CITATION REPORT List of articles citing

Universal sample preparation method for proteome analysis

DOI: 10.1038/nmeth.1322 Nature Methods, 2009, 6, 359-62.

Source: https://exaly.com/paper-pdf/46337879/citation-report.pdf

Version: 2024-04-28

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

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

#	Paper	IF	Citations
2200	FLEXITau: Quantifying Post-translational Modifications of Tau Protein in Vitro and in Human Disease.		
2199	Single Cell Proteomics Using Frog (Xenopus laevis) Blastomeres Isolated from Early Stage Embryos, Which Form a Geometric Progression in Protein Content.		
2198	Multiplexed Post-Experimental Monoisotopic Mass Refinement (mPE-MMR) to Increase Sensitivity and Accuracy in Peptide Identifications from Tandem Mass Spectra of Cofragmentation.		
2197	Comparative Evaluation of Small Molecular Additives and Their Effects on Peptide/Protein Identification.		
2196	Adapting Data-Independent Acquisition for Mass Spectrometry-Based Protein Site-Specific NGlycosylation Analysis.		
2195	MPA Portable: A Stand-Alone Software Package for Analyzing Metaproteome Samples on the Go.		
2194			
2193	glyXtoolMS: An Open-Source Pipeline for Semiautomated Analysis of Glycopeptide Mass Spectrometry Data.		
2192	LFAQ: Toward Unbiased Label-Free Absolute Protein Quantification by Predicting Peptide Quantitative Factors.		
2191	Comprehensive Analysis of Protein NTerminome by Guanidination of Terminal Amines.		
2190	A Single In-Vial Dual Extraction Strategy for the Simultaneous Lipidomics and Proteomics Analysis of HDL and LDL Fractions.		
2189	Differences between Platelets Derived from Neonatal Cord Blood and Adult Peripheral Blood Assessed by Mass Spectrometry.		
2188	Click-MS: Tagless Protein Enrichment Using Bioorthogonal Chemistry for Quantitative Proteomics.		
2187	Intracellularly Generated Immunological Gold Nanoparticles for Combinatorial Photothermal Therapy and Immunotherapy against Tumor.		
2186	Characterization of Gain-of-Function Mutant Provides New Insights into ClpP Structure.		
2185	Low-Background Acyl-Biotinyl Exchange Largely Eliminates the Coisolation of NonSAcylated Proteins and Enables Deep SAcylproteomic Analysis.		
2184	Chemical Proteomic Profiling of Lysophosphatidic Acid-Binding Proteins.		

2183	Hormonal inhibition of feeding and death in octopus: control by optic gland secretion. 1977 , 198, 948-51	124
2182	Fundamentals and Advances of Orbitrap Mass Spectrometry. 2000 , 1-36	1
2181	Pre-fractionation of rat liver cytosol proteins prior to mass spectrometry-based proteomic analysis using tandem biomimetic affinity chromatography. 2010 , 23, 93-100	6
2180	Spin filter-based sample preparation for shotgun proteomics. <i>Nature Methods</i> , 2009 , 6, 785; author reply 785-6	65
2179	Reply to Spin filterBased sample preparation for shotgun proteomics Nature Methods, 2009, 6, 785-786 21.6	38
2178	Improved visualization of protein consensus sequences by iceLogo. <i>Nature Methods</i> , 2009 , 6, 786-7	496
2177	Caenorhabditis elegans has a phosphoproteome atypical for metazoans that is enriched in developmental and sex determination proteins. 2009 , 8, 4039-49	59
2176	Global analysis of the yeast osmotic stress response by quantitative proteomics. 2009 , 5, 1337-46	108
2175	Combination of FASP and StageTip-based fractionation allows in-depth analysis of the hippocampal membrane proteome. 2009 , 8, 5674-8	426
2174	Proteomic Analyses of a Variety of Intracellular Bacterial Species Infecting Different Host Cell Lines. 2010 , 7, 222-232	5
2173	Establishment of a protein frequency library and its application in the reliable identification of specific protein interaction partners. 2010 , 9, 861-79	52
2172	Current technological challenges in biomarker discovery and validation. 2010 , 16, 101-21	17
2171	Prodynorphin mutations cause the neurodegenerative disorder spinocerebellar ataxia type 23. 2010 , 87, 593-603	86
2170	Depletion of abundant plasma proteins and limitations of plasma proteomics. 2010 , 9, 4982-91	246
2169	Direct cellular lysis/protein extraction protocol for soil metaproteomics. 2010 , 9, 6615-22	146
2168	What does the future hold for Top Down mass spectrometry?. 2010 , 21, 193-202	98
2167	A novel (18)O inverse labeling-based workflow for accurate bottom-up mass spectrometry quantification of proteins separated by gel electrophoresis. 2010 , 31, 3407-19	9
2166	Dried polyacrylamide gel absorption: a method for efficient elimination of the interferences from SDS-solubilized protein samples in mass spectrometry-based proteome analysis. 2010 , 31, 3816-22	10

