer Membranes of Mitochondria and Plastids. 2018 , 10,	15
964	Data-Independent Acquisition Mass Spectrometry To Quantify Protein Levels in FFPE Tumor Biopsies for Molecular Diagnostics. 2019 , 18, 426-435	11
963	Development of parallel reaction monitoring (PRM)-based quantitative proteomics applied to HER2-Positive breast cancer. 2018 , 9, 33762-33777	13
962	Ethylene Receptors, CTRs and EIN2 Target Protein Identification and Quantification Through Parallel Reaction Monitoring During Tomato Fruit Ripening. 2018 , 9, 1626	25
961	Interactome and Proteome Dynamics Uncover Immune Modulatory Associations of the Pathogen Sensing Factor cGAS. 2018 , 7, 627-642.e6	24
960	Targeted Quantitative Profiling of GTP-Binding Proteins in Cancer Cells Using Isotope-Coded GTP Probes. 2018 , 90, 14339-14346	11
959	Roles of Small GTPases in Acquired Tamoxifen Resistance in MCF-7 Cells Revealed by Targeted, Quantitative Proteomic Analysis. 2018 , 90, 14551-14560	5
958	Evaluation of Different Decellularization Protocols on the Generation of Pancreas-Derived Hydrogels. 2018 , 24, 697-708	37
957	HLA-B57 micropolymorphism defines the sequence and conformational breadth of the immunopeptidome. 2018 , 9, 4693	19
956	Analysis of significant protein abundance from multiple reaction-monitoring data. 2018 , 12, 123	
955	Distinct Roles of Two Histone Methyltransferases in Transmitting H3K36me3-Based Epigenetic Memory Across Generations in. 2018 , 210, 969-982	16
954	The depolymerase activity of MCAK shows a graded response to Aurora B kinase phosphorylation through allosteric regulation. 2019 , 132,	11
953	Absolute Quantification of in Grapevine Leaf and Petiole Tissues by Proteomics. 2018 , 9, 1735	8
952	Rapid Multiplexed Proteomic Screening for Primary Immunodeficiency Disorders From Dried Blood Spots. 2018 , 9, 2756	15
951	Comparison of the Whole Cell Proteome and Secretome of Epidemic Strains From the 2008-2012 Australian Epidemic Under Sulfate-Modulating Conditions. 2018 , 9, 2851	8
950	Irisin Mediates Effects on Bone and Fat via α 5 β 1 Integrin Receptors. 2018 , 175, 1756-1768.e17	207
949	Comparative Flavivirus-Host Protein Interaction Mapping Reveals Mechanisms of Dengue and Zika Virus Pathogenesis. 2018 , 175, 1931-1945.e18	148
948	Co-occurring KRAS mutation/LKB1 loss in non-small cell lung cancer cells results in enhanced metabolic activity susceptible to caloric restriction: an in vitro integrated multilevel approach. 2018 , 37, 302	14

947	Discovery and Quantification of Nonhuman Proteins in Human Milk. 2019 , 18, 225-238	16
946	Quantitative Proteomics Evaluation of Human Multipotent Stromal Cell for Cell Regeneration. 2018 , 25, 2524-2536.e4	6
945	Proteomic Analysis of S-Palmitoylated Proteins in Ocular Lens Reveals Palmitoylation of AQP5 and MP20. 2018 , 59, 5648-5658	5
944	200+ Protein Concentrations in Healthy Human Blood Plasma: Targeted Quantitative SRM SIS Screening of Chromosomes 18, 13, Y, and the Mitochondrial Chromosome Encoded Proteome. 2019 , 18, 120-129	12
943	Chromatogram libraries improve peptide detection and quantification by data independent acquisition mass spectrometry. 2018 , 9, 5128	143
942	Combined Targeted Analysis of Metabolites and Proteins in Tear Fluid With Regard to Clinical Applications. 2018 , 7, 22	11
941	Sensoproteomics: A New Approach for the Identification of Taste-Active Peptides in Fermented Foods. 2018 , 66, 11092-11104	15
940	Glucocerebrosidase deficiency promotes protein aggregation through dysregulation of extracellular vesicles. 2018 , 14, e1007694	19
939	Infection-Induced Peroxisome Biogenesis Is a Metabolic Strategy for Herpesvirus Replication. 2018 , 24, 526-541.e7	36
938	New Antibody-Free Mass Spectrometry-Based Quantification Reveals That C9ORF72 Long Protein Isoform Is Reduced in the Frontal Cortex of Hexanucleotide-Repeat Expansion Carriers. 2018 , 12, 589	14
937	Identification of Helicase Proteins as Clients for HSP90. 2018 , 90, 11751-11755	13
936	In vivo Proteomics Approaches for the Analysis of Bacterial Adaptation Reactions in Host-Pathogen Settings. 2018 , 1841, 207-228	
935	SRM-MS Method Development for Hepcidin-25 Peptide. 2018 , 2018, 9653747	3
934	Expanding the Use of Spectral Libraries in Proteomics. 2018 , 17, 4051-4060	26
933	Combining Chemical Genetics with Proximity-Dependent Labeling Reveals Cellular Targets of Poly(ADP-ribose) Polymerase 14 (PARP14). 2018 , 13, 2841-2848	23
932	RNA editing derived epitopes function as cancer antigens to elicit immune responses. 2018 , 9, 3919	54
931	Microbial Proteomics. 2018 ,	
930	Quantification of Vitamin B-Related Proteins in Marine Microbial Systems Using Selected Reaction Monitoring Mass Spectrometry. 2018 , 1849, 87-98	1

929	Accurate quantification of Hexosaminidase released from laboratory of allergic diseases 2 cells via liquid chromatography tandem mass spectrometry method. 2018 , 1578, 106-111	7
928	Protein Dynamics in Solution by Quantitative Crosslinking/Mass Spectrometry. 2018 , 43, 908-920	34
927	Enhanced validation of antibodies for research applications. 2018 , 9, 4130	48
926	Memory enhancement by ferulic acid ester across species. 2018 , 4, eaat6994	11
925	Identification of Novel Protein Lysine Acetyltransferases in Escherichia coli. 2018 , 9,	39
924	Drug response prediction model using a hierarchical structural component modeling method. 2018 , 19, 288	1
923	Targeted LC-MS/MS Reveals Similar Contents of α -Amylase/Trypsin-Inhibitors as Putative Triggers of Nonceliac Gluten Sensitivity in All Wheat Species except Einkorn. 2018 , 66, 12395-12403	42
922	A dual regulatory circuit consisting of S-adenosylmethionine decarboxylase protein and its reaction product controls expression of the paralogous activator prozyme in Trypanosoma brucei. 2018 , 14, e1007404	3
921	Application of Proteomics Technologies in Oil Palm Research. 2018 , 37, 473-499	4
920	PWWP2A binds distinct chromatin moieties and interacts with an MTA1-specific core NuRD complex. 2018 , 9, 4300	22
919	Humanization of the Blood-Brain Barrier Transporter ABCB1 in Mice Disrupts Genomic Locus - Lessons from Three Unsuccessful Approaches. 2018 , 8, 78-86	2
918	apQuant: Accurate Label-Free Quantification by Quality Filtering. 2019 , 18, 535-541	33
917	Calibration Using a Single-Point External Reference Material Harmonizes Quantitative Mass Spectrometry Proteomics Data between Platforms and Laboratories. 2018 , 90, 13112-13117	18
916	Plasma lipoproteome in Alzheimer's disease: a proof-of-concept study. 2018 , 15, 31	7
915	Detection of Residual Proteins UL5 and UL29 Using a Targeted Proteomics Approach in HSV29, a Replication-Deficient HSV-2 Vaccine Candidate. 2018 , 107, 3022-3031	3
914	A surface endogalactanase in Bacteroides thetaiotaomicron confers keystone status for arabinogalactan degradation. 2018 , 3, 1314-1326	57
913	A comparative analysis of label-free liquid chromatography-mass spectrometry liver proteomic profiles highlights metabolic differences between pig breeds. 2018 , 13, e0199649	7
912	Functional Proteomics and Deep Network Interrogation Reveal a Complex Mechanism of Action of Midostaurin in Lung Cancer Cells. 2018 , 17, 2434-2447	9

911	Streamlined microfluidic analysis of phosphopeptides using stable isotope-labeled synthetic peptides and MRM-MS detection. 2018 , 39, 3171-3184	3
910	Combining discovery and targeted proteomics reveals a prognostic signature in oral cancer. 2018 , 9, 3598	81
909	Challenges and Opportunities for Biological Mass Spectrometry Core Facilities in the Developing World. 2018 , 29, 4-15	4
908	Phosphotyrosine profiling of human cerebrospinal fluid. 2018 , 15, 29	12
907	Proteomic Response to Thaxtomin Phytotoxin Elicitor Cellobiose and to Deletion of Cellulose Utilization Regulator CebR in <i>Streptomyces scabies</i> . 2018 , 17, 3837-3852	6
906	Differential Roles of the Thylakoid Luminal Deg Protease Homologs in Chloroplast Proteostasis. 2018 , 178, 1065-1080	14
905	Comparative Targeted Proteomics of the Central Metabolism and Photosystems in SigE Mutant Strains of sp. PCC 6803. 2018 , 23,	8
904	The MAP4 Kinase SIK1 Ensures Robust Extracellular ROS Burst and Antibacterial Immunity in Plants. 2018 , 24, 379-391.e5	57
903	Identification of Peptide Biomarkers for Discrimination of Shrimp Species through SWATH-MS-Based Proteomics and Chemometrics. 2018 , 66, 10567-10574	23
902	Label-Free Proteomic Approach to Characterize Protease-Dependent and -Independent Effects of sarA Inactivation on the <i>Staphylococcus aureus</i> Exoproteome. 2018 , 17, 3384-3395	12
901	Layers of regulation of cell-cycle gene expression in the budding yeast <i>Saccharomyces cerevisiae</i> . 2018 , 29, 2644-2655	6
900	Identification of Changing Ribosome Protein Compositions using Mass Spectrometry. 2018 , 18, e1800217	18
899	Proteomics. 2018 , 1-17	1
898	Stability of histone post-translational modifications in samples derived from liver tissue and primary hepatic cells. 2018 , 13, e0203351	3
897	The Protein Coded by a Short Open Reading Frame, Not by the Annotated Coding Sequence, Is the Main Gene Product of the Dual-Coding Gene. 2018 , 17, 2402-2411	26
896	Assembling the Community-Scale Discoverable Human Proteome. 2018 , 7, 412-421.e5	68
895	Selenocysteine-Specific Mass Spectrometry Reveals Tissue-Distinct Selenoproteomes and Candidate Selenoproteins. 2018 , 25, 1380-1388.e4	20
894	A <i>Bordetella pertussis</i> MgtC homolog plays a role in the intracellular survival. 2018 , 13, e0203204	8

893	Mapping Cellular Polarity Networks Using Mass Spectrometry-based Strategies. 2018 , 430, 3545-3564	5
892	Quantification of Serum High Mobility Group Box 1 by Liquid Chromatography/High-Resolution Mass Spectrometry: Implications for Its Role in Immunity, Inflammation, and Cancer. 2018 , 90, 7552-7560	10
891	Activity-dependent neuroprotective protein recruits HP1 and CHD4 to control lineage-specifying genes. 2018 , 557, 739-743	68
890	Curcumin exerts its antitumor effects in a context dependent fashion. 2018 , 182, 65-72	10
889	Nano-LC/NSI MS Refines Lipidomics by Enhancing Lipid Coverage, Measurement Sensitivity, and Linear Dynamic Range. 2018 , 90, 8093-8101	54
888	Concentration-dependent protein loading of extracellular vesicles released by <i>Histoplasma capsulatum</i> after antibody treatment and its modulatory action upon macrophages. 2018 , 8, 8065	45
887	Global untargeted serum metabolomic analyses nominate metabolic pathways responsive to loss of expression of the orphan metallo β -lactamase, MBLAC1. 2018 , 14, 142-155	4
886	Naturally Occurring Variants in LRP1 (Low-Density Lipoprotein Receptor-Related Protein 1) Affect HDL (High-Density Lipoprotein) Metabolism Through ABCA1 (ATP-Binding Cassette A1) and SR-B1 (Scavenger Receptor Class B Type 1) in Humans. 2018 , 38, 1440-1453	10
885	MRMAssayDB: an integrated resource for validated targeted proteomics assays. <i>Bioinformatics</i> , 2018 , 34, 3566-3571	7.2 20
884	Identification of potential biomarkers of head and neck squamous cell carcinoma using iTRAQ based quantitative proteomic approach. 2018 , 19, 1124-1130	6
883	Tools and protocol for quantification of myosin phosphorylation with MRM-MS. 2018 , 5, 466-474	
882	Early urinary candidate biomarker discovery in a rat thioacetamide-induced liver fibrosis model. 2018 , 61, 1369-1381	15
881	The clinical outcome of LMNA missense mutations can be associated with the amount of mutated protein in the nuclear envelope. 2018 , 20, 1404-1412	10
880	A new method for measuring thyroid hormones using nano-LC-MS/MS. 2018 , 1093-1094, 24-30	13
879	Proteomic characterization of six Taiwanese snake venoms: Identification of species-specific proteins and development of a SISCAPA-MRM assay for cobra venom factors. 2018 , 187, 59-68	18
878	Analysis of <i>Staphylococcus aureus</i> proteins secreted inside infected human epithelial cells. 2018 , 308, 664-674	2
877	Kinome rewiring reveals AURKA limits PI3K-pathway inhibitor efficacy in breast cancer. 2018 , 14, 768-777	39
876	Proteomics Approach To Trace Site-Specific Damage in Aquatic Extracellular Enzymes During Photoinactivation. 2018 , 52, 7671-7679	6

875	Polyprotein strategy for stoichiometric assembly of nitrogen fixation components for synthetic biology. 2018 , 115, E8509-E8517	44
874	Co-regulatory networks of human serum proteins link genetics to disease. 2018 , 361, 769-773	183
873	A Targeted Quantitative Proteomic Approach Assesses the Reprogramming of Small GTPases during Melanoma Metastasis. 2018 , 78, 5431-5445	14
872	Discovery of the Consistently Well-Performed Analysis Chain for SWATH-MS Based Pharmacoproteomic Quantification. 2018 , 9, 681	52
871	Mechanistic insights into the cellular effects of a novel FN1 variant associated with a spondylometaphyseal dysplasia. 2018 , 94, 429-437	7
870	Proteomics reveals Rictor as a noncanonical TGF- β signaling target during aneurysm progression in Marfan mice. 2018 , 315, H1112-H1126	12
869	Pharmacokinetics, Safety, and Clinical Efficacy of Cannabidiol Treatment in Osteoarthritic Dogs. 2018 , 5, 165	74
868	Discrimination and quantification of homologous keratins from goat and sheep with dual protease digestion and PRM assays. 2018 , 186, 38-46	1
867	Proteomic Methods of Detection and Quantification of Protein Toxins. 2018 , 10,	33
866	Using Skyline to Analyze Data-Containing Liquid Chromatography, Ion Mobility Spectrometry, and Mass Spectrometry Dimensions. 2018 , 29, 2182-2188	33
865	Impact of Phosphoproteomics in the Era of Precision Medicine for Prostate Cancer. 2018 , 8, 28	15
864	Systems pharmacology using mass spectrometry identifies critical response nodes in prostate cancer. 2018 , 4, 26	7
863	A large-scale and robust dynamic MRM study of colorectal cancer biomarkers. 2018 , 187, 80-92	12
862	Comprehensive overview and recent advances in proteomics MS based methods for food allergens analysis. 2018 , 106, 21-36	47
861	MS analysis of a dilution series of bacteria:phytoplankton to improve detection of low abundance bacterial peptides. 2018 , 8, 9276	2
860	Molecular phenotyping of laboratory mouse strains using 500 multiple reaction monitoring mass spectrometry plasma assays. 2018 , 1, 78	15
859	Adverse Outcome Pathway-Driven Analysis of Liver Steatosis in Vitro: A Case Study with Cyproconazole. 2018 , 31, 784-798	34
858	Reconstituting Arabidopsis CRY2 Signaling Pathway in Mammalian Cells Reveals Regulation of Transcription by Direct Binding of CRY2 to DNA. 2018 , 24, 585-593.e4	18

857	Structural and functional changes in RNase A originating from tyrosine and histidine cross-linking and oxidation induced by singlet oxygen and peroxy radicals. 2018 , 126, 73-86	22
856	H drives metabolic rearrangements in gas-fermenting. 2018 , 11, 55	62
855	Current Mass Spectrometric Tools for the Bioanalyses of Therapeutic Monoclonal Antibodies and Antibody-Drug Conjugates. 2018 , 34, 397-406	19
854	Comparative salivary proteomics analysis of children with and without dental caries using the iTRAQ/MRM approach. 2018 , 16, 11	21
853	Proteomics-based insights into mitogen-activated protein kinase inhibitor resistance of cerebral melanoma metastases. 2018 , 15, 13	8
852	Potential molecular mechanisms of overgrazing-induced dwarfism in sheepgrass (<i>Leymus chinensis</i>) analyzed using proteomic data. 2018 , 18, 81	3
851	Computational Methods for Understanding Mass Spectrometry-Based Shotgun Proteomics Data. 2018 , 1, 207-234	82
850	Monitoring of Plant Protein Post-translational Modifications Using Targeted Proteomics. 2018 , 9, 1168	32
849	Improved Sensitivity and Separations for Phosphopeptides using Online Liquid Chromatography Coupled with Structures for Lossless Ion Manipulations Ion Mobility-Mass Spectrometry. 2018 , 90, 10889-10896 ²⁴	24
848	Tissue Proteomics. 2018 ,	
847	Evaluation of Serum Glycoprotein Biomarker Candidates for Detection of Esophageal Adenocarcinoma and Surveillance of Barrett's Esophagus. 2018 , 17, 2324-2334	14
846	A Novel LC System Embeds Analytes in Pre-formed Gradients for Rapid, Ultra-robust Proteomics. 2018 , 17, 2284-2296	133
845	Assessing the reproducibility of an O-glycopeptide enrichment method with a novel software, Pinnacle. 2018 , 39, 3142-3147	2
844	Axonal G3BP1 stress granule protein limits axonal mRNA translation and nerve regeneration. 2018 , 9, 3358	59
843	Targeted LC-MS/MS for the evaluation of proteomics biomarkers in the blood of neonates with necrotizing enterocolitis and late-onset sepsis. 2018 , 410, 7163-7175	11
842	Determining Allele-Specific Protein Expression (ASPE) Using a Novel Quantitative Concatamer Based Proteomics Method. 2018 , 17, 3606-3612	14
841	XCMS-MRM and METLIN-MRM: a cloud library and public resource for targeted analysis of small molecules. 2018 , 15, 681-684	69
840	Data-independent acquisition-based SWATH-MS for quantitative proteomics: a tutorial. 2018 , 14, e8126	389

839	Basis of Mass Spectrometry. 2018 , 19-45	0
838	Absolute two-point quantification of proteins using dimethylated proteotypic peptides. 2018 , 143, 4359-4365	1
837	statTarget: A streamlined tool for signal drift correction and interpretations of quantitative mass spectrometry-based omics data. 2018 , 1036, 66-72	57
836	Parkin and PINK1 mitigate STING-induced inflammation. 2018 , 561, 258-262	509
835	A decade of understanding secondary metabolism in <i>Pseudomonas</i> spp. for sustainable agriculture and pharmaceutical applications. 2018 , 1, 3-17	9
834	Seasonal Changes in Endocannabinoid Concentrations between Active and Hibernating Marmots (<i>Marmota flaviventris</i>). 2018 , 33, 388-401	13
833	Insights into the role of androgen receptor in human testicular peritubular cells. 2018 , 6, 756-765	13
832	Target Selection Strategies for LC-MS/MS Food Allergen Methods. 2018 , 101, 146-151	14
831	Sex steroids mediate discrete effects on HDL cholesterol efflux capacity and particle concentration in healthy men. 2018 , 12, 1072-1082	12
830	Assessment of Recovery of Milk Protein Allergens from Processed Food for Mass Spectrometry Quantification. 2018 , 101, 152-161	8
829	A Targeted LC-MS/MS Method for the Simultaneous Detection and Quantitation of Egg, Milk, and Peanut Allergens in Sugar Cookies. 2018 , 101, 108-117	29
828	Targeted brain proteomics uncover multiple pathways to Alzheimer's dementia. 2018 , 84, 78-88	56
827	Serum Proteomic Profiling to Identify Biomarkers of Premature Carotid Atherosclerosis. 2018 , 8, 9209	12
826	Type 2 diabetes is associated with loss of HDL endothelium protective functions. 2018 , 13, e0192616	36
825	The <i>Xanthomonas euvesicatoria</i> type III effector XopAU is an active protein kinase that manipulates plant MAP kinase signaling. 2018 , 14, e1006880	18
824	Post-translational quantitation by SRM/MRM: applications in cardiology. 2018 , 15, 477-502	5
823	Comparative analysis of fermentation and enzyme expression profiles among industrial <i>Saccharomyces cerevisiae</i> strains. 2018 , 102, 7071-7081	3
822	Future Prospects of Spectral Clustering Approaches in Proteomics. 2018 , 18, e1700454	10

821	Expression of dopamine D2 and D3 receptors in the human retina revealed by positron emission tomography and targeted mass spectrometry. 2018 , 175, 32-41	9
820	Quantification of Inflammasome Adaptor Protein ASC in Biological Samples by Multiple-Reaction Monitoring Mass Spectrometry. 2018 , 41, 1396-1408	4
819	Obesity and Insulin Resistance Promote Atherosclerosis through an IFN γ -Regulated Macrophage Protein Network. 2018 , 23, 3021-3030	41
818	D-Cateslytin: a new antifungal agent for the treatment of oral <i>Candida albicans</i> associated infections. 2018 , 8, 9235	10
817	Novel Approaches for the MS-Based Detection of Food Allergens: High Resolution, MS \square and Beyond. 2018 , 101, 124-131	11
816	Proteomic Analysis of Aqueous Humor from Primary Open Angle Glaucoma Patients on Drug Treatment Revealed Altered Complement Activation Cascade. 2018 , 17, 2499-2510	14
815	Using Stepwise Pharmacogenomics and Proteomics to Predict Hepatitis C Treatment Response in Difficult to Treat Patient Populations. 2019 , 13, e1800006	1
814	Automated workflow composition in mass spectrometry-based proteomics. <i>Bioinformatics</i> , 2019 , 35, 656-664	7.2 23
813	Phenotyping and relative quantification of vitamin D binding protein in a paediatric population by using liquid chromatography-tandem mass spectrometry. 2019 , 56, 56-63	
812	Proteomics Mass Spectrometry Data Analysis Tools. 2019 , 84-95	2
811	The Prion Protein Regulates Synaptic Transmission by Controlling the Expression of Proteins Key to Synaptic Vesicle Recycling and Exocytosis. 2019 , 56, 3420-3436	7
810	Combination of label-free quantitative proteomics and transcriptomics reveals intraspecific venom variation between the two strains of <i>Tetrastichus brontispae</i> , a parasitoid of two invasive beetles. 2019 , 192, 37-53	14
809	Ariadne's Thread in the Analytical Labyrinth of Membrane Proteins: Integration of Targeted and Shotgun Proteomics for Global Absolute Quantification of Membrane Proteins. 2019 , 91, 11972-11980	4
808	hSWATH: Unlocking SWATH's Full Potential for an Untargeted Histone Perspective. 2019 , 18, 3840-3849	8
807	Lysozyme-Assisted Photothermal Eradication of Methicillin-Resistant Infection and Accelerated Tissue Repair with Natural Melanosome Nanostructures. 2019 , 13, 11153-11167	49
806	Maternal-to-zygotic transition as a potential target for niclosamide during early embryogenesis. 2019 , 380, 114699	7
805	HSP90 inhibitors stimulate DNAJB4 protein expression through a mechanism involving N-methyladenosine. 2019 , 10, 3613	15
804	Oxidative stress adaptation improves the heat tolerance of <i>Pseudomonas fluorescens</i> SN15-2. 2019 , 138, 104070	7

803	Manganese and iron deficiency in Southern Ocean <i>Phaeocystis antarctica</i> populations revealed through taxon-specific protein indicators. 2019 , 10, 3582	22
802	Mutations in <i>RABL3</i> alter <i>KRAS</i> prenylation and are associated with hereditary pancreatic cancer. 2019 , 51, 1308-1314	31
801	Attenuation of Equine Lentivirus Alters Mitochondrial Protein Expression Profile from Inflammation to Apoptosis. 2019 , 93,	2
800	<i>cindr</i> , the <i>Drosophila</i> Homolog of the <i>CD2AP</i> Alzheimer's Disease Risk Gene, Is Required for Synaptic Transmission and Proteostasis. 2019 , 28, 1799-1813.e5	16
799	Rebuilding core abscisic acid signaling pathways of <i>Arabidopsis</i> in yeast. 2019 , 38, e101859	15
798	Potential roles of gut microbiome and metabolites in modulating ALS in mice. 2019 , 572, 474-480	240
797	A conserved role of the insulin-like signaling pathway in diet-dependent uric acid pathologies in <i>Drosophila melanogaster</i> . 2019 , 15, e1008318	20
796	Serum glycoprotein biomarker validation for esophageal adenocarcinoma and application to Barrett's surveillance.	1
795	DIA-NN: Deep neural networks substantially improve the identification performance of Data-independent acquisition (DIA) in proteomics.	1
794	Urine proteome changes in a TNBS-induced colitis rat model.	0
793	A comparative analysis of label-free liquid chromatography-mass spectrometry liver proteomic profiles highlights metabolic differences between pig breeds.	0
792	Rapidly Assessing the Quality of Targeted Proteomics Experiments Through Monitoring Stable-isotope Labeled Standards.	
791	FlashPack: Fast and simple preparation of ultra-high performance capillary columns for LC-MS.	0
790	New insights into the ORF2 capsid protein, a key player of the hepatitis E virus lifecycle.	
789	Pacific geoduck (<i>Panopea generosa</i>) resilience to natural pH variation.	0
788	Massively parallel fitness profiling reveals multiple novel enzymes in <i>Pseudomonas putida</i> lysine metabolism.	1
787	Comprehensive proteomic and metabolomic profiling of <i>mcr-1</i> mediated colistin resistance in <i>Escherichia coli</i> .	
786	Hetero-oligomeric CPN60 resembles highly symmetric group I chaperonin structure revealed by Cryo-EM.	

- 785 Characterization of Pacific oyster (*Crassostrea gigas*) proteomic response to natural environmental differences.
- 784 Data-Independent Acquisition Mass Spectrometry to Localize Phosphosites.
- 783 Screening a Resource of Recombinant Protein Fragments for Targeted Proteomics. 1
- 782 Identification of Human Blood Plasma Proteins Using Spike-In Peptides in Shotgun Proteomics. **2019**, 2, e00093
- 781 Advances in Mass Spectrometry-Based Proteomics and Its Application in Cancer Research. **2019**, 89-112
- 780 Cindr, the *Drosophila* Homolog of the CD2AP Alzheimer's Disease Susceptibility Gene, is Required for Synaptic Transmission and Proteostasis. 0
- 779 Neuropeptidomics of the Mammalian Brain. **2019**, 161-177
- 778 Measuring amber initiator tRNA orthogonality in a genomically recoded organism.
- 777 Sweet revenge - *Streptococcus pyogenes* showcases first example of immune evasion through specific IgG glycan hydrolysis.
- 776 An essential RNA-binding lysine residue in the Nab3 RRM domain undergoes mono and trimethylation.
- 775 Avant-garde: An automated data-driven DIA data curation tool. 2
- 774 CRK2 and C-terminal phosphorylation of NADPH oxidase RBOHD regulate ROS production in *Arabidopsis*. 1
- 773 Scalable data analysis in proteomics and metabolomics using BioContainers and workflows engines. 0
- 772 MetaMSD: meta analysis for mass spectrometry data. **2019**, 7, e6699 1
- 771 Automated high-throughput proteome and phosphoproteome analysis using paramagnetic bead technology.
- 770 Fast and accurate bacterial species identification in biological samples using LC-MS/MS mass spectrometry and machine learning.
- 769 Generating high-quality libraries for DIA-MS with empirically-corrected peptide predictions. 1
- 768 MAP2 is Differentially Phosphorylated in Schizophrenia, Altering its Function. 0

- 767 Targeted Clinical Metabolomics Platform for the Stratification of Diabetic Patients. 1
- 766 Targeted phosphoproteomics of the Ras signaling network reveal regulatory mechanisms mediated by oncogenic KRAS. 1
- 765 Mass Spectrometry-Based Plasma Proteomics: Considerations from Sample Collection to Achieving Translational Data. 1
- 764 Loss of function from widely distributed, synonymous mutations at single codons.
- 763 Domain model explains propagation dynamics and stability of K27 and K36 methylation landscapes.
- 762 Methyl-Metabolite Depletion Elicits Adaptive Responses to Support Heterochromatin Stability and Epigenetic Persistence.
- 761 Differential urine proteome analysis of a bovine IRBP induced uveitis rat model by discovery and parallel reaction monitoring proteomics.
- 760 HIGD2A is required for assembly of the COX3 module of human mitochondrial complex IV. 2
- 759 Reference glycan structure libraries of primary human cardiomyocytes and pluripotent stem cell-derived cardiomyocytes reveal cell-type and culture stage-specific glycan phenotypes.
- 758 Chemical genetics of AGC-kinases reveals shared targets of Ypk1, Protein Kinase A and Sch9.
- 757 Novel insights into N-glycan fucosylation and core xylosylation in *C. reinhardtii*.
- 756 Maternally-transferred thyroid hormones and life-history variation in birds.
- 755 Adaptive iron utilization compensates for the lack of an inducible uptake system in *Naegleria fowleri* and represents a potential target for therapeutic intervention.
- 754 Measurement of organ-specific and acute-phase blood protein levels in early Lyme disease.
- 753 Sphingosine 1-phosphate-regulated transcriptomes in heterogeneous arterial and lymphatic endothelium of the aorta.
- 752 Absolute quantification of transcription factors reveals principles of gene regulation in erythropoiesis. 0
- 751 The proteome of small urinary extracellular vesicles after kidney transplantation as an indicator of renal cellular biology and a source for markers predicting outcome.
- 750 Neutrophil extracellular trap formation correlates with improved overall survival in ovarian cancer.