2165	Advances in shotgun proteomics and the analysis of membrane proteomes. 2010 , 73, 2078-91	97
2164	Strain identification of commercial influenza vaccines by mass spectrometry. 2010 , 406, 193-203	10
2163	The Asia Oceania Human Proteome Organisation Membrane Proteomics Initiative. Preparation and characterisation of the carbonate-washed membrane standard. 2010 , 10, 4142-8	22
2162	Analysis of phagosomal proteomes: from latex-bead to bacterial phagosomes. 2010 , 10, 4098-116	20
2161	A targeted siRNA screen to identify SNAREs required for constitutive secretion in mammalian cells. 2010 , 11, 1191-204	90
2160	Super-SILAC mix for quantitative proteomics of human tumor tissue. <i>Nature Methods</i> , 2010 , 7, 383-5 21.6	431
2159	High-stringency tandem affinity purification of proteins conjugated to ubiquitin-like moieties. 2010 , 5, 873-82	15
2158	Decoding signalling networks by mass spectrometry-based proteomics. 2010 , 11, 427-39	484
2157	Proteomics, the red blood cell and transfusion medicine. 2010 , 5, 63-72	1
2156	Perfluorooctanoic acid for shotgun proteomics. 2010 , 5, e15332	27
2155	Defining the transcriptome and proteome in three functionally different human cell lines. 2010 , 6, 450	269
2154	The cargo-selective retromer complex is a recruiting hub for protein complexes that regulate endosomal tubule dynamics. 2010 , 123, 3703-17	178
2153	Toward quantitative proteomics of organ substructures: implications for renal physiology. 2010 , 30, 487-99	7
2152	Brain phosphoproteome obtained by a FASP-based method reveals plasma membrane protein topology. 2010 , 9, 3280-9	221
2151	Overview of peptide and protein analysis by mass spectrometry. 2010 , Chapter 16, Unit16.1	25
2150	Quantitative phosphoproteomics reveals widespread full phosphorylation site occupancy during mitosis. 2010 , 3, ra3	1106
2149	Proteome, phosphoproteome, and N-glycoproteome are quantitatively preserved in formalin-fixed paraffin-embedded tissue and analyzable by high-resolution mass spectrometry. 2010 , 9, 3688-700	193
2148	Feasibility of large-scale phosphoproteomics with higher energy collisional dissociation fragmentation. 2010 , 9, 6786-94	139

(2011-2010)

2147	efficiency of human plasma proteins by trypsin. 2010 , 9, 5422-37	265
2146	Yeast expression proteomics by high-resolution mass spectrometry. 2010 , 470, 259-80	8
2145	Precision mapping of an in vivo N-glycoproteome reveals rigid topological and sequence constraints. 2010 , 141, 897-907	700
2144	Quantitative interaction proteomics and genome-wide profiling of epigenetic histone marks and their readers. 2010 , 142, 967-80	579
2143	Mass spectrometry-based proteomics in cell biology. 2010 , 190, 491-500	310
2142	The bottleneck in the cancer biomarker pipeline and protein quantification through mass spectrometry-based approaches: current strategies for candidate verification. 2010 , 56, 212-22	140
2141	Red blood cell proteomics. 2010 , 17, 151-64	14
2140	Top-down and bottom-up proteomics of SDS-containing solutions following mass-based separation. 2010 , 9, 2863-70	119
2139	CDK2AP1/DOC-1 is a bona fide subunit of the Mi-2/NuRD complex. 2010 , 6, 1700-6	43
2138	An integrated global strategy for cell lysis, fractionation, enrichment and mass spectrometric analysis of phosphorylated peptides. 2010 , 6, 822-9	28
2137	Proteomic analysis of surface and endosomal membrane proteins from the avian LMH epithelial cell line. 2011 , 10, 3973-82	11
2136	A protein processing filter method for bacterial identification by mass spectrometry-based proteomics. 2011 , 10, 907-12	16
2135	Enhanced reliability of avian influenza virus (AIV) and Newcastle disease virus (NDV) identification using matrix-assisted laser desorption/ionization-mass spectrometry (MALDI-MS). 2011 , 83, 1717-25	6
2134	Improvements in proteomic metrics of low abundance proteins through proteome equalization using ProteoMiner prior to MudPIT. 2011 , 10, 3690-700	76
2133	Label-free proteomics and systems biology analysis of mycobacterial phagosomes in dendritic cells and macrophages. 2011 , 10, 2425-39	17
2132	Subcellular tissue proteomics of hepatocellular carcinoma for molecular signature discovery. 2011 , 10, 5070-83	34
2131	Absolute SILAC-compatible expression strain allows Sumo-2 copy number determination in clinical samples. 2011 , 10, 4869-75	33
2130	Pulsed stable isotope labeling of amino acids in cell culture uncovers the dynamic interactions between HIV-1 and the monocyte-derived macrophage. 2011 , 10, 2852-62	18