- 749 Mechanism underlying autoinducer recognition in the *Vibrio cholerae* DPO-VqmA quorum-sensing pathway.
- 748 Prevalence and impact of oprD mutations in *Pseudomonas aeruginosa* strains in cystic fibrosis.
- 747 Parental effects via glyphosate-based herbicides in a bird model? ○
- 746 Quantification of the anti-murine PD-1 monoclonal antibody RMP1-14 in BALB/c mouse plasma by liquid chromatography-tandem mass spectrometry and application to a pharmacokinetic study. **2020, 412, 739-752**
- 745 Lysine Acetylation Reshapes The Downstream Signaling Landscape of Vav1 in Lymphocytes. ○
- 744 Development of a novel method for the quantification of tyrosine 39 phosphorylated alpha-synuclein in human cerebrospinal fluid.
- 743 DPHL: A pan-human protein mass spectrometry library for robust biomarker discovery. 1
- 742 Development of a novel method for the quantification of tyrosine 39 phosphorylated alpha-synuclein in human cerebrospinal fluid.
- 741 Technical Report: Targeted Proteomic Analysis Reveals Enrichment of Atypical Ubiquitin Chains in Contractile Murine Tissues.
- 740 Wnt-inducible Lrp6-APEX2 Interacting Proteins Identify ESCRT Machinery and Trk-Fused Gene as Components of the Wnt Signaling Pathway.
- 739 Computational modeling reveals cell-cycle dependent kinetics of H4K20 methylation states during *Xenopus* embryogenesis.
- 738 Genome modularization reveals overlapped gene topology is necessary for efficient viral reproduction. ○
- 737 Rub1/NEDD8, a ubiquitin-like modifier, is also a ubiquitin modifier.
- 736 Identification and Evaluation of Serum Protein Biomarkers Which Differentiate Psoriatic from Rheumatoid Arthritis.
- 735 Functional Characterization of the Lin28/let-7 Circuit during Forelimb Regeneration in *Ambystoma mexicanum* and its Influence on Metabolic Reprogramming.
- 734 Selected reaction monitoring for the quantification of *Escherichia coli* ribosomal proteins.
- 733 Mitotic activity shapes stage-specific histone modification profiles during *Xenopus* embryogenesis.
- 732 Peak identification and quantification by proteomic mass spectrogram decomposition.

731	DIAFree enables untargeted open-search identification for Data-Independent Acquisition data.	
730	Detection of Discordant Peptide Quantities in Shotgun Proteomics Data by Peptide Correlation Analysis (PeCorA).	1
729	The roseoloviruses downregulate the protein tyrosine phosphatase PTPRC (CD45).	0
728	Deciphering the Interregional and Interhemisphere Proteome of the Human Brain in the Context of the Human Proteome Project. 2021 , 20, 5280-5293	3
727	Data-Independent Acquisition Mass Spectrometry of the Human Lens Enhances Spatiotemporal Measurement of Fiber Cell Aging. 2021 , 32, 2755-2765	0
726	Design of a Quantitative LC-MS Method for Residual Toxins Adenylate Cyclase Toxin (ACT), Dermonecrotic Toxin (DNT) and Tracheal Cytotoxin (TCT) in Vaccines. 2021 , 13,	
725	Proteomic analysis of hypothalamus in prepubertal and pubertal female goat. 2022 , 251, 104411	0
724	Isolation and Identification of Dengue Virus Interactome with Human Plasma Proteins by Affinity Purification-Mass Spectrometry. 2022 , 2409, 133-153	
723	The hepatocyte export carrier inhibition assay improves the separation of hepatotoxic from non-hepatotoxic compounds. 2021 , 351, 109728	4
722	DeepLC can predict retention times for peptides that carry as-yet unseen modifications. 2021 , 18, 1363-1369	18
721	A simple tool extends TIMSTOF compatibility with historic data processing tools and enables ion mobility-enhanced spectral libraries.	
720	Intramuscular Evaluation of Chimeric Locked Nucleic Acid/2'Methyl-Modified Antisense Oligonucleotides for Targeted Exon 23 Skipping in Mdx Mice. 2021 , 14,	
719	The innate immunity protein C1QBP functions as a negative regulator of circulative transmission of Potato leafroll virus by aphids.	
718	Estimating the number of protein molecules in a plant cell: protein and amino acid homeostasis during drought. 2021 , 185, 385-404	8
717	Honeybee gut microbiota modulates host behaviors and neurological processes.	1
716	Plasma Amino Acid Response to Whey Protein Ingestion Following 28 Days of Probiotic (DE111) Supplementation in Active Men and Women. 2020 , 6,	2
715	The infection-tolerant mammalian reservoir of Lyme disease and other zoonoses broadly counters the inflammatory effects of endotoxin.	
714	Targeted quantification of phosphorylation sites identifies STRIPAK-dependent phosphorylation of the Hippo pathway-related kinase SmKIN3.	

- 713 Functional Significance of Conserved Cysteines in the Extracellular Loops of the ATP Binding Cassette Transporter Pdr11p. **2020**, 7, 1
- 712 Prochlorococcus extracellular vesicles: Molecular composition and adsorption to diverse microbes.
- 711 Selected reaction monitoring for the quantification of Escherichia coli ribosomal proteins. **2020**, 15, e0236850 1
- 710 A tale of solving two computational challenges in protein science: neoantigen prediction and protein structure prediction. **2021**, 0
- 709 Omics Approaches to determine protease degradomes in complex biological matrices. **2022**, 209-228
- 708 Elucidation of xenoestrogen metabolism by non-targeted, stable isotope-assisted mass spectrometry in breast cancer cells. **2021**, 158, 106940 1
- 707 Development of an analytical method to detect simultaneously 219 new psychoactive substances and 65 other substances in urine specimens using LC-QqQ MS/MS with CriticalPairFinder and TransitionFinder. **2022**, 238, 122979 1
- 706 Broad and thematic remodeling of the surface glycoproteome on isogenic cells transformed with driving proliferative oncogenes.
- 705 Protein Interactome of the Cancerous Inhibitor of Protein Phosphatase 2A (CIP2A) in Th17 Cells.
- 704 A Consensus Proteomic Analysis of Alzheimer's Disease Brain and Cerebrospinal Fluid Reveals Early Changes in Energy Metabolism Associated with Microglia and Astrocyte Activation. 1
- 703 Bioinformatics Tools for SRM-MS. **2020**, 115-144
- 702 Intermittent hypoxia promotes functional neuroprotection from retinal ischemia in untreated first-generation offspring.
- 701 The Nucleosome Remodeling and Deacetylase complex has an asymmetric, dynamic, and modular architecture.
- 700 Fast quantitative analysis of timsTOF PASEF data with MSFragger and IonQuant. 3
- 699 A comprehensive proteomic SWATH-MS workflow for profiling blood extracellular vesicles: a new avenue for glioma tumour surveillance. 0
- 698 Recapitulating evolutionary divergence in a single cis-regulatory element is sufficient to cause expression changes of the lens gene Tdrd7.
- 697 Organized cannabinoid receptor distribution in neurons revealed by super-resolution fluorescence imaging.
- 696 A PEROXO-Tag enables rapid isolation of peroxisomes from human cells. 1

- 695 Cryo-EM structure of coronavirus-HKU1 haemagglutinin esterase reveals architectural changes arising from prolonged circulation in humans.
- 694 A multiplexed work-flow for absolute quantification of *Klebsiella oxytoca* Nif proteins.
- 693 Development of a novel method for the quantification of tyrosine 39 phosphorylated α - and β -synuclein in human cerebrospinal fluid.
- 692 Light contamination in stable isotope-labelled internal peptide standards is frequent and a potential source of false discovery and quantitation error in proteomics.
- 691 Down-Regulation of Phosphoenolpyruvate Carboxylase Kinase in Grapevine Cell Cultures and Leaves Is Linked to Enhanced Resveratrol Biosynthesis. **2021**, 11, 0
- 690 In vitro reconstitution of the *Escherichia coli* 70S ribosome with a full set of recombinant ribosomal proteins. **2021**, 1
- 689 Peptide barcoding for one-pot evaluation of sequence-function relationships of nanobodies. **2021**, 11, 21516
- 688 SmartPeak automates targeted and quantitative metabolomics data processing.
- 687 Protein kinase A controls the hexosamine pathway by tuning the feedback inhibition of GFAT-1.
- 686 ELOVL2 is required for robust visual function in zebrafish.
- 685 A TMT-based quantitative proteomic analysis provides insights into the protein changes in the seeds of high- and low- protein content soybean cultivars. **2020**, 47, 209-217 3
- 684 Proteomics study of colorectal cancer and adenomatous polyps identifies TFR1, SAHH, and HV307 as potential biomarkers for screening.
- 683 Rice Calcium/Calmodulin-Dependent Protein Kinase Directly Phosphorylates a Mitogen-Activated Protein Kinase Kinase to Regulate Abscisic Acid Responses.
- 682 SETD2 regulates the methylation of translation elongation factor eEF1A1 in clear cell renal cell carcinoma. 0
- 681 Intra-axonal translation of *Khsrp* mRNA slows axon regeneration by destabilizing localized mRNAs.
- 680 Targeted detection and quantitation of histone modifications from 1,000 cells. **2020**, 15, e0240829 0
- 679 Targeted Proteomics Reveals Quantitative Differences in Low Abundance Glycosyltransferases of Patients with Congenital Disorders of Glycosylation. 0
- 678 Mapping Isoform Abundance and Interactome of the Endogenous TMPRSS2-ERG Fusion Protein with Orthogonal Immunoprecipitation-Mass Spectrometry Assays.

677	First 3D-Structural Data of Full-length Rod-Outer-Segment Guanylyl Cyclase 1 in Bovine Retina by Cross-linking/Mass Spectrometry.	
676	SARS-CoV-2 Innate Effector Associations and Viral Load in Early Nasopharyngeal Infection. 2020 ,	1
675	A Recombinant Protein Biomarker DDA Library Increases DIA Coverage of Low Abundance Plasma Proteins.	
674	Peptide Ancestry Informative Markers in Uterine Neoplasms from Women of European, African and Asian Ancestry.	
673	ProteoSushi: a software tool to biologically annotate and quantify modification-specific, peptide-centric proteomics datasets.	
672	Deciphering the LRRK code: LRRK1 and LRRK2 phosphorylate distinct Rab proteins and are regulated by diverse mechanisms.	0
671	Quantification of individual proteins in silicone hydrogel contact lens deposits. 2013 , 19, 390-9	8
670	Differential proteomics analysis of mononuclear cells in cerebrospinal fluid of Parkinson's disease. 2015 , 8, 15462-6	2
669	Investigation of cattle plasma proteome in response to pain and inflammation using next generation proteomics technique, SWATH-MS. 2021 ,	0
668	Mitochondrial proteomics reveals new insights into embryogenic competence acquisition in <i>Carica papaya</i> L. callus. 2021 , 252, 104434	
667	Targeted Mass Spectrometry Enables Multiplexed Quantification of Immunomodulatory Proteins in Clinical Biospecimens. 2021 , 12, 765898	3
666	Proteomics of : From the Lab to the Clinic. 2021 , 22,	2
665	Novel protein markers of androgen activity in humans: proteomic study of plasma from young chemically castrated men.	0
664	<i>Prochlorococcus</i> extracellular vesicles: molecular composition and adsorption to diverse microbes. 2021 ,	1
663	SARS-CoV-2 ORF8 encoded protein contains a histone mimic, disrupts chromatin regulation, and enhances replication.	0
662	DeepPhospho accelerates DIA phosphoproteome profiling through in silico library generation. 2021 , 12, 6685	4
661	Proteomics Profiling to Distinguish DOCK8 Deficiency From Atopic Dermatitis.. 2021 , 2, 774902	1
660	Semi-Quantitative Multiplex Profiling of the Complement System Identifies Associations of Complement Proteins with Genetic Variants and Metabolites in Age-Related Macular Degeneration.. 2021 , 11,	0

659	Patterns of gene expression in pollen of cotton (<i>Gossypium hirsutum</i>) indicate down-regulation as a feature of thermotolerance. 2021 ,	0
658	Development of a Standardized Microflow LC Gradient to Enable Sensitive and Long-Term Detection of Synthetic Anabolic-Androgenic Steroids for High-Throughput Doping Controls. 2021 , 93, 15590-15596	0
657	Targeted Detection of SARS-CoV-2 Nucleocapsid Sequence Variants by Mass Spectrometric Analysis of Tryptic Peptides. 2021 ,	2
656	Increased carvone production in <i>Escherichia coli</i> by balancing limonene conversion enzyme expression via targeted quantification concatamer proteome analysis. 2021 , 11, 22126	0
655	Potential Use of Serum Proteomics for Monitoring COVID-19 Progression to Complement RT-PCR Detection. 2021 ,	1
654	Insight into ALKBH8-related intellectual developmental disability based on the first pathogenic missense variant. 2021 , 1	2
653	Does Data-Independent Acquisition Data Contain Hidden Gems? A Case Study Related to Alzheimer's Disease. 2021 ,	1
652	Application of Skyline for Analysis of Protein-Protein Interactions In Vivo. 2021 , 26,	0
651	Posttranscriptional Regulation of the Human LDL Receptor by the U2-Spliceosome. 2021 ,	2
650	Global ubiquitylation analysis of mitochondria in primary neurons identifies endogenous Parkin targets following activation of PINK1. 2021 , 7, eabj0722	5
649	Post-translational modification patterns on β -myosin heavy chain are altered in ischemic and non-ischemic human hearts.	
648	Multilayered regulation of autophagy by the Atg1 kinase orchestrates spatial and temporal control of autophagosome formation. 2021 ,	3
647	Uncovering Xenobiotics in the Dark Metabolome using Ion Mobility Spectrometry, Mass Defect Analysis and Machine Learning.	0
646	Plasma cell dependence on histone/protein deacetylase 11 reveals a therapeutic target in multiple myeloma. 2021 ,	3
645	Targeted Selected Reaction Monitoring Verifies Histology Specific Peptide Signatures in Epithelial Ovarian Cancer. 2021 , 13,	
644	Candesartan prevents arteriopathy progression in cerebral autosomal recessive arteriopathy with subcortical infarcts and leukoencephalopathy model. 2021 , 131,	3
643	Min waves without MinC can pattern FtsA-FtsZ filaments on model membranes.	
642	Proteomic analysis of liver tissue reveals <i>Aeromonas hydrophila</i> infection mediated modulation of host metabolic pathways in <i>Labeo rohita</i> .	0

641	Integrative Transcriptomics and Proteomics Analyses to Reveal the Developmental Regulation of : A Neglected Trematode With Potential Carcinogenic Implications.. 2021 , 11, 783662	
640	Improving the Speed and Selectivity of Newborn Screening Using Ion Mobility Spectrometry-Mass Spectrometry. 2021 ,	7
639	Convergent Cerebrospinal Fluid Proteomes and Metabolic Ontologies in Humans and Animal Models of Rett Syndrome.	
638	Quantitative Chemoproteomic Profiling with Data-Independent Acquisition-Based Mass Spectrometry.. 2022 ,	3
637	Integrated proteomic and metabolomic analyses of the mitochondrial neurodegenerative disease MELAS.. 2022 ,	1
636	Associations of established breast cancer risk factors with urinary estrogens in postmenopausal women.. 2022 , 1	
635	Debottlenecking 4-hydroxybenzoate hydroxylation in <i>Pseudomonas putida</i> KT2440 improves muconate productivity from p-coumarate.. 2022 , 70, 31-42	3
634	Autoantibody and hormone activation of the thyrotropin G protein-coupled receptor.	0
633	Omega-6 and Omega-3 Fatty Acid-Derived Oxylipins from the Lipoxygenase Pathway in Maternal and Umbilical Cord Plasma at Delivery and Their Relationship with Infant Growth.. 2022 , 23,	0
632	Getting more out of FLAG-Tag co-immunoprecipitation mass spectrometry experiments using FAIMS.. 2022 , 254, 104473	0
631	Mass spectrometric detection of KRAS protein mutations using molecular imprinting. 2021 ,	2
630	Development of a Standardized MRM Method for the Quantification of One Carbon Metabolism Enzymes.. 2022 , 2420, 159-175	0
629	Organ-Based Proteome and Post-Translational Modification Profiling of a Widely Cultivated Tropical Water Fish, .. 2021 ,	2
628	Multi-omic profiling of histone variant H3.3 lysine 27 methylation reveals a distinct role from canonical H3 in stem cell differentiation.. 2022 ,	
627	Enabling Quantitative Analysis of Surface Small Molecules for Exposomics and Behavioral Studies.. 2022 ,	
626	Needler: An Algorithm to Develop a Comprehensive Targeted MS Method Capable of Monitoring the Human Proteome.	
625	Mice harboring the FXN I151F pathological point mutation present decreased frataxin levels, a Friedreich ataxia-like phenotype, and mitochondrial alterations.. 2022 , 79, 74	1
624	Targeted Profiling of Epitranscriptomic Reader, Writer, and Eraser Proteins Accompanied with Radioresistance in Breast Cancer Cells.. 2022 ,	3

623	The Parallel Reaction Monitoring-Parallel Accumulation-Serial Fragmentation (prm-PASEF) Approach for Multiplexed Absolute Quantitation of Proteins in Human Plasma.. 2022,	7
622	Mechanisms for Improving Hepatic Glucolipid Metabolism by Cinnamic Acid and Cinnamic Aldehyde: An Insight Provided by Multi-Omics.. 2021, 8, 794841	0
621	Differential Histone Posttranslational Modifications Induced by DNA Hypomethylating Agents.. 2022, 29, 10732748221074051	0
620	Quantitative proteomics revealed new functions of ALKBH4.. 2021, e2100231	
619	Integrated transcriptome and proteome analysis reveals brassinosteroid-mediated regulation of cambium initiation and patterning in woody stem.. 2022, 9,	1
618	Effect of the Post-Harvest Processing on Protein Modification in Green Coffee Beans by Phenolic Compounds.. 2022, 11,	2
617	Mannose-binding lectin and complement mediate follicular localization and enhanced immunogenicity of diverse protein nanoparticle immunogens.. 2022, 38, 110217	1
616	DIA proteomics data from a UPS1-spiked protein mixture processed with six software tools.. 2022, 41, 107829	0
615	Quantitative proteomics and phosphoproteomics of urinary extracellular vesicles define diagnostic and prognostic biosignatures for Parkinson's Disease.	0
614	Thiamine-dependent regulation of mammalian brain pyridoxal kinase in vitro and in vivo.. 2022,	1
613	Methods for Quantification of Glycopeptides by Liquid Separation and Mass Spectrometry.. 2022,	0
612	Mutations in SARS-CoV-2 variants of concern link to increased spike cleavage and virus transmission.. 2022,	23
611	Complex marine microbial communities partition metabolism of scarce resources over the diel cycle.. 2022,	1
610	Chromatin alterations during the epididymal maturation of mouse sperm refine the paternally inherited epigenome.. 2022, 15, 2	0
609	Codon optimality is the primary contributor to the exceptional mutational sensitivity of CcdA antitoxin in its operonic context.	0
608	Peptide ancestry informative markers in uterine neoplasms from women of European, African, and Asian ancestry.. 2022, 25, 103665	0
607	SecMS analysis of selenoproteins with selenocysteine insertion sequence and beyond.. 2022, 662, 227-240	
606	Data-Independent Acquisition Approach to Proteome: A Case Study and a Spectral Library for Mass Spectrometry-Based Investigation of .. 2022,	

605	Nascent peptide-induced translation discontinuation in eukaryotes impacts biased amino acid usage in proteomes.	
604	Small Heat Shock Protein 22 Improves Cognition and Learning in the Tauopathic Brain.. 2022 , 23,	0
603	Amplification of human interneuron progenitors promotes brain tumors and neurological defects.. 2022 , 375, eabf5546	7
602	Comparative Proteomic Analysis Reveals Metformin Improves the Expression of Biomarkers of Endometrial Receptivity in Infertile Women with Minimal/Mild Endometriosis.. 2022 , 1	0
601	Distinct salinity-induced changes in wheat metabolic machinery in different root tissue types.. 2022 , 256, 104502	1
600	Molecular mechanisms involved in Atlantic halibut (<i>Hippoglossus hippoglossus</i>) egg quality: impairments at transcription and protein folding levels induce inefficient protein and energy homeostasis during early development.	
599	Mass spectrometry and proteome analysis to identify SARS-CoV-2 protein from COVID-19 patient swab samples.. 2022 , 3, 101177	0
598	High-performance nano-flow liquid chromatography column combined with high- and low-collision energy data-independent acquisition enables targeted and discovery identification of modified ribonucleotides by mass spectrometry.. 2022 , 1665, 462803	2
597	Spotlight on alternative frame coding: Two long overlapping genes in are translated and under purifying selection.. 2022 , 25, 103844	2
596	Significant impact of mTORC1 and ATF4 pathways in CHO cell recombinant protein production induced by CDK4/6 inhibitor.. 2022 ,	0
595	Acarbose suppresses symptoms of mitochondrial disease in a mouse model of Leigh Syndrome.	
594	A rapid and simple signature peptides-based method for species authentication of three main commercial <i>Pheretima</i> .. 2021 , 255, 104456	1
593	Revealing AMP mechanisms of action through resistance evolution and quantitative proteomics.. 2022 , 663, 259-271	
592	A proximity-based in silico approach to identify redox-labile disulfide bonds: The example of FVIII.. 2022 , 17, e0262409	0
591	Quantitative proteomic analysis of serum-purified exosomes identifies putative pre-eclampsia-associated biomarkers.. 2022 , 19, 5	1
590	Improving the proteome coverage of <i>Daphnia magna</i> - implications for future ecotoxicoproteomics studies.. 2022 , e2100289	1
589	CACNB4 overexpression decreases dendritic spine density in sex-specific manner.	
588	Longitudinal Plasma Proteomics Analysis Reveals Novel Candidate Biomarkers in Acute COVID-19.. 2022 ,	4

587	Light contamination in stable isotope-labelled internal peptide standards is frequent and a potential source of false discovery and quantitation error in proteomics.. 2022 , 414, 2545	1
586	High-Field Asymmetric Waveform Ion Mobility Spectrometry and Parallel Reaction Monitoring Increases Sensitivity for Clinical Biomarker Quantitation from Formalin-Fixed, Paraffin-Embedded Tumor Biopsies.	
585	Glycomic and Glycoproteomic Techniques in Neurodegenerative Disorders and Neurotrauma: Towards Personalized Markers.. 2022 , 11,	0
584	Toward optimal clearance - A universal affinity based mass spectrometry approach for comprehensive ELISA reagent coverage evaluation and HCP hitchhiker analysis.. 2022 , e3244	0
583	Proteomic Exploration of Porcine Oocytes During Meiotic Maturation Using an Accurate TMT-Based Quantitative Approach.. 2021 , 8, 792869	0
582	Pan-cancer quantitation of epithelial-mesenchymal transition dynamics using parallel reaction monitoring-based targeted proteomics approach.. 2022 , 20, 84	1
581	Specificities of G α subunits for the SNARE complex before and after stimulation of β adrenergic receptors.. 2021 , 14, eabc4970	0
580	Next-Generation Serology by Mass Spectrometry: Readout of the SARS-CoV-2 Antibody Repertoire. 2021 ,	4
579	Fluorinated rhamnosides inhibit cellular fucosylation. 2021 , 12, 7024	1
578	[Research progress and application of retention time prediction method based on deep learning]. 2021 , 39, 211-218	2
577	Assay design for unambiguous identification and quantification of circulating pathogen-derived peptide biomarkers.. 2022 , 12, 2948-2962	
576	Democratizing data-independent acquisition proteomics analysis on public cloud infrastructures via the Galaxy framework.. 2022 , 11,	4
575	An In Vivo Stable Isotope Labeling Method to Investigate Individual Matrix Protein Synthesis, Ribosomal Biogenesis, and Cellular Proliferation in Murine Articular Cartilage.. 2022 , 3, zqac008	0
574	Laboratory Techniques in Cellular and Molecular Medicine.	
573	Tumor Suppressor Role of Wild-Type P53-Dependent Secretome and Its Proteomic Identification in PDAC.. 2022 , 12,	1
572	Shotgun Proteomics Identifies Active Metabolic Pathways in Bleached Coral Tissue and Intraskelatal Compartments. 2022 , 9,	
571	Accelerating the Validation of Endogenous On-Target Engagement and In-cellulo Kinetic Assessment for Covalent Inhibitors of KRASG12C in Early Drug Discovery.	
570	Targeting insulin-like growth factor-1 receptor (IGF1R) for brain delivery of biologics.. 2022 , 36, e22208	1

569	Discovery and Visualization of Uncharacterized Drug-Protein Adducts Using Mass Spectrometry.. 2022,	0
568	Data-Independent Acquisition Enables Robust Quantification of 400 Proteins in Non-Depleted Canine Plasma.. 2022, 10,	1
567	Activity dependent dissociation of the Homer1 interactome.. 2022, 12, 3207	1
566	HIV-1 and methamphetamine alter galectins -1, -3, and -9 in human monocyte-derived macrophages.. 2022, 1	0
565	The Mycobacterium tuberculosis protein O-phosphorylation landscape.	0
564	Changes in Whey Proteome between Mediterranean and Murrah Buffalo Colostrum and Mature Milk Reflect Their Pharmaceutical and Medicinal Value.. 2022, 27,	2
563	Study of Dimorphism Transition Mechanism of Based on Comparative Proteomics.. 2022, 8,	
562	Multiple reaction monitoring-mass spectrometry enables robust quantitation of plasma proteins regardless of whole blood processing delays that may occur in the clinic.. 2022, 100212	2
561	In-Depth Serum Proteomics by DIA-MS with Spectral Libraries Reveals Dynamics during the Active Phase of Systemic Juvenile Idiopathic Arthritis.. 2022, 7, 7012-7023	2
560	Proteome Analysis of Urinary Biomarkers in a Bovine IRBP-Induced Uveitis Rat Model Data-Independent Acquisition and Parallel Reaction Monitoring Proteomics.. 2022, 9, 831632	
559	Modular automated bottom-up proteomic sample preparation for high-throughput applications.. 2022, 17, e0264467	
558	Systematic dissection of phosphorylation-dependent YAP1 complex formation elucidates a key role for PTPN14 in Hippo signal integration.	
557	Mapping Tyrosine Kinases Based on a TK Activity-Representing Peptide Library Reveals a Role for SRC in H1975 Drug Resistance.. 2022,	3
556	Tryptophan depletion results in tryptophan-to-phenylalanine substitutants.. 2022,	3
555	Cancer proteogenomics: current impact and future prospects.. 2022,	7
554	Early Endosome Capture Proteomics and its Application to Amyloid Precursor Protein Intramembrane Processing by β and γ -Secretases.	
553	Gel-Based and Gel-Free Phosphoproteomics to Measure and Characterize Mitochondrial Phosphoproteins.. 2022, 2, e390	2
552	Targeted proteomics and specific immunoassays reveal the presence of shared allergens between the zoonotic nematodes Anisakis simplex and Pseudoterranova decipiens.. 2022, 12, 4127	1

551	Data-Independent Acquisition for the Detection of Mononucleoside RNA Modifications by Mass Spectrometry.. 2022 ,	2
550	Profiling the diversity of agonist-selective effects on the proximal proteome environment of G protein-coupled receptors.	1
549	Evaluation of Acquisition Modes for Semi-Quantitative Analysis by Targeted and Untargeted Mass Spectrometry.. 2022 , e9308	0
548	High-throughput and high-sensitivity biomarker monitoring in body fluid by FAIMS-enhanced fast LC SureQuant ^{MS} targeted quantitation.	
547	Quantitative proteomics analysis of human vitreous in rhegmatogenous retinal detachment associated with choroidal detachment by data-independent acquisition mass spectrometry.. 2022 , 1	0
546	Posttranslational modification of the RHO of plants protein RACB by phosphorylation and cross-kingdom conserved ubiquitination.. 2022 , 17, e0258924	0
545	Mitochondrial respiration supports autophagy to provide stress resistance during quiescence.. 2022 , 1-18	1
544	Profiling Mouse Brown and White Adipocytes to Identify Metabolically Relevant Small ORFs and Functional Microproteins.	
543	DIAMetAlyzer allows automated false-discovery rate-controlled analysis for data-independent acquisition in metabolomics.. 2022 , 13, 1347	1
542	Over-Expression of a Wheat Late Maturity Alpha-Amylase Type 1 Impact on Starch Properties During Grain Development and Germination.. 2022 , 13, 811728	1
541	Blockade of redox second messengers inhibits JAK/STAT and MEK/ERK signaling sensitizing FLT3-mutant acute myeloid leukemia to targeted therapies.	0
540	Development and Validation of a High-Resolving Power Absolute Quantitative PFAS method Incorporating Skyline Data Processing.. 2022 , e9295	0
539	Semen Proteomics of COVID-19 Convalescent Men Reveals Disruption of Key Biological Pathways Relevant to Male Reproductive Function.. 2022 , 7, 8601-8612	2
538	Functional genomics of RAP proteins and their role in mitoribosome regulation in Plasmodium falciparum.. 2022 , 13, 1275	1
537	Novel protein markers of androgen activity in humans: proteomic study of plasma from young chemically castrated men.. 2022 , 11,	0
536	RGI-GOLVEN signaling promotes cell surface immune receptor abundance to regulate plant immunity.. 2022 , e53281	1
535	CEST-2.2 overexpression alters lipid metabolism and extends longevity of mitochondrial mutants.. 2022 , e52606	1
534	Fast and Sensitive Quantification of AccQ-Tag Derivatized Amino Acids and Biogenic Amines by UHPLC-UV Analysis from Complex Biological Samples.. 2022 , 12,	0

533	Distinct Roles of Honeybee Gut Bacteria on Host Metabolism and Neurological Processes.. 2022 , e0243821	0
532	An approach to measuring protein turnover in human induced pluripotent stem cell organoids by mass spectrometry.. 2022 ,	1
531	CD14 and lipopolysaccharide-binding protein as novel biomarkers for sarcoidosis by proteomics of serum extracellular vesicles.. 2022 ,	0
530	Bisphenol A replacement chemicals, BPF and BPS, induce protumorigenic changes in human mammary gland organoid morphology and proteome.. 2022 , 119, e2115308119	0
529	Mical modulates Tau toxicity via cysteine oxidation in vivo.. 2022 , 10, 44	0
528	Secreted phospholipase A modifies extracellular vesicles and accelerates B cell lymphoma.. 2022 ,	2
527	Pulmonary Surfactant Protein B Carried by HDL Predicts Incident Cardiovascular Disease in Patients with Type 1 Diabetes.. 2022 , 100196	1
526	SP3-enabled Rapid and High Coverage Chemoproteomic Identification of Cell-State Dependent Redox-Sensitive Cysteines.. 2022 , 100218	0
525	Proteomic analysis of coarse and fine skin tissues of Liaoning cashmere goat.. 2022 ,	
524	Identification and validation of new ERK substrates by phosphoproteomic technologies including Phos-tag SDS-PAGE.. 2022 , 104543	2
523	Significance of both alkB and P450 alkane-degrading systems in Tsukamurella tyrosinosolvens: proteomic evidence.. 2022 , 1	0
522	A fly GWAS for purine metabolites identifies human FAM214 homolog medusa, which acts in a conserved manner to enhance hyperuricemia-driven pathologies by modulating purine metabolism and the inflammatory response.. 2022 , 1	
521	Integration Analysis of Transcriptome and Proteome Reveal the Mechanisms of Goat Wool Bending.. 2022 , 10, 836913	0
520	Targeted Proteomics and Support Vector Classification Reveal Potential Biomarkers for the Early Detection of High-grade Serous Ovarian Cancer.	0
519	Proteomic analysis reveals exercise training induced remodelling of hepatokine secretion and uncovers syndecan-4 as a regulator of hepatic lipid metabolism.. 2022 , 101491	0
518	Absolute Proteome Quantification in the Gas-Fermenting Acetogen .. 2022 , e0002622	0
517	Characterization of the secretome, transcriptome and proteome of human cell line EndoC-β1.. 2022 , 100229	1
516	Redox-dependent structure and dynamics of macrophage migration inhibitory factor reveal sites of latent allostery.. 2022 ,	2