2129	Molecular architecture of the human Mediator-RNA polymerase II-TFIIF assembly. 2011 , 9, e1000603	77
2128	GeLCMS for in-depth protein characterization and advanced analysis of proteomes. 2011 , 753, 143-55	31
2127	Peptide extraction from formalin-fixed paraffin-embedded tissue. 2011 , Chapter 23, Unit23.5	9
2126	Formalin-Fixed Paraffin-Embedded Tissues. 2011 ,	4
2125	Mapping intact protein isoforms in discovery mode using top-down proteomics. 2011 , 480, 254-8	520
2124	Deep proteome and transcriptome mapping of a human cancer cell line. 2011 , 7, 548	723
2123	Supervised regularized canonical correlation analysis: integrating histologic and proteomic measurements for predicting biochemical recurrence following prostate surgery. 2011 , 12, 483	26
2122	Receptor Signal Transduction Protocols. 2011 ,	1
2121	DNA mediated chromatin pull-down for the study of chromatin replication. 2011 , 1, 95	45
2120	Quantitative analysis of the intra- and inter-individual variability of the normal urinary proteome. 2011 , 10, 637-45	175
2119	Proteomics under pressure: development of essential sample preparation techniques in proteomics using ultrahigh hydrostatic pressure. 2011 , 10, 5536-46	24
2118	Accurate proteome-wide protein quantification from high-resolution 15N mass spectra. 2011 , 12, R122	15
2117	Mass spectrometry at the interface of proteomics and genomics. 2011 , 7, 284-91	33
2116	Intact proteome fractionation strategies compatible with mass spectrometry. 2011 , 8, 787-800	35
2115	Analytical aspects of proteomics: 2009-2010. 2011 , 83, 4407-26	26
2114	Peptide affinity purification for the isolation and identification of GPCR-associated protein complexes. 2011 , 746, 389-98	
2113	Tandem affinity purification and identification of GPCR-associated protein complexes. 2011 , 746, 399-409	5
2112	Preparation and application of a partially degradable gel in mass spectrometry-based proteomic analysis. 2011 , 879, 2957-62	8

(2011-2011)

2111	Non-invasive proteomic analysis of human skin keratins: screening of methionine oxidation in keratins by mass spectrometry. 2011 , 75, 435-49	17
2110	The importance of the digest: proteolysis and absolute quantification in proteomics. 2011 , 54, 351-60	115
2109	Mass spectrometry-based phosphoproteomics reveals multisite phosphorylation on mammalian brain voltage-gated sodium and potassium channels. 2011 , 22, 153-9	24
2108	High recovery FASP applied to the proteomic analysis of microdissected formalin fixed paraffin embedded cancer tissues retrieves known colon cancer markers. 2011 , 10, 3040-9	228
2107	The host defense proteome of human and bovine milk. 2011 , 6, e19433	167
2106	Characterizing the Escherichia coli O157:H7 proteome including protein associations with higher order assemblies. 2011 , 6, e26554	16
2105	Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC) [an Introduction for Biologists. 2011 , 8, 2-16	3
2104	A novel strategy for the comprehensive analysis of the biomolecular composition of isolated plasma membranes. 2011 , 7, 541	32
2103	Comparative proteomics and activity of a green sulfur bacterium through the water column of Lake Cadagno, Switzerland. 2011 , 13, 203-215	32
2102	Proteomic reactors and their applications in biology. 2011 , 278, 3796-806	32
2101	Quantitative proteomics of Chlorobaculum tepidum: insights into the sulfur metabolism of a phototrophic green sulfur bacterium. 2011 , 323, 142-50	12
2100	Use of stable isotope labeling by amino acids in cell culture as a spike-in standard in quantitative proteomics. 2011 , 6, 147-57	232
2099	Monitoring protein expression in whole-cell extracts by targeted label- and standard-free LC-MS/MS. 2011 , 6, 859-69	50
2098	Critical assessment of accelerating trypsination methods. 2011 , 56, 1069-78	53
2097	Filter-aided sample preparation with dimethyl labeling to identify and quantify milk fat globule membrane proteins. 2011 , 75, 34-43	91
2096	Proteomic biosignatures for monocyte-macrophage differentiation. 2011 , 271, 239-55	17
2095	Microproteomic analysis of 10,000 laser captured microdissected breast tumor cells using short-range sodium dodecyl sulfate-polyacrylamide gel electrophoresis and porous layer open tubular liquid chromatography tandem mass spectrometry. 2011 , 1218, 8168-74	53
2094	Quantitative, high-resolution proteomics for data-driven systems biology. 2011 , 80, 273-99	550

2093	Standardization of a sample preparation and analytical workflow for proteomics of archival endometrial cancer tissue. 2011 , 10, 5264-71	33
2092	In vivo quantitative proteomics: the SILAC mouse. 2012 , 757, 435-50	69
2091	Large-scale phosphosite quantification in tissues by a spike-in SILAC method. <i>Nature Methods</i> , 2011 , 8, 655-8	126
2090	Analysis of intact protein isoforms by mass spectrometry. 2011 , 286, 25451-8	83
2089	100% protein sequence coverage: a modern form of surrealism in proteomics. 2011 , 41, 291-310	79
2088	Observed peptide pI and retention time shifts as a result of post-translational modifications in multidimensional separations using narrow-range IPG-IEF. 2011 , 40, 697-711	24
2087	Tools for phospho- and glycoproteomics of plasma membranes. 2011 , 41, 223-33	16
2086	Analysis of membrane and hydrophilic proteins simultaneously derived from the mouse brain using cloud-point extraction. 2011 , 400, 2827-36	25
2085	Skeletal muscle proteomics: current approaches, technical challenges and emerging techniques. 2011 , 1, 6	76
2084	Proteomic analysis of outer membrane vesicles derived from Pseudomonas aeruginosa. 2011 , 11, 3424-9	162
2083	Lights and shadows of proteomic technologies for the study of protein species including isoforms, splicing variants and protein post-translational modifications. 2011 , 11, 590-603	17
2082	A systematic analysis of the effects of increasing degrees of serum immunodepletion in terms of depth of coverage and other key aspects in top-down and bottom-up proteomic analyses. 2011 , 11, 2222-35	55
2081	Site-specific analysis of bacterial phosphoproteomes. 2011 , 11, 3002-11	39
2080	Comparison between procedures using SDS for shotgun proteomic analyses of complex samples. 2011 , 11, 2931-5	45
2079	Characterization of the Asia Oceania Human Proteome Organisation Membrane Proteomics Initiative Standard using SDS-PAGE shotgun proteomics. 2011 , 11, 4376-84	17
2078	OFFgel-based multidimensional LC-MS/MS approach to the cataloguing of the human platelet proteome for an interactomic profile. 2011 , 32, 686-95	28
2077	Quantitative proteomics for epigenetics. 2011 , 12, 224-34	54
2076	Comprehensive proteomics. 2011 , 22, 3-8	72

(2011-2011)