515	Absolute quantification of viral proteins during single-round replication of MDCK suspension cells.. 2022 , 259, 104544	0
514	The production of preconditioned freeze-dried <i>Oenococcus oeni</i> primes its metabolism to withstand environmental stresses encountered upon inoculation into wine.. 2022 , 369, 109617	0
513	MSSort-DIA: A deep learning classification tool of the peptide precursors quantified by OpenSWATH.. 2022 , 104542	0
512	Analysis of protein phosphorylation sites in the hypothalamus tissues of pubescent goats.. 2022 , 260, 104574	0
511	The emerging role of mass spectrometry-based proteomics in molecular pharming practices.. 2022 , 68, 102133	1
510	Targeted proteomics for rapid and robust peanut allergen quantification.. 2022 , 383, 132592	2
509	Human Serum Albumin Cys34 Adducts in Newborn Dried Blood Spots: Associations With Air Pollution Exposure During Pregnancy.. 2021 , 9, 730369	0
508	Deep learning approaches for data-independent acquisition proteomics.. 2021 ,	2
507	Integrated Proteomic and Metabolomic Analyses of the Mitochondrial Neurodegenerative Disease MELAS.	0
506	A multiplex protein panel assay determines disease severity and is prognostic about outcome in COVID-19 patients.	
505	New advances in quantitative proteomics research and current applications in asthma. 2021 ,	0
504	Activation mechanism of PINK1.. 2021 ,	5
503	Limited, but potentially functional translation of non-coding transcripts in the HEK293T cellular cytosol.	
502	HLA Allele-Specific Quantitative Profiling of Type 1 Diabetic B Lymphocyte Immunopeptidome.. 2021 ,	0
501	RPL3L-containing ribosomes modulate mitochondrial activity in the mammalian heart.	0
500	FastCAT accelerates absolute quantification of proteins by using multiple short non-purified chimeric standards.	
499	A Lactic Acid Bacteria Consortium Impacted the Content of Casein-Derived Biopeptides in Dried Fresh Cheese.. 2021 , 27,	0
498	Prebiotic membranes and micelles do not inhibit peptide formation during dehydration. 2021 ,	1

497	Sample Size-Comparable Spectral Library Enhances Data-Independent Acquisition-Based Proteome Coverage of Low-Input Cells.. 2021 , 93, 17003-17011	2
496	MITOL regulates phosphatidic acid-binding activity of RMDN3/PTPIP51.. 2021 ,	1
495	Effects of Neck-Arm Restraint Suspension of Beef Carcasses on Meat Quality and Proteome of Different Muscles During Post-mortem Aging.. 2021 , 8, 774529	
494	Broad application of CYP3A4 LC-MS protein quantification in hepatocyte cytochrome P450 induction assays identifies nonuniformity in mRNA and protein induction responses. 2021 ,	0
493	Tissue Plasminogen Activator Effects on Fibrin Volume and the Ocular Proteome in a Juvenile Rabbit Model of Lensectomy. 2021 , 10, 7	1
492	LC-MS peak assignment based on unanimous selection by six machine learning algorithms. 2021 , 11, 23411	0
491	Developments and Perspectives in High-Throughput Protein Glycomics: Enabling the Analysis of Thousands of Samples.. 2022 ,	1
490	Mice with a deficiency in Peroxisomal Membrane Protein 4 (PXMP4) display mild changes in hepatic lipid metabolism.. 2022 , 12, 2512	1
489	Quantitative Cell Proteomic Atlas: Pathway-scale targeted mass spectrometry for high-resolution functional profiling of cell signaling.	
488	The PeptideAtlas of a widely cultivated fish <i>Labeo rohita</i> : A resource for the Aquaculture Community.. 2022 , 9, 171	2
487	automRm: An R Package for Fully Automatic LC-QQQ-MS Data Preprocessing Powered by Machine Learning.. 2022 ,	2
486	Quantitative Proteogenomic Characterization of Inflamed Murine Colon Tissue Using an Integrated Discovery, Verification, and Validation Proteogenomic Workflow.. 2022 , 10,	0
485	High-Resolution Demultiplexing (HRdm) Ion Mobility Spectrometry-Mass Spectrometry for Aspartic and Isoaspartic Acid Determination and Screening.. 2022 ,	2
484	Proteomic Profiling and Functional Analysis of B Cell-Derived Exosomes upon Infection.. 2022 , 2022, 5187166	0
483	Simple, efficient and thorough shotgun proteomic analysis with PatternLab V.. 2022 ,	3
482	Data_Sheet_1.zip. 2020 ,	
481	Image_1.TIF. 2020 ,	
480	Image_2.TIF. 2020 ,	

479 Image_3.TIF. 2020,

478 Image_4.TIF. 2020,

477 Image_5.TIF. 2020,

476 Presentation_1.pdf. 2020,

475 Data_Sheet_1.pdf. 2020,

474 Table_1.DOCX. 2020,

473 Data_Sheet_1.docx. 2020,

472 Table_1.xlsx. 2020,

471 Image_1.jpg. 2020,

470 Image_2.JPEG. 2020,

469 Image_3.jpg. 2020,

468 Image_4.JPEG. 2020,

467 Image_5.JPEG. 2020,

466 Image_6.JPEG. 2020,

465 Table_1.pdf. 2020,

464 Table_2.pdf. 2020,

463 Table_3.pdf. 2020,

462 Image_1.TIF. 2020,

461 Table_1.XLSX. 2020,

460 Table_2.XLSX. 2020,

459 Table_3.XLSX. 2020,

458 Table_4.XLSX. 2020,

457 Table_5.XLSX. 2020,

456 Table_6.XLSX. 2020,

455 Table_7.XLSX. 2020,

454 Data_Sheet_1.PDF. 2020,

453 Image_1.tif. 2018,

452 Image_2.TIF. 2018,

451 Table_1.XLSX. 2018,

450 Table_2.XLSX. 2018,

449 Table_3.XLSX. 2018,

448 Table_4.XLSX. 2018,

447 Table_5.XLSX. 2018,

446 Table_6.XLSX. 2018,

445 Table_7.XLSX. 2018,

444 Table_8.XLSX. 2018,

443 Data_Sheet_1.PDF. **2019**,

442 Table_1.XLSX. **2019**,

441 Table_2.XLSX. **2019**,

440 Data_Sheet_1.pdf. **2020**,

439 Data_Sheet_2.xlsx. **2020**,

438 Data_Sheet_1.PDF. **2019**,

437 Table_1.xlsx. **2019**,

436 Table_2.xlsx. **2019**,

435 Table_3.xlsx. **2019**,

434 Table_4.xlsx. **2019**,

433 Table_5.xlsx. **2019**,

432 Table_6.xlsx. **2019**,

431 Table_7.xlsx. **2019**,

430 Table_8.XLSX. **2019**,

429 Data_Sheet_1.docx. **2020**,

428 Data_Sheet_2.docx. **2020**,

427 Table_1.docx. **2020**,

426 Table_2.xlsx. **2020**,

425 Table_3.xlsx. 2020,

424 Table_4.xlsx. 2020,

423 Table_5.xlsx. 2020,

422 Table_6.xlsx. 2020,

421 Table_7.xlsx. 2020,

420 Table_8.xlsx. 2020,

419 Table_9.xlsx. 2020,

418 Image_1.JPEG. 2018,

417 Image_2.JPEG. 2018,

416 Image_3.jpg. 2018,

415 Image_4.JPEG. 2018,

414 Table_1.docx. 2018,

413 Data_Sheet_1.pdf. 2018,

412 Table_1.xlsx. 2018,

411 DataSheet_1.xls. 2020,

410 DataSheet_2.xlsx. 2020,

409 Image_1.pdf. 2020,

408 Image_2.pdf. 2020,

407 Image_3.pdf. **2020**,

406 Image_4.pdf. **2020**,

405 Image_5.pdf. **2020**,

404 Image_6.pdf. **2020**,

403 Image_7.pdf. **2020**,

402 Image_8.pdf. **2020**,

401 Image_9.pdf. **2020**,

400 Table_1.pdf. **2020**,

399 Table_2.pdf. **2020**,

398 Table_3.pdf. **2020**,

397 DataSheet_1.zip. **2019**,

396 Data_Sheet_1.PDF. **2018**,

395 Presentation_1.pptx. **2018**,

394 Presentation_2.PPTX. **2018**,

393 Presentation_3.pptx. **2018**,

392 Table_1.xlsx. **2018**,

391 Table_2.xlsx. **2018**,

390 Table_3.xlsx. **2018**,

389	Table_4.docx. 2018 ,	
388	Table_5.docx. 2018 ,	
387	OUP accepted manuscript.	0
386	A fast and sensitive absolute quantification assay for the detection of SARS-CoV?2 peptides using Parallel Reaction Monitoring Mass Spectrometry.	
385	Multi-Site Observational Study to Assess Biomarkers for Susceptibility or Resilience to Chronic Pain: The Acute to Chronic Pain Signatures (A2CPS) Study Protocol.. 2022 , 9, 849214	0
384	Comprehensive Assessment of Host Cell Protein Expression after Extended Culture and Bioreactor Production of CHO Cell Lines.. 2022 ,	0
383	Characterization of Cytochrome P450s with Key Roles in Determining Herbicide Selectivity in Maize.	2
382	Post-translational modification patterns on ̢myosin heavy chain are altered in ischemic and nonischemic human hearts.. 2022 , 11,	1
381	Single-Shot 10K Proteome Approach: Over 10,000 Protein Identifications by Data-Independent Acquisition-Based Single-Shot Proteomics with Ion Mobility Spectrometry.. 2022 ,	0
380	Intra-axonal translation of Khsrp mRNA slows axon regeneration by destabilizing localized mRNAs.. 2022 ,	0
379	Isolation of fucoxanthin chlorophyll protein complexes of the centric diatom Thalassiosira pseudonana associated with the xanthophyll cycle enzyme diadinoxanthin de-epoxidase.. 2022 ,	
378	Ultrastructural Assessment and Proteomic Analysis in Myofibrillogenesis in the Heart Primordium After Heartbeat Initiation in Rats. 2022 , 13,	
377	Novel Antibody-Peptide Binding Assay Indicates Presence of Immunoglobulins against EGFR Phospho-Site S1166 in High-Grade Glioma.. 2022 , 23,	1
376	FastCAT Accelerates Absolute Quantification of Proteins Using Multiple Short Nonpurified Chimeric Standards.. 2022 ,	0
375	A TRUSTED targeted mass spectrometry assay for pan-herpesvirus protein detection.. 2022 , 39, 110810	0
374	Modulation of huntingtin degradation by cAMP-dependent protein kinase A (PKA) phosphorylation of C-HEAT domain Ser2550.	
373	An antibody-free enrichment approach enabled by reductive glutaraldehydation for monomethyllysine proteome analysis.. 2022 , e2100378	1
372	Benchmarking of analysis strategies for data-independent acquisition proteomics using a large-scale dataset comprising inter-patient heterogeneity.. 2022 , 13, 2622	2

- 371 A data-independent acquisition (DIA)-based quantification workflow for proteome analysis of 5000 cells.. **2022**, 216, 114795 ○
- 370 A ubiquitinome analysis to study the functional roles of the proteasome associated deubiquitinating enzymes USP14 and UCH37.. **2022**, 262, 104592 ○
- 369 Evaluation of the Major Seed Storage Proteins, the Conglutins, Across Genetically Diverse Narrow-Leafed Lupin Varieties. **2022**, 9,
- 368 Comparative proteomic analysis identifies differentially expressed proteins and reveals potential mechanisms of traumatic heterotopic ossification progression. **2022**, 34, 42-59
- 367 Proteomic Analysis of Human Neural Stem Cell Differentiation by SWATH-MS.. **2022**,
- 366 Comparison of anti-peptide and anti-protein antibody-based purification techniques for detection of SARS-CoV-2 by targeted LC-MS/MS. **2022**, 2, 100018
- 365 The Nuclear DNA Sensor IFI16 Indiscriminately Binds to and Diminishes Accessibility of the HSV-1 Genome to Suppress Infection.. **2022**, e0019822 1
- 364 Zn-regulated GTPase metalloprotein activator 1 modulates vertebrate zinc homeostasis.. **2022**, 5
- 363 Sensoproteomic Discovery of Taste-Modulating Peptides and Taste Re-engineering of Soy Sauce.. **2022**, 1
- 362 Human OTULIN haploinsufficiency impairs cell-intrinsic immunity to staphylococcal α -toxin.. **2022**, eabm6380 1
- 361 Maternal serum CFHR4 protein is a potential non-invasive marker of ventricular septal defects in offspring: evidence from a comparative proteomics study.. **2022**, 19, 17
- 360 Proteomic characterization of four subtypes of M2 macrophages derived from human THP-1 cells.. **2022**, 23, 407-422 ○
- 359 Glycopeptide-Centric Approaches for the Characterization of Microbial Glycoproteomes. **2022**, 153-171
- 358 Mining Proteomics Datasets to Uncover Functional Pseudogenes. **2022**, 241-251
- 357 Automating Assignment, Quantitation, and Biological Annotation of Redox Proteomics Datasets with ProteoSushi. **2022**, 61-84
- 356 A rapid and universal liquid chromatograph-mass spectrometry-based platform, refmAb-Q nSMOL, for monitoring monoclonal antibody therapeutics.
- 355 High-throughput and high-sensitivity biomarker monitoring in body fluid by FAIMS-enhanced fast LC SureQuant^{MS} targeted quantitation. **2022**, 100251
- 354 Targeted LC-MS/MS-based metabolomics and lipidomics on limited hematopoietic stem cell numbers. **2022**, 3, 101408 ○

- 353 Identifying Reactive Sites on Diacylglycerol Kinases for Covalent Binding in Cells.
- 352 Iron-Regulated Assembly of the Cytosolic Iron-Sulfur Cluster Biogenesis Machinery. **2022**, 102094 0
- 351 Biochemical and structural insights into SARS-CoV-2 polyprotein processing by Mpro.
- 350 The proto-oncogene DEK regulates neuronal excitability and tau accumulation in Alzheimer's disease vulnerable neurons.
- 349 Quantitative measurement of HER2 expression to subclassify ERBB2 unamplified breast cancer. 3
- 348 Rise of the SARS-CoV-2 Variants: Can proteomics be the silver bullet?. 0
- 347 Differential cofactor dependencies define distinct types of human enhancers. 2
- 346 Optimization of Microflow LC Coupled with Scanning SWATH and Its Application in Hepatocellular Carcinoma Tissues. 1
- 345 Recapitulation of endogenous 4R tau expression and formation of insoluble tau in directly reprogrammed human neurons. **2022**, 29, 918-932.e8 1
- 344 Uncovering PFAS and Other Xenobiotics in the Dark Metabolome Using Ion Mobility Spectrometry, Mass Defect Analysis, and Machine Learning. 1
- 343 Substrate-selective positive allosteric modulation of PTPRD's phosphatase by flavonols. **2022**, 202, 115109 0
- 342 Liquid chromatography coupled to tandem mass spectrometry for comprehensive quantification of crustacean tropomyosin and arginine kinase in food matrix. **2022**, 140, 109137 1
- 341 Intraoperative Plasma Proteomic Changes in Cardiac Surgery: In Search of Biomarkers of Post-operative Delirium.
- 340 A hybrid inorganic-biological artificial photosynthesis system for energy-efficient food production. **2022**, 3, 461-471 3
- 339 Parallel Reaction Monitoring Mass Spectrometry for Rapid and Accurate Identification of β -Lactamases Produced by Enterobacteriaceae. 13,
- 338 Power of mzRAPP-Based Performance Assessments in MS1-Based Nontargeted Feature Detection. **2022**, 94, 8588-8595 1
- 337 Enhanced metabolism and negative regulation of ER stress support higher erythropoietin production in HEK293 cells. **2022**, 39, 110936 0
- 336 Profiling the Plasma Apolipoproteome of Normo- and Hyperlipidemic Mice by Targeted Mass Spectrometry.