2075	Comparison of ultrafiltration units for proteomic and N-glycoproteomic analysis by the filter-aided sample preparation method. 2011 , 410, 307-9	138
2074	Comparison of surfactant-assisted shotgun methods using acid-labile surfactants and sodium dodecyl sulfate for membrane proteome analysis. 2011 , 698, 36-43	37
2073	Rapid and enhanced proteolytic digestion using electric-field-oriented enzyme reactor. 2011 , 74, 1030-5	18
2072	A workflow for peptide-based proteomics in a poorly sequenced plant: a case study on the plasma membrane proteome of banana. 2011 , 74, 1218-29	30
2071	Challenges and solutions for the identification of membrane proteins in non-model plants. 2011 , 74, 1165-81	27
2070	Recent progress in liquid chromatography-based separation and label-free quantitative plant proteomics. 2011 , 72, 963-74	65
2069	Liquid chromatography-mass spectrometry-based proteomics of Nitrosomonas. 2011 , 486, 465-82	17
2068	Quantification of proteins and their modifications using QconCAT technology. 2011 , 500, 113-31	7
2067	Accurate quantification of more than 4000 mouse tissue proteins reveals minimal proteome changes during aging. 2011 , 10, M110.004523	101
2066	Mining recent brain proteomic databases for ion channel phosphosite nuggets. 2011 , 137, 3-16	23
2065	Proteomics in the microbial sciences. 2011 , 2, 17-30	17
2064	Identification and characterization of a novel ubiquitous nucleolar protein 'NARR' encoded by a gene overlapping the rab34 oncogene. 2011 , 39, 7103-13	5
2063	Rare cell proteomic reactor applied to stable isotope labeling by amino acids in cell culture (SILAC)-based quantitative proteomics study of human embryonic stem cell differentiation. 2011 , 10, M110.000679	50
2062	A robust method for quantitative high-throughput analysis of proteomes by 18O labeling. 2011 , 10, M110.003	33655
2061	Beta1 integrin cytoplasmic tyrosines promote skin tumorigenesis independent of their phosphorylation. 2011 , 108, 15213-8	28
2060	Arabidopsis thaliana high-affinity phosphate transporters exhibit multiple levels of posttranslational regulation. 2011 , 23, 1523-35	158
2059	Challenges in plasma membrane phosphoproteomics. 2011 , 8, 483-94	14
2058	Proteomic characterization of pseudorabies virus extracellular virions. 2011 , 85, 6427-41	70

2057	Target identification using drug affinity responsive target stability (DARTS). 2011, 3, 163-180	104
2056	Sample preparation techniques for the untargeted LC-MS-based discovery of peptides in complex biological matrices. 2011 , 2011, 245291	58
2055	The quantitative proteome of a human cell line. 2011 , 7, 549	586
2054	Methods for identification of CA125 from ovarian cancer ascites by high resolution mass spectrometry. 2012 , 13, 9942-58	20
2053	The RNA-binding E3 ubiquitin ligase MEX-3C links ubiquitination with MHC-I mRNA degradation. 2012 , 31, 3596-606	60
2052	Quantitative proteomics reveals that Hsp90 inhibition preferentially targets kinases and the DNA damage response. 2012 , 11, M111.014654	77
2051	A crucial role for Mim2 in the biogenesis of mitochondrial outer membrane proteins. 2012 , 125, 3464-73	60
2050	Analysis of high accuracy, quantitative proteomics data in the MaxQB database. 2012 , 11, M111.014068	116
2049	Novel roles of Caenorhabditis elegans heterochromatin protein HP1 and linker histone in the regulation of innate immune gene expression. 2012 , 32, 251-65	28
2048	Proteomic portrait of human breast cancer progression identifies novel prognostic markers. 2012 , 72, 2428-39	107
2047	Comparative proteomics reveals a significant bias toward alternative protein isoforms with conserved structure and function. 2012 , 29, 2265-83	64
2046	On marathons and Sprints: an integrated quantitative proteomics and transcriptomics analysis of differences between slow and fast muscle fibers. 2012 , 11, M111.010801	65
2045	Mapping yeast N-glycosites with isotopically recoded glycans. 2012 , 11, M111.015339	22
2044	DNA and chromatin modification networks distinguish stem cell pluripotent ground states. 2012 , 11, 1036-47	12
2043	Quantitative measurement of allele-specific protein expression in a diploid yeast hybrid by LC-MS. 2012 , 8, 602	27
2042	Sequence and structural characterization of great salt lake bacteriophage CW02, a member of the T7-like supergroup. 2012 , 86, 7907-17	27
2041	Evidence for a genetic and physical interaction between nonstructural proteins NS1 and NS4B that modulates replication of West Nile virus. 2012 , 86, 7360-71	111
2040	An overview of the vaccinia virus infectome: a survey of the proteins of the poxvirus-infected cell. 2012 , 86, 1487-99	14

2039	Investigation of receptor interacting protein (RIP3)-dependent protein phosphorylation by quantitative phosphoproteomics. 2012 , 11, 1640-51	56
2038	Mining the proteome: the application of tandem mass spectrometry to endocrine cancer research. 2012 , 19, R149-61	3
2037	Miniaturized mass-spectrometry-based analysis system for fully automated examination of conditioned cell culture media. 2012 , 2012, 290457	3
2036	Pathobiochemical changes in diabetic skeletal muscle as revealed by mass-spectrometry-based proteomics. 2012 , 2012, 893876	13
2035	Phosphoproteome of Pristionchus pacificus provides insights into architecture of signaling networks in nematode models. 2012 , 11, 1631-9	11
2034	Novel proteomic tools reveal essential roles of SRP and importance of proper membrane protein biogenesis. 2012 , 11, M111.011585	12
2033	System-wide perturbation analysis with nearly complete coverage of the yeast proteome by single-shot ultra HPLC runs on a bench top Orbitrap. 2012 , 11, M111.013722	313
2032	Targeted proteomics of the secretory pathway reveals the secretome of mouse embryonic fibroblasts and human embryonic stem cells. 2012 , 11, 1829-39	24
2031	Peptide production and decay rates affect the quantitative accuracy of protein cleavage isotope dilution mass spectrometry (PC-IDMS). 2012 , 11, 814-23	58
2030	A Protein Epitope Signature Tag (PrEST) library allows SILAC-based absolute quantification and multiplexed determination of protein copy numbers in cell lines. 2012 , 11, O111.009613	116
2029	Proteomic analysis of formalin-fixed paraffin-embedded pancreatic tissue using liquid chromatography tandem mass spectrometry. 2012 , 41, 175-85	25
2028	Proteomic responses of Roseobacter litoralis OCh149 to starvation and light regimen. 2012 , 27, 430-42	12
2027	Establishment of two-dimensional gel electrophoresis profiles of the human acute promyelocytic leukemia cell line NB4. 2012 , 6, 570-4	4
2026	Longitudinal characterization of the brain proteomes for the tg2576 amyloid mouse model using shotgun based mass spectrometry. 2012 , 11, 6159-74	22
2025	Neuroproteomic profiling of human brain tissue using multidimensional separation techniques and selective enrichment of membrane proteins. 2012 , 33, 3779-85	7
2024	Consecutive proteolytic digestion in an enzyme reactor increases depth of proteomic and phosphoproteomic analysis. 2012 , 84, 2631-7	229
2023	Loss of perivascular adipose tissue on peroxisome proliferator-activated receptor-ldeletion in smooth muscle cells impairs intravascular thermoregulation and enhances atherosclerosis. 2012 , 126, 1067-78	227
2022	Shotgun analysis of membrane proteomes by an improved SDS-assisted sample preparation method coupled with liquid chromatography-tandem mass spectrometry. 2012 , 911, 6-14	6

2021	Extensive quantitative remodeling of the proteome between normal colon tissue and adenocarcinoma. 2012 , 8, 611	174
2020	Proteomic analysis of Chinese hamster ovary cells. 2012 , 11, 5265-76	128
2019	Label-free quantification and shotgun analysis of complex proteomes by one-dimensional SDS-PAGE/NanoLC-MS: evaluation for the large scale analysis of inflammatory human endothelial cells. 2012 , 11, 527-39	58
2018	Proteomic characteristics of the liver and skeletal muscle in the Chinese tree shrew (Tupaia belangeri chinensis). 2012 , 3, 691-700	9
2017	Sample preparation and analytical strategies for large-scale phosphoproteomics experiments. 2012 , 23, 843-53	35
2016	SILAC-based proteomic analysis to investigate the impact of amyloid precursor protein expression in neuronal-like B103 cells. 2012 , 33, 3728-37	14
2015	Patient-specific protein aggregates in myofibrillar myopathies: laser microdissection and differential proteomics for identification of plaque components. 2012 , 12, 3598-609	18
2014	Comprehensive mapping of the bull sperm surface proteome. 2012 , 12, 3559-79	70
2013	SDS-PAGE-free protocol for comprehensive identification of cytochrome P450 enzymes and uridine diphosphoglucuronosyl transferases in human liver microsomes. 2012 , 12, 3464-9	4
2012	Enhanced N-glycosylation site exploitation of sialoglycopeptides by peptide IPG-IEF assisted TiO2 chromatography. 2012 , 29, 433-43	11
2011	A census of human soluble protein complexes. 2012 , 150, 1068-81	612
2010	Increased expression of LDL receptor-related protein 1 during human cytomegalovirus infection reduces virion cholesterol and infectivity. 2012 , 12, 86-96	48
2009	Long noncoding RNAs are rarely translated in two human cell lines. 2012 , 22, 1646-57	292
2008	Ultrasmall gold nanoparticles for highly specific isolation/enrichment of N-linked glycosylated peptides. 2012 , 137, 991-8	28
2007	Quantitative functions of Argonaute proteins in mammalian development. 2012 , 26, 693-704	131
2006	Proteomic profiling of infiltrating ductal carcinoma reveals increased cellular interactions with tissue microenvironment. 2012 , 11, 2236-46	3
2005	Proteomic plasma membrane profiling reveals an essential role for gp96 in the cell surface expression of LDLR family members, including the LDL receptor and LRP6. 2012 , 11, 1475-84	55
2004	Global snapshot of the influence of endocytosis upon EGF receptor signaling output. 2012 , 11, 5157-66	15