335	A streamlined platform for analyzing tera-scale DDA and DIA mass spectrometry data enables highly sensitive immunopeptidomics. 2022 , 13,	0
334	Cullin-independent recognition of HHARI substrates by a dynamic RBR catalytic domain. 2022 ,	0
333	Deconvoluting signals downstream of growth and immune receptor kinases by phosphocodes of the BSU1 family phosphatases. 2022 , 8, 646-655	1
332	On-Chip Preconcentration Microchip Capillary Electrophoresis Based CE-PRM-LIVE for High-Throughput Selectivity Profiling of Deubiquitinase Inhibitors.	0
331	Microanalysis of Brain Angiotensin Peptides Using Ultrasensitive Capillary Electrophoresis Trapped Ion Mobility Mass Spectrometry.	1
330	Comprehensive Mapping and Dynamics of Site-Specific Prolyl-Hydroxylation, Lysyl-Hydroxylation and Lysyl O-Glycosylation of Collagens Deposited in ECM During Zebrafish Heart Regeneration. 9,	1
329	A Current Encyclopedia of Bioinformatics Tools, Data Formats and Resources for Mass Spectrometry Lipidomics. 2022 , 12, 584	3
328	Metabolome changes with diet-induced remission in pediatric Crohn's disease. 2022 ,	3
327	A Novel Proteogenomic Integration Strategy Expands the Breadth of Neo-Epitope Sources. 2022 , 14, 3016	0
326	A multiplex protein panel assay for severity prediction and outcome prognosis in patients with COVID-19: An observational multi-cohort study. 2022 , 49, 101495	2
325	Immunoassay for quantification of antigen-specific IgG fucosylation. 2022 , 81, 104109	0
324	Plasma proteomic changes in response to surgical trauma and a novel transdermal analgesic treatment in dogs. 2022 , 265, 104648	0
323	A fast and sensitive absolute quantification assay for the detection of SARS-CoV-2 peptides using parallel reaction monitoring mass spectrometry. 2022 , 265, 104664	
322	Effects of age on subcutaneous adipose tissue proteins in Chinese indigenous Ningxiang pig by TMT-labeled quantitative proteomics. 2022 , 265, 104650	1
321	Horizontal Integration: OMICS Mass Spectrometry-Based Proteomics in Systems Biology Research. 2022 ,	
320	Histone malonylation is regulated by SIRT5 and KAT2A.	0
319	A rapid and non-invasive proteomic analysis using DBS and buccal swab for multiplexed second-tier screening of Pompe disease and Mucopolysaccharidosis type I. 2022 ,	1
318	Development of Parallel Reaction Monitoring Mass Spectrometry Assay for the Detection of Human Norovirus Major Capsid Protein. 2022 , 14, 1416	

317	Comprehensive proteomic quantification of bladder stone progression in a cystinuric mouse model using data-independent acquisitions. 2022 , 17, e0250137	0
316	Monitoring Protein Import into the Endoplasmic Reticulum in Living Cells with Proximity Labeling. 2022 , 17, 1963-1977	0
315	Peptidomic Approaches and Observations in Neurodegenerative Diseases. 2022 , 23, 7332	
314	The SKBR3 cell-membrane proteome reveals telltales of aberrant cancer cell proliferation and targets for precision medicine applications. 2022 , 12,	2
313	prolfqua: A Comprehensive R-package for Proteomics Differential Expression Analysis.	1
312	New Insights into Cypermethrin Insecticide Resistance Mechanisms of <i>Culex pipiens pallens</i> by Proteome Analysis.	1
311	Diet and feeding pattern modulate diurnal dynamics of the ileal microbiome and transcriptome. 2022 , 40, 111008	5
310	Machine Learning-Based Fragment Selection Improves the Performance of Qualitative PRM Assays.	0
309	Dendritic cell-mediated cross presentation of tumor-derived peptides is biased against plasma membrane proteins. 2022 , 10, e004159	0
308	Phosphorylation of eIF4E in the stroma drives the production and spatial organisation of collagen type I in the mammary gland. 2022 ,	2
307	The conformational change of the protease inhibitor α -macroglobulin is triggered by the retraction of the cleaved bait region from a central channel.. 2022 , 102230	
306	Structural basis of interdomain communication in PPAR α	3
305	Prognosis of Alzheimer's Disease Using Quantitative Mass Spectrometry of Human Blood Plasma Proteins and Machine Learning. 2022 , 23, 7907	2
304	Transcriptional drifts associated with environmental changes in endothelial cells.	
303	An Ovarian Steroid Metabolomic Pathway Analysis in Basal and Polycystic Ovary Syndrome (PCOS) like Gonadotropin Conditions Reveals a Hyperandrogenic Phenotype Measured by Mass Spectrometry. 2022 , 10, 1646	2
302	Utilizing Skyline to analyze lipidomics data containing liquid chromatography, ion mobility spectrometry and mass spectrometry dimensions.	2
301	Neuromelanin granules of the substantia nigra: proteomic profile provides links to tyrosine hydroxylase, stress granules and lysosomes.	0
300	Limited evidence for protein products of non-coding transcripts in the HEK293T cellular cytosol. 2022 , 100264	1

- 299 Englerin A Rewires Phosphosignaling via Hsp27 Hyperphosphorylation to Induce Cytotoxicity in Renal Cancer Cells. ○
- 298 AlphaViz: Visualization and validation of critical proteomics data directly at the raw data level. ○
- 297 Tissue-Based Proteomic Profiling in Patients with Hyperplasia and Endometrial Cancer. **2022**, 11, 2119 ○
- 296 Serum amyloid P component and pro-platelet basic protein in extracellular vesicles or serum are novel markers of liver fibrosis in chronic hepatitis C patients. **2022**, 17, e0271020 ○
- 295 Min waves without MinC can pattern FtsA-anchored FtsZ filaments on model membranes. **2022**, 5,
- 294 Dynamic acylome reveals metabolite driven modifications in *Syntrophomonas wolfei*.
- 293 Accelerating the Validation of Endogenous On-Target Engagement and In Cellulo Kinetic Assessment for Covalent Inhibitors of KRASG12C in Early Drug Discovery. 2
- 292 MAVEN2: An Updated Open-Source Mass Spectrometry Exploration Platform. **2022**, 12, 684 ○
- 291 Amnion Cells in Tailored Hydrogels Deposit Human Amnion Native Extracellular Matrix. 2204543 1
- 290 Relative quantification of sulfenic acids in plasma proteins using differential labelling and mass spectrometry coupled with 473nm photo-dissociation analysis: A multiplexed approach applied to an Alzheimer's disease cohort. **2022**, 250, 123745
- 289 A Targeted Liquid Chromatography-Tandem Mass Spectrometry Method for Simultaneous Quantification of Peptides from the Carboxyl-terminal Region of Type III Procollagen, Biomarkers of Collagen Turnover. ○
- 288 Characterization and Preclinical Treatment of Rotational Force-Induced Brain Injury.
- 287 SP3-FAIMS-Enabled High-Throughput Quantitative Profiling of the Cysteinome. **2022**, 2,
- 286 Huntingtin turnover: modulation of huntingtin degradation by cAMP-dependent protein kinase A (PKA) phosphorylation of C-HEAT domain Ser2550.
- 285 Phosphoproteomics of three exercise modalities identifies canonical signaling and C18ORF25 as an AMPK substrate regulating skeletal muscle function. **2022**, ○
- 284 Evaluating Peptide Fragment Ion Detection Using Traveling Wave Ion Mobility Spectrometry with Signal-Enhanced MSE (SEMSE). **2022**, 94, 10930-10941 1
- 283 Prediction of peptide mass spectral libraries with machine learning. ○
- 282 Plasma Proteome Perturbation for CMV DNAemia in Kidney Transplantation.

- 281 Ocular proteomic and transcriptomic changes with aging in a rabbit model of lensectomy with intraocular lens insertion. **2022**, 109219
- 280 Pro-inflammatory cytokines in aqueous humor from dogs with anterior uveitis and post-operative ocular hypertension following phacoemulsification, primary glaucoma, and normal healthy eyes. **2022**, 17, e0273449
- 279 A toolbox for class I HDACs reveals isoform specific roles in gene regulation and protein acetylation. **2022**, 18, e1010376 0
- 278 In-depth Analysis of the Sirtuin 5-regulated Mouse Brain Acylome using Library-free Data-Independent Acquisitions.
- 277 Surrogate peptide selection and internal standardization for accurate quantification of endogenous proteins.
- 276 Proteomic Investigation of the Antibacterial Mechanism of Cefiderocol against Escherichia coli.
- 275 Development of multiple reaction monitoring (MRM) assays to identify Brucella abortus proteins in the serum of humans and livestock. 2200009
- 274 Evaluation of autoantibody signatures in Pituitary Adenoma patients using human proteome arrays. 2100111 3
- 273 Proteomic analysis of the meristematic root zone in contrasting genotypes reveals new insights in drought tolerance in rice. 2200100
- 272 The addition of FAIMS increases targeted proteomics sensitivity from FFPE tumor biopsies. **2022**, 12, 0
- 271 A multidimensional metabolomics workflow to image biodistribution and evaluate pharmacodynamics in adult zebrafish. **2022**, 15, 0
- 270 Histone Acid Extraction and High Throughput Mass Spectrometry to Profile Histone Modifications in Arabidopsis thaliana. **2022**, 2,
- 269 Restructured membrane contacts rewire organelles for human cytomegalovirus infection. **2022**, 13, 0
- 268 Autoantibody mimicry of hormone action at the thyrotropin receptor. 0
- 267 Novel Diagnostic Biomarkers for High-Grade Serous Ovarian Cancer Uncovered by Data-Independent Acquisition Mass Spectrometry. 0
- 266 Urinary Proteome Analysis of Global Cerebral Ischemia/Reperfusion Injury Rat Model via Data-Independent Acquisition and Parallel Reaction Monitoring Proteomics. **2022**, 72, 2020-2029 0
- 265 Early prediction of COVID-19 patient survival by targeted plasma multi-omics and machine learning. **2022**, 100277 3
- 264 The CLP and PREP protease systems coordinate maturation and degradation of the chloroplast proteome in Arabidopsis thaliana. 0

263	Baseline proteomics characterisation of the emerging host biomanufacturing organism Halomonas bluephagenesis. 2022 , 9,	
262	Spectral Library-Based Single-Cell Proteomics Resolves Cellular Heterogeneity. 2022 , 11, 2450	1
261	Convergent Cerebrospinal Fluid Proteomes and Metabolic Ontologies in Humans and Animal Models of Rett Syndrome.. 2022 , 104966	0
260	Molecular processes underlying the ROS -induced changes in muscle hardness in grass carp: Insights from a dietary pro-oxidant and oxidant approach.	
259	Characterization and optimization of microwave-assisted extraction of B-phycoerythrin from Porphyridium purpureum using response surface methodology and Doehlert design. 2022 , 19, 101212	0
258	Quantitative proteome profiling reveals molecular hallmarks of egg quality in Atlantic halibut: impairments of transcription and protein folding impede protein and energy homeostasis during early development. 2022 , 23,	0
257	Identification of trypsin-degrading commensals in the large intestine. 2022 , 609, 582-589	3
256	Comparison of protein extraction protocols and allergen mapping from black soldier fly Hermetia illucens. 2022 , 269, 104724	1
255	Bio-distribution and longevity of mesenchymal stromal cell derived membrane particles. 2022 , 350, 642-651	0
254	Comparative maternal protein profiling of mouse biparental and uniparental embryos. 2022 , 11,	1
253	Quantitative Detection of Protein Splice Variants by Selected Reaction Monitoring (SRM) Mass Spectrometry. 2022 , 231-246	0
252	A rapid and universal liquid chromatograph-mass spectrometry-based platform, refmAb-Q nSMOL, for monitoring monoclonal antibody therapeutics. 2022 , 147, 4275-4284	1
251	Pyrrroloquinoline quinone regulates glycolipid metabolism in the jejunum via inhibiting AMPK phosphorylation of weaned pigs. 2022 , 13, 9610-9621	0
250	Tear proteomic analysis of young glasses, orthokeratology, and soft contact lens wearers. 2023 , 270, 104738	0
249	Transmissibility of anisakid allergenic peptides from animal feed to chicken meat: Proof of concept. 2023 , 115, 104939	0
248	Absolute and relative quantitation of amylase/trypsin-inhibitors by LC-MS/MS from wheat lines obtained by CRISPR-Cas9 and RNAi. 13,	0
247	OHP2 is not required for psbA translation in Chlamydomonas.	0
246	Critical Analysis of Multi-Omic Data From a Strain of Plutella xylostella Resistant to Bacillus thuringiensis Cry1Ac Toxin. 2022 , 70, 11419-11428	0

- 245 Addressing the Protease Bias in Quantitative Proteomics. **2022**, 21, 2526-2534 ○
- 244 Dear-DIAXMBD: deep autoencoder for data-independent acquisition proteomics. ○
- 243 Myosins and MyomiR Network in Patients with Obstructive Hypertrophic Cardiomyopathy. **2022**, 10, 2180 ○
- 242 Hydropersulfides inhibit lipid peroxidation and ferroptosis by scavenging radicals. 6
- 241 Proteomic analysis of the regulatory networks of ClpX in a model cyanobacterium *Synechocystis* sp. PCC 6803. 13, ○
- 240 Predicting treatment outcome using kinome activity profiling in HER2+ breast cancer biopsies. ○
- 239 TurnoverR: A Skyline External Tool for Analysis of Protein Turnover in Metabolic Labeling Studies. ○
- 238 Sex-specific impacts of CACNB4 overexpression on dendritic spine density: relevance to schizophrenia. ○
- 237 Serum plays an important role in reprogramming the seasonal transcriptional profile of brown bear adipocytes. **2022**, 105084 ○
- 236 A multiplexed parallel reaction monitoring assay to monitor bovine pregnancy-associated glycoproteins throughout pregnancy and after gestation. **2022**, 17, e0271057 ○
- 235 Phosphorylation of the receptor protein Pex5p modulates import of proteins into peroxisomes. **2022**, ○
- 234 Sex differences in brain tumor glutamine metabolism reveal sex-specific vulnerabilities to treatment. **2022**, ○
- 233 SERUM BNEKLERIDE ALFA-2-MAKROGLUBULIN TAYIN 966-977 ○
- 232 Data-independent acquisition proteomics methods for analyzing post-translational modifications. 2200046 1
- 231 Mitochondrial protein import clogging as a mechanism of disease. ○
- 230 Oncohistone interactome profiling uncovers contrasting oncogenic mechanisms and identifies potential therapeutic targets in high grade glioma. ○
- 229 Quantitative Mass Spectrometry Analysis of Cerebrospinal Fluid Biomarker Proteins Reveals Stage-Specific Changes in Alzheimer's Disease. ○
- 228 Tuning heterologous glucan biosynthesis in yeast to understand and exploit plant starch diversity. **2022**, 20, ○