2003	Online nanoscale ERLIC-MS outperforms RPLC-MS for shotgun proteomics in complex mixtures. 2012 , 11, 5059-64	20
2002	Fully automated multifunctional ultrahigh pressure liquid chromatography system for advanced proteome analyses. 2012 , 11, 4373-81	16
2001	Nano-LC FTICR tandem mass spectrometry for top-down proteomics: routine baseline unit mass resolution of whole cell lysate proteins up to 72 kDa. 2012 , 84, 2111-7	35
2000	Centrifugation assisted microreactor enables facile integration of trypsin digestion, hydrophilic interaction chromatography enrichment, and on-column deglycosylation for rapid and sensitive N-glycoproteome analysis. 2012 , 84, 5146-53	84
1999	Comparative proteomic analysis of eleven common cell lines reveals ubiquitous but varying expression of most proteins. 2012 , 11, M111.014050	566
1998	Coupling methanol denaturation, immobilized trypsin digestion, and accurate mass and time tagging for liquid-chromatography-based shotgun proteomics of low nanogram amounts of RAW 264.7 cell lysate. 2012 , 84, 8715-21	21
1997	Prefractionation and separation by C8 stationary phase: effective strategies for integral membrane proteins analysis. 2012 , 88, 567-72	11
1996	Protein turnover quantification in a multilabeling approach: from data calculation to evaluation. 2012 , 11, 512-26	17
1995	Evaluation of the compact high-field orbitrap for top-down proteomics of human cells. 2012, 11, 4308-14	75
1994	Advancing formaldehyde cross-linking towards quantitative proteomic applications. 2012 , 404, 1057-67	43
1993	Deep proteome profiling of circulating granulocytes reveals bactericidal/permeability-increasing protein as a biomarker for severe atherosclerotic coronary stenosis. 2012 , 11, 5235-44	16
1992	A simple protocol for Matrix Assisted Laser Desorption Ionization- time of flight-mass spectrometry (MALDI-TOF-MS) analysis of lipids and proteins in single microsamples of paintings. 2012 , 718, 1-10	40
1991	Mapping N-glycosylation sites across seven evolutionarily distant species reveals a divergent substrate proteome despite a common core machinery. 2012 , 46, 542-8	199
1990	Mapping in vivo signal transduction defects by phosphoproteomics. 2012 , 18, 43-51	33
1989	Shotgun analysis of membrane proteomes using a novel combinative strategy of solution-based sample preparation coupled with liquid chromatography-tandem mass spectrometry. 2012 , 901, 18-24	12
1988	Label-free quantitative proteomics reveals differentially regulated proteins in the latex of sticky diseased Carica papaya L. plants. 2012 , 75, 3191-8	28
1987	MHC class I target recognition, immunophenotypes and proteomic profiles of natural killer cells within the spleens of day-14 chick embryos. 2012 , 37, 446-56	11
1986	Combination of FASP and fully automated 2D-LC-MS/MS allows in-depth proteomic characterization of mouse zymogen granules. 2013 , 27, 407-8	9