227	Protective alpha1-antitrypsin effects in autoimmune vasculitis are compromised by methionine oxidation.	0
226	Ecological Monitoring and Omics: A Comprehensive Comparison of Workflows for Mass Spectrometry-Based Quantitative Proteomics of Fish (<i>Labeo rohita</i>) Liver Tissue. 2022 , 26, 489-503	0
225	Chemotaxonomic patterns in intracellular metabolites of marine microbial plankton. 9,	0
224	Fanconi anemia-isogenic head and neck cancer cell line pairs - a basic and translational science resource.	0
223	Quantitative Cell Proteomic Atlas: Pathway-Scale Targeted Mass Spectrometry for High-Resolution Functional Profiling of Cell Signaling. 2022 , 21, 2535-2544	0
222	A High-Throughput Ion Mobility Spectrometry/Mass Spectrometry Screening Method for Opioid Profiling. 2022 , 33, 1904-1913	1
221	Calcineurin dephosphorylates topoisomerase II β and regulates the formation of neuronal-activity-induced DNA breaks. 2022 ,	0
220	A membrane integral methyltransferase catalysing N-terminal histidine methylation of lytic polysaccharide monooxygenases.	0
219	SARS-CoV-2 disrupts host epigenetic regulation via histone mimicry.	4
218	The salmonella effector Hcp modulates infection response, and affects salmonella adhesion and egg contamination incidences in ducks. 12,	0
217	Characterization of KDM5 lysine demethylase family substrate preference and identification of novel substrates.	0
216	Murine endothelial serine palmitoyltransferase 1 (SPTLC1) is required for vascular development and systemic sphingolipid homeostasis. 11,	0
215	The human disease gene LYSET is essential for lysosomal enzyme transport and viral infection. 2022 , 378,	4
214	The Brain Protein Acylation System Responds to Seizures in the Rat Model of PTZ-Induced Epilepsy. 2022 , 23, 12302	0
213	Proteomic consequences of TDA1 deficiency in <i>Saccharomyces cerevisiae</i> : Protein kinase Tda1 is essential for Hxk1 and Hxk2 serine 15 phosphorylation. 2022 , 12,	0
212	Global profiling of arginine dimethylation in regulating protein phase separation by a steric effectBased chemical-enrichment method. 2022 , 119,	1
211	Levels of soluble complement regulators predict severity of COVID-19 symptoms. 13,	0
210	SETD2 regulates the methylation of translation elongation factor eEF1A1 in clear cell renal cell carcinoma. 2022 , 1-14	0

209	Construction of an rAAV Producer Cell Line through Synthetic Biology. 2022 , 11, 3285-3295	1
208	Intraventricular B7-H3 CAR T cells for diffuse intrinsic pontine glioma: preliminary first-in-human bioactivity and safety.	3
207	Unique and shared proteome responses of rice plants (<i>Oryza sativa</i>) to individual abiotic stresses.	0
206	Is nontargeted data acquisition for target analysis (nDATA) in mass spectrometry a forward-thinking analytical approach?.	1
205	Preserving the Phosphoproteome of Clinical Biopsies Using a Quick-Freeze Collection Device. 2022 , 20, 436-445	0
204	One-stop analysis of DIA proteomics data using MSFragger-DIA and FragPipe computational platform.	0
203	A class of anti-inflammatory lipids decrease with aging in the central nervous system.	0
202	Phosphatase protector alpha4 (P4) is involved in adipocyte maintenance and mitochondrial homeostasis through regulation of insulin signaling. 2022 , 13,	1
201	Targeted Proteomic Analysis of Small GTPases in Radioresistant Breast Cancer Cells. 2022 , 94, 14925-14930	0
200	Proteomic response of early juvenile Pacific oysters (<i>Crassostrea gigas</i>) to temperature. 10, e14158	0
199	Proteome alterations during clonal isolation of established human pancreatic cancer cell lines. 2022 , 79,	0
198	OzFAD: Ozone-enabled fatty acid discovery reveals unexpected diversity in the human lipidome.	1
197	Longitudinal Evaluation of Biomarkers in Wound Fluids from Venous Leg Ulcers and Split-thickness Skin Graft Donor Site Wounds Treated with a Protease-modulating Wound Dressing.	0
196	Comparison of Genome and Plasmid-Based Engineering of Multigene Benzylglucosinolate Pathway in <i>Saccharomyces cerevisiae</i> .	0
195	GwAAP: A genome-wide amino acid coding-decoding quantitative proteomics system. 2022 , 105471	0
194	Lipid hydroperoxides and oxylipins are mediators of denervation induced muscle atrophy. 2022 , 57, 102518	1
193	Deep Phosphoproteome Landscape of Interhemispheric Functionality of Neuroanatomical Regions of the Human Brain.	0
192	Nontargeted and Targeted Metabolomics Identifies Dietary Exposure Biomarkers for Navy Bean and Rice Bran Consumption in Children and Adults.	0

191	Improvement of mutated peptide identification through MS/MS signals searching against the protein libraries generated from transcriptome and translome. 2023 , 483, 116965	0
190	Reversed-Phase Liquid Chromatography of Peptides for Bottom-Up Proteomics: A Tutorial.	5
189	Proteomic analysis of spermathecal fluid reveals factors related to long-term sperm storage in ant queens.	0
188	Comprehensive data and workflow for mapping global proteome and post-translational modifications in Indian Major Carp, <i>Labeo rohita</i> . 2022 , 108746	0
187	Dynamic acylome reveals metabolite driven modifications in <i>Syntrophomonas wolfei</i> . 13,	0
186	Near-Physiological in vitro Assembly of 50S Ribosomes Involves Parallel Pathways.	0
185	A Peptide-Centric Quantitative Proteomics Dataset for the Phenotypic Assessment of Alzheimer's Disease.	0
184	Connecting multiple microenvironment proteomes uncovers the biology in head and neck cancer. 2022 , 13,	0
183	Impact of alcohol exposure on neural development and network formation in human cortical organoids.	1
182	An extracellular receptor tyrosine kinase motif orchestrating intracellular STAT activation. 2022 , 13,	0
181	Integrated Exposomics/Metabolomics for Rapid Exposure and Effect Analyses.	0
180	Proteomic genotyping of SNP of Complement Factor H (CFH) Y402H and I62V using multiple reaction monitoring (MRM) assays. 2022 , 12,	0
179	The Proteome of Neuromelanin Granules in Dementia with Lewy Bodies. 2022 , 11, 3538	0
178	Proteomes of Extracellular Vesicles From Pancreatic Cancer Cells and Cancer-Associated Fibroblasts. 2022 , 51, 790-799	0
177	LC-MS / MS -Based Proteomics Methods for Quantifying Drug-Metabolizing Enzymes and Transporters. 2022 , 143-176	0
176	Clonal amplification-enhanced gene expression for cell-free directed evolution.	0
175	Cold-Induced Physiological and Biochemical Alternations and Proteomic Insight into the Response of <i>Saccharum spontaneum</i> to Low Temperature. 2022 , 23, 14244	1
174	Proteins in Tumor-Derived Plasma Extracellular Vesicles Indicate Tumor Origin. 2023 , 22, 100476	0

- 173 Defective determination of synthetic cathinones in blood for forensic investigation. **2023**, 539, 122-129 ○
- 172 Assessment of inconsistencies in the solvent-accessible surfaces of proteins between crystal structures and solution structures observed by LC-MS. **2023**, 640, 97-104 ○
- 171 Proteomics analysis indicates the involvement of immunity and inflammation in the onset stage of SOD1-G93A mouse model of ALS. **2023**, 272, 104776 ○
- 170 Multiomics data analysis workflow to assess severity in longitudinal plasma samples of COVID-19 patients. **2023**, 46, 108765 ○
- 169 Development and validation of a LCMS/MS method for quantitation of recombinant human growth hormone in rat plasma and application to a pharmacokinetic study. **2023**, 224, 115188 ○
- 168 Proteomic analysis of antiviral innate immunity. **2023**, 58, 101291 ○
- 167 Software Tool for Visualization and Validation of Protein Turnover Rates Using Heavy Water Metabolic Labeling and LC-MS. **2022**, 23, 14620 1
- 166 Differential phosphorylation of Clr4 SUV39H by Cdk1 accompanies a histone H3 methylation switch that is essential for gametogenesis. ○
- 165 Calredoxin regulates the chloroplast NADPH-dependent thioredoxin reductase in *Chlamydomonas reinhardtii*. ○
- 164 Integrative Proteomics and Transcriptomics Profiles of the Oviduct Reveal the Prolificacy-Related Candidate Biomarkers of Goats (*Capra hircus*) in Estrous Periods. **2022**, 23, 14888 1
- 163 Tryptophan Metabolism Hub Gene Expression Associates with Increased Inflammation and Severe Disease Outcomes in COVID-19 Infection and Inflammatory Bowel Disease. **2022**, 23, 14776 ○
- 162 Confinement induces oxidative damage and synaptic dysfunction in mice. 13, ○
- 161 Targeted and Explorative Profiling of Kallikrein Proteases and Global Proteome Biology of Pancreatic Ductal Adenocarcinoma, Chronic Pancreatitis, and Normal Pancreas Highlights Disease-Specific Proteome Remodelling. ○
- 160 Secure Food-Allergen Determination by Combining Smartphone-Based Raw Image Analyses and Liquid Chromatography-Mass Spectrometry for the Quantification of Proteins Contained in Lateral Flow Assays. **2022**, 94, 17046-17054 3
- 159 Fungal antibiotics control bacterial community diversity in the cheese rind microbiome. ○
- 158 Grabody B, an IGF1 receptor-based shuttle, mediates efficient delivery of biologics across the blood-brain barrier. **2022**, 2, 100338 ○
- 157 Simulation of mass spectrometry-based proteomics data with Synthedia. 1
- 156 A single protein to multiple peptides: Investigation of protein-peptide relationship using targeted alpha-2-macroglobulin analysis. ○

- 155 Isobaric crosslinking mass spectrometry technology for studying conformational and structural changes in proteins and complexes. ○
- 154 DNA Repair Mechanisms are Activated in Circulating Lymphocytes of Hospitalized Covid-19 Patients. Volume 15, 6629-6644 ○
- 153 Lipo-Chitooligosaccharides Induce Specialized Fungal Metabolite Profiles That Modulate Bacterial Growth. **2022**, 7, ○
- 152 Biochemical and structural insights into SARS-CoV-2 polyprotein processing by Mpro. **2022**, 8, 1
- 151 A combination of molecular and clinical parameters provides a new strategy for high-grade serous ovarian cancer patient management. **2022**, 20, ○
- 150 Complementary hepatic metabolomics and proteomics reveal the adaptive mechanisms of dairy cows to the transition period. **2022**, ○
- 149 An oncogene addiction phosphorylation signature and its derived scores inform tumor responsiveness to targeted therapies. **2023**, 80, ○
- 148 Analysis of Golgi Protein Acetylation Using In Vitro Assays and Parallel Reaction Monitoring Mass Spectrometry. **2023**, 721-741 ○
- 147 Population divergence in maternal investment and embryo energy use and allocation reveals adaptive responses to cool climates. ○
- 146 Dynamic Data Independent Acquisition Mass Spectrometry with Real-Time Retrospective Alignment. ○
- 145 Unique and Shared Proteome Responses of Rice Plants (*Oryza sativa*) to Individual Abiotic Stresses. **2022**, 23, 15552 ○
- 144 Targeted Proteomics Analysis of Staphylococcal Superantigenic Toxins in Menstrual Fluid from Women with Menstrual Toxic Shock Syndrome (mTSS). **2022**, 14, 886 ○
- 143 In-depth analysis of the Sirtuin 5-regulated mouse brain malonylome and succinylome using library-free data-independent acquisitions. 2100371 1
- 142 Nascent peptide-induced translation discontinuation in eukaryotes impacts biased amino acid usage in proteomes. **2022**, 13, ○
- 141 The loss of cardiac SIRT3 decreases metabolic flexibility and proteostasis in an age-dependent manner. ○
- 140 Effects of small molecule-induced dimerization on the programmed death ligand 1 protein life cycle. **2022**, 12, 2
- 139 TB500/TB1000 and SGF1000: A scientific approach for a better understanding of misbranded and adulterated drugs. ○
- 138 Epigenetic reprogramming shapes the cellular landscape of schwannoma. ○

137	The first Pituitary Proteome Landscape from matched anterior and posterior lobes for a better understanding of the Pituitary Gland. 2022 , 100478	0
136	Acetic Acid Ion Pairing Additive for Reversed-Phase HPLC Improves Detection Sensitivity in Bottom-up Proteomics Compared to Formic Acid.	0
135	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
134	Absolute quantification of cellular levels of photosynthesis-related proteins in <i>Synechocystis</i> sp. PCC 6803.	0
133	Intraoperative Plasma Proteomic Changes in Cardiac Surgery: In Search of Biomarkers of Post-operative Delirium. 2200066	0
132	Bile Proteome Analysis by High-Precision Mass Spectrometry to Examine Novel Biomarkers of Primary Sclerosing Cholangitis.	0
131	Proteomic analysis of digestive tract peptidases and lipases from the invasive gastropod <i>Pomacea canaliculata</i> .	0
130	Interrogation of an ovine serum peptide spectral library to annotate ambiguous clinicopathological biomarkers using data-independent acquisition. 11, 1433	0
129	An E3 ligase network engages GCN1 to promote the degradation of translation factors on stalled ribosomes. 2023 ,	1
128	Targeted Quantitative Mass Spectrometry Analysis of Protein Biomarkers From Previously Stained Single Formalin-Fixed Paraffin-Embedded Tissue Sections. 2023 , 100052	0
127	DPHL v2: An updated and comprehensive DIA pan-human assay library for quantifying more than 14,000 proteins.	0
126	Proteomic profiling of urinary small extracellular vesicles in children with pneumonia: a pilot study.	0
125	Scribe: next-generation library searching for DDA experiments.	1
124	Characterization and implications of host-cell protein aggregates in biopharmaceutical processing.	0
123	Proteomics Standards Initiative at Twenty Years: Current Activities and Future Work.	0
122	Proteome Mapping of Cervical Mucus and Its Potential as a Source of Biomarkers in Female Tract Disorders. 2023 , 24, 1038	0
121	Profiling mouse brown and white adipocytes to identify metabolically relevant small ORFs and functional microproteins. 2023 , 35, 166-183.e11	0
120	Fibrinogen beta chain may be a potential predict biomarker for pre-eclampsia: A preliminary study. 2023 , 539, 206-214	0

119	Integrative Analysis of Proteomics and Transcriptomics of Longissimus dorsi with Different Feeding Systems in Yaks. 2023 , 12, 257	0
118	Hyper-phosphorylation of Hepatic Proteome Characterizes Non-alcoholic Fatty Liver Disease in S-adenosylmethionine Deficiency. 2023 , 105987	0
117	Developing quantitative assays for six urinary glycoproteins using parallel reaction monitoring, data-independent acquisition, and TMT-based data-dependent acquisition. 2200072	0
116	Development of an LC-MRM-MS-Based Candidate Reference Measurement Procedure for Standardization of Serum Apolipoprotein (a) Tests.	1
115	Benchmarking commonly used software suites and analysis workflows for DIA proteomics and phosphoproteomics. 2023 , 14,	0
114	Degradation Kinetics of Lignocellulolytic Enzymes in a Biogas Reactor Using Quantitative Mass Spectrometry. 2023 , 9, 67	0
113	Development of a simple and reliable LC-MS/MS method to simultaneously detect walnut and almond as specified in food allergen labelling regulations in processed foods. 2023 , 6, 100444	1
112	Differential Susceptibility of Fetal Retinal Pigment Epithelial Cells, hiPSC- Retinal Stem Cells, and Retinal Organoids to Zika Virus Infection. 2023 , 15, 142	1
111	ONE-HELIX PROTEIN 2 is not required for the synthesis of photosystem II subunit D1 in Chlamydomonas.	0
110	Chemical Proteomics with Novel Fully Functionalized Fragments and Stringent Target Prioritization Identifies the Glutathione-Dependent Isomerase GSTZ1 as a Lung Cancer Target.	0
109	Targeted and explorative profiling of kallikrein proteases and global proteome biology of pancreatic ductal adenocarcinoma, chronic pancreatitis, and normal pancreas highlights disease-specific proteome remodelling. 2023 , 36, 100871	0
108	Integrated Proteotranscriptomics of the Hypothalamus Reveals Altered Regulation Associated with the FecB Mutation in the BMPR1B Gene That Affects Prolificacy in Small Tail Han Sheep. 2023 , 12, 72	0
107	Covalent Library Screening by Targeted Mass Spectrometry for Rapid Binding Site Identification.	0
106	Apolipoprotein Proteomics for Residual Lipid-Related Risk in Coronary Heart Disease.	1
105	Identification of Highly Sensitive Pleural Effusion Protein Biomarkers for Malignant Pleural Mesothelioma by Affinity-Based Quantitative Proteomics. 2023 , 15, 641	0
104	Aurora B Kinase Dependent Phosphorylation of Keratin 8 is required for Cytokinesis in Mammalian Cells of Epithelial Origin.	0
103	Combination of untargeted and targeted proteomics for secretome analysis of L-WRN cells.	0
102	Targeted Quantification of Protein Phosphorylation and Its Contributions towards Mathematical Modeling of Signaling Pathways. 2023 , 28, 1143	0

101	PrIntMap-R: An Online Application for Intraprotein Intensity and Peptide Visualization from Bottom-Up Proteomics. 2023 , 22, 432-441	1
100	Trem2 H157Y increases soluble TREM2 production and reduces amyloid pathology. 2023 , 18,	1
99	Development of an Orthotopic HPV16-Dependent Base of Tongue Tumor Model in MHC-Humanized Mice. 2023 , 12, 188	0
98	Scribe: Next Generation Library Searching for DDA Experiments. 2023 , 22, 482-490	0
97	Mis-spliced transcripts generatede novoproteins in TDP-43-related ALS/FTD.	0
96	The Mycobacterium tuberculosis protein O-phosphorylation landscape.	0
95	Glycoproteomics in Cerebrospinal Fluid Reveals Brain-Specific Glycosylation Changes. 2023 , 24, 1937	0
94	Absolute Quantitative Targeted Proteomics Assays for Plasma Proteins. 2023 , 439-473	0
93	Quantitative analysis of high-throughput biological data.	0
92	Liquid ChromatographyMass Spectrometry Analysis of Frataxin Proteoforms in Whole Blood as Biomarkers of the Genetic Disease Friedreich's Ataxia. 2023 , 95, 4251-4260	0
91	Precise diagnosis and typing of early-stage renal immunoglobulin-derived amyloidosis by label-free quantification of parallel reaction monitoring-based targeted proteomics. 2023 , 24,	0
90	Breast cancer cell secretome analysis to decipher miRNA regulating the tumor microenvironment and discover potential biomarkers. 2023 , e15421	0
89	Placental Remote Control of Fetal Metabolism: Trophoblast mTOR Signaling Regulates Liver IGFBP-1 Phosphorylation and IGF-1 Bioavailability. 2023 , 24, 7273	0
88	Proteomic analysis of liver tissue reveals Aeromonas hydrophila infection mediated modulation of host metabolic pathways in Labeo rohita. 2023 , 279, 104870	0
87	Determining plasma and cerebrospinal fluid concentrations of EGFR-TKI in lung cancer patients. 2023 , 669, 115115	0
86	Comparative transcriptomic and proteomic analysis of nutritional quality-related molecular mechanisms of Qianmei 419 and Qianfu 4 varieties of Camellia sinensis. 2023 , 865, 147329	0
85	A highly sensitive and robust LC-MS platform for host cell protein characterization in biotherapeutics. 2023 , 82, 101675	0
84	Proteomic and N-glycoproteomic analyses of total subchondral bone protein in patients with primary knee osteoarthritis. 2023 , 280, 104896	0

- 83 Understanding mobile phase buffer composition and chemical structure effects on electrospray ionization mass spectrometry response. **2023**, 1696, 463966 ○
- 82 Egg protein profile and dynamics during embryogenesis in *Haemaphysalis flava* ticks. **2023**, 14, 102180 ○
- 81 Exogenous aralar/slc25a12 can replace citrin/slc25a13 as malate aspartate shuttle component in liver. **2023**, 35, 100967 ○
- 80 Chronic BMAA exposure combined with TDP-43 mutation elicits motor neuron dysfunction phenotypes in mice. **2023**, 126, 44-57 ○
- 79 Common mouse models of tauopathy reflect early but not late human disease. **2023**, 18, ○
- 78 Metaproteomic analysis of nasopharyngeal swab samples to identify microbial peptides and potential co-infection status in COVID-19 patients. ○
- 77 VGLL3 is a mechanosensitive protein that promotes cardiac fibrosis through liquid-liquid phase separation. **2023**, 14, ○
- 76 Organ Protection by Caloric Restriction Depends on Activation of the De Novo NAD⁺ Synthesis Pathway. **2023**, Publish Ahead of Print, ○
- 75 Generation of a high yield vaccine backbone for influenza B virus in embryonated chicken eggs. **2023**, 8, ○
- 74 Phosphoproteomics Profiling Defines a Target Landscape of the Basophilic Protein Kinases AKT, S6K, and RSK in Skeletal Myotubes. **2023**, 22, 768-789 ○
- 73 Cell-selective inhibition of DNA damage response signaling by nitric oxide is associated with an attenuation in glucose uptake. **2023**, 299, 102994 ○
- 72 Perturbed post-translational modification (PTM) network atlas of collagen I during stent-induced neointima formation. **2023**, 276, 104842 ○
- 71 Apolipoprotein C3 induces inflammasome activation only in its delipidated form. **2023**, 24, 408-411 ○
- 70 Quantification of Proteins in Blood by Absorptive Microtiter Plate-Based Affinity Purification Coupled to Liquid Chromatography-Mass Spectrometry. **2023**, 221-233 ○
- 69 Exploration of associations among dietary tryptophan, microbiome composition and function, and symptom severity in irritable bowel syndrome. ○
- 68 Histone malonylation is regulated by SIRT5 and KAT2A. **2023**, 26, 106193 ○
- 67 Bioinformatics Tools and Knowledgebases to Assist Generating Targeted Assays for Plasma Proteomics. **2023**, 557-577 ○
- 66 An Optimized Data-Independent Acquisition Strategy for Comprehensive Analysis of Human Plasma Proteome. **2023**, 93-107 ○

- 65 Benchmarking Bioinformatics Pipelines in Data-Independent Acquisition Mass Spectrometry for Immunopeptidomics. **2023**, 22, 100515 ○
- 64 Targeted proteomics using stable isotope labeled protein fragments enables precise and robust determination of total apolipoprotein(a) in human plasma. **2023**, 18, e0281772 ○
- 63 Plasma, urine, and stool metabolites in response to dietary rice bran and navy bean supplementation in adults at high-risk for colorectal cancer. 2, ○
- 62 Simultaneous measurement of kynurenine metabolites and explorative metabolomics using liquid chromatography-mass spectrometry: A novel accurate method applied to serum and plasma samples from a large healthy cohort. **2023**, 227, 115304 ○
- 61 Highly sensitive in vivo detection of dynamic changes in enkephalins following acute stress. ○
- 60 Metabolic heterogeneity and cross-feeding within isogenic yeast populations captured by DILAC. **2023**, 8, 441-454 ○
- 59 Endo-lysosomal protein concentrations in CSF from patients with frontotemporal dementia caused by CHMP2B mutation. **2023**, 15, ○
- 58 Evolutionary origins and interactomes of human, young microproteins and small peptides translated from short open reading frames. **2023**, 83, 994-1011.e18 ○
- 57 A qualitative peptide biomarker approach to identify piscine gelatine in products to support food security. **2023**, 40, 465-474 ○
- 56 Prophylactic and therapeutic vaccination protects sperm health from *Chlamydia muridarum*-induced abnormalities. ○
- 55 Immunolyser: A web-based computational pipeline for analysing and mining immunopeptidomic data. **2023**, 21, 1678-1687 ○
- 54 Comparison between articular chondrocytes and mesenchymal stromal cells for the production of articular cartilage implants. 11, ○
- 53 The structural components of the *Azotobacter vinelandii* iron-only nitrogenase, AnfDKG, form a protein complex within the plant mitochondrial matrix. ○
- 52 Using protein-per-mRNA differences among human tissues in codon optimization. **2023**, 24, ○
- 51 Complete Workflow for High Throughput Human Single Skeletal Muscle Fiber Proteomics. ○
- 50 Cyclin A and Cks1 promote kinase consensus switching to non-proline-directed CDK1 phosphorylation. **2023**, 42, 112139 ○
- 49 Cdk5 mediates rotational force-induced brain injury. **2023**, 13, ○
- 48 Tandem mass tag-based quantitative proteomic profiling identifies candidate serum biomarkers of drug-induced liver injury in humans. **2023**, 14, ○

- 47 Design of *Lactococcus lactis* Strains Producing Garvicin A and/or Garvicin Q, Either Alone or Together with Nisin A or Nisin Z and High Antimicrobial Activity against *Lactococcus garvieae*. **2023**, 12, 1063 ○
- 46 Cold Exposure-Induced Alterations in the Brain Peptidome and Gut Microbiome Are Linked to Energy Homeostasis in Mice. **2023**, 22, 100525 ○
- 45 Engineered hypermutation adapts cyanobacterial photosynthesis to combined high light and high temperature stress. **2023**, 14, ○
- 44 Dynamic interplay between RPL3- and RPL3L-containing ribosomes modulates mitochondrial activity in the mammalian heart. ○
- 43 The Past and Future of Lipidomics Bioinformatics. **2023**, 271-290 ○
- 42 Impact of Spontaneous Fermentation and Inoculum with Natural Whey Starter on Peptidomic Profile and Biological Activities of Cheese Whey: A Comparative Study. **2023**, 9, 270 ○
- 41 Phosphorylation-linked complex profiling identifies assemblies required for Hippo signal integration. **2023**, 19, ○
- 40 Proteomics of high-density lipoprotein subfractions and subclinical atherosclerosis in type 1 diabetes mellitus: a case-control study. **2023**, 15, ○
- 39 Functional and targeted proteomics characterization of a human primary endothelial cell model of the blood-brain barrier (BBB) for drug permeability studies. **2023**, 465, 116456 ○
- 38 Fanconi anemia-isogenic head and neck cancer cell line pairs: A basic and translational science resource. ○
- 37 Parasitic nematode secreted phospholipase A2 suppresses cellular and humoral immunity by targeting hemocytes in *Drosophila melanogaster*. 14, ○
- 36 Structure-activity relationships of actively FhuE transported rifabutin derivatives with potent activity against *Acinetobacter baumannii*. **2023**, 252, 115257 ○
- 35 Effects of *n*-butanol production on metabolism and the photosystem in *Synechococcus elongatus*; PCC 7942 based on metabolic flux and target proteome analyses. **2023**, ○
- 34 prolfqa: A Comprehensive R-Package for Proteomics Differential Expression Analysis. **2023**, 22, 1092-1104 ○
- 33 Integrative transcriptome and proteome analysis reveals maize responses to *Fusarium verticillioides* infection inside the stalks. ○
- 32 Global Discovery and Temporal Changes of Human Albumin Modifications by Pan-Protein Adductomics: Initial Application to Air Pollution Exposure. **2023**, 34, 595-607 ○
- 31 A Large-Scale Proteomics Resource of Circulating Extracellular Vesicles for Biomarker Discovery in Pancreatic Cancer. ○
- 30 Long-read proteogenomics to connect disease-associated sQTLs to the protein isoform effectors of disease. ○

- 29 Interlaboratory Evaluation of a User-Friendly Benchtop Mass Spectrometer for Multiple-Attribute Monitoring Studies of a Monoclonal Antibody. **2023**, 28, 2855 ○
- 28 Metabolic Difference Analysis of Clostridium cellulovorans Grown on Glucose and Cellulose. **2023**, 9, 321 ○
- 27 Transcriptional drifts associated with environmental changes in endothelial cells. 12, ○
- 26 Blockade of ROS production inhibits oncogenic signaling in acute myeloid leukemia and amplifies response to precision therapies. **2023**, 16, ○
- 25 Kinetic proteomics identifies targeted changes in liver metabolism and the ribo-interactome by dietary sulfur amino acid restriction. ○
- 24 Combined physicochemical and functional assessment of pertuzumab integrity supports extended in-use stability. ○
- 23 Peptidomics. **2023**, 3, ○
- 22 Targeted Blood Plasma Proteomics and Hemostasis Assessment of Post COVID-19 Patients with Acute Myocardial Infarction. **2023**, 24, 6523 ○
- 21 Clonal Amplification-Enhanced Gene Expression in Synthetic Vesicles. **2023**, 12, 1187-1203 ○
- 20 Ribosomal protein RPL39L is an efficiency factor in the cotranslational folding of proteins with alpha helical domains. ○
- 19 MSstats Version 4.0: Statistical Analyses of Quantitative Mass Spectrometry-Based Proteomic Experiments with Chromatography-Based Quantification at Scale. ○
- 18 Analytical characterization of host-cell-protein-rich aggregates in monoclonal antibody solutions. ○
- 17 Label-Free Quantification Mass Spectrometry Identifies Protein Markers of Chemotherapy Response in High-Grade Serous Ovarian Cancer. **2023**, 15, 2172 ○
- 16 Performance assessment of an equine metabolomics model for screening a range of anabolic agents. **2023**, 19, ○
- 15 Evaluating proteomics imputation methods with improved criteria. ○
- 14 Targeted MRM Quantification of Urinary Proteins in Chronic Kidney Disease Caused by Glomerulopathies. **2023**, 28, 3323 ○
- 13 A peptide-centric quantitative proteomics dataset for the phenotypic assessment of Alzheimer's disease. **2023**, 10, ○
- 12 Bromodomain Protein Inhibitors Reorganize the Chromatin of Synovial Fibroblasts. **2023**, 12, 1149 ○

- 11 Proteomics and machine learning identify a distinct biomarker panel to detect prodromal and early Parkinson disease. ○
- 10 EGFR+lung adenocarcinomas coopt alveolar macrophage metabolism and function to support EGFR signaling and growth. ○
- 9 Increasing Proteome Depth While Maintaining Quantitative Precision in Short-Gradient Data-Independent Acquisition Proteomics. ○
- 8 Epigenetic Control of Translation Checkpoint and Tumor Progression via RUVBL1-EEF1A1 Axis. ○
- 7 Targeted Proteomic Profiling Revealed Roles of Small GTPases during Osteogenic Differentiation. ○
- 6 RNA binding protein SYNCRIP maintains proteostasis and self-renewal of hematopoietic stem and progenitor cells. **2023**, 14, ○
- 5 Regulation of adaptive growth decisions via phosphorylation of the TRAPP11 complex in Arabidopsis. ○
- 4 MslImpute: Estimation of missing peptide intensity data in label-free quantitative mass spectrometry. **2023**, 100558 ○
- 3 Alternative splicing decouples local from global PRC2 activity. ○
- 2 Localization and Quantification of Post-Translational Modifications of Proteins Using Electron Activated Dissociation Fragmentation on a Fast-Acquisition Time-of-Flight Mass Spectrometer. ○
- 1 HIC1 interacts with FOXP3 multi protein complex: a novel mechanism to regulate human regulatory T cell differentiation and function. ○