1985	Evaluation of SDS depletion using an affinity spin column and IMS-MS detection. 2012 , 12, 3138-42	25
1984	Comparison of total and cytoplasmic mRNA reveals global regulation by nuclear retention and miRNAs. 2012 , 13, 574	30
1983	Development stage-specific proteomic profiling uncovers small, lineage specific proteins most abundant in the Aspergillus Fumigatus conidial proteome. 2012 , 10, 30	47
1982	Optimization of iTRAQ labelling coupled to OFFGEL fractionation as a proteomic workflow to the analysis of microsomal proteins of Medicago truncatula roots. 2012 , 10, 37	28
1981	Integrated next-generation sequencing of 16S rDNA and metaproteomics differentiate the healthy urine microbiome from asymptomatic bacteriuria in neuropathic bladder associated with spinal cord injury. 2012 , 10, 174	268
1980	Novel mass spectrometric method for phosphorylation quantification using cerium oxide nanoparticles and tandem mass tags. 2012 , 84, 2466-73	18
1979	Tumour suppressor p16(INK4a) - anoikis-favouring decrease in N/O-glycan/cell surface sialylation by down-regulation of enzymes in sialic acid biosynthesis in tandem in a pancreatic carcinoma model. 2012 , 279, 4062-80	96
1978	Super-SILAC allows classification of diffuse large B-cell lymphoma subtypes by their protein expression profiles. 2012 , 11, 77-89	135
1977	Comprehensive phosphoproteome analysis of INS-1 pancreatic I-cells using various digestion strategies coupled with liquid chromatography-tandem mass spectrometry. 2012 , 11, 2206-23	21
1976	Classification of inhibitors of hepatic organic anion transporting polypeptides (OATPs): influence of protein expression on drug-drug interactions. 2012 , 55, 4740-63	245
1975	ZIC-cHILIC as a fractionation method for sensitive and powerful shotgun proteomics. 2012 , 7, 2041-55	29
1974	Advances in phosphopeptide enrichment techniques for phosphoproteomics. 2012 , 43, 1009-24	90
1973	Sample preparation for the analysis of membrane proteomes by mass spectrometry. 2012 , 3, 661-8	8
1972	The Plasmodium falciparum schizont phosphoproteome reveals extensive phosphatidylinositol and cAMP-protein kinase A signaling. 2012 , 11, 5323-37	110
1971	Targeted proteomics for metabolic pathway optimization. 2012 , 944, 237-49	16
1970	Comparison of extraction methods for the comprehensive analysis of mouse brain proteome using shotgun-based mass spectrometry. 2012 , 11, 2441-51	47
1969	HPLC-SEC characterization of membrane protein-detergent complexes. 2012 , Chapter 29, Unit 29.5.1-12	10
1968	Proteome-wide selected reaction monitoring assays for the human pathogen Streptococcus pyogenes. 2012 , 3, 1301	62

1967	Limits of Proteomics: Protein Solubilisation Issues. 2012 ,	1
1966	Identifying chromatin readers using a SILAC-based histone peptide pull-down approach. 2012 , 512, 137-60	9
1965	Comparative study of workflows optimized for in-gel, in-solution, and on-filter proteolysis in the analysis of plasma membrane proteins. 2012 , 11, 3030-4	55
1964	Comprehensive quantification of monolignol-pathway enzymes in Populus trichocarpa by protein cleavage isotope dilution mass spectrometry. 2012 , 11, 3390-404	38
1963	Integrated SDS removal and peptide separation by strong-cation exchange liquid chromatography for SDS-assisted shotgun proteome analysis. 2012 , 11, 818-28	31
1962	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
1961	Integrin and Cell Adhesion Molecules. 2012,	2
1960	Simple sodium dodecyl sulfate-assisted sample preparation method for LC-MS-based proteomics applications. 2012 , 84, 2862-7	63
1959	GOFAST: an integrated approach for efficient and comprehensive membrane proteome analysis. 2012 , 84, 9008-14	20
1958	In-depth analysis of the Magnaporthe oryzae conidial proteome. 2012 , 11, 5827-35	28
1957	Coupling a detergent lysis/cleanup methodology with intact protein fractionation for enhanced proteome characterization. 2012 , 11, 6008-18	63
1956	Comparative SILAC proteomic analysis of Trypanosoma brucei bloodstream and procyclic lifecycle stages. 2012 , 7, e36619	122
1955	The adenomatous polyposis coli protein contributes to normal compaction of mitotic chromatin. 2012 , 7, e38102	10
1954	Identification of a candidate proteomic signature to discriminate multipotent and non-multipotent stromal cells. 2012 , 7, e38954	6
1953	The biochemical anatomy of cortical inhibitory synapses. 2012 , 7, e39572	43
1952	Short-chain 3-hydroxyacyl-coenzyme A dehydrogenase associates with a protein super-complex integrating multiple metabolic pathways. 2012 , 7, e35048	16
1951	Distribution and functions of TonB-dependent transporters in marine bacteria and environments: implications for dissolved organic matter utilization. 2012 , 7, e41204	73
1950	GTSE1 is a microtubule plus-end tracking protein that regulates EB1-dependent cell migration. 2012 , 7, e51259	40

1949	Organelle proteomics in skeletal muscle biology. 2012 , 2,	6
1948	Perfluorooctanoic acid and ammonium perfluorooctanoate: volatile surfactants for proteome analysis?. 2012 , 26, 523-31	12
1947	Proteomic analysis of rat microglia establishes a high-confidence reference data set of over 3000 proteins. 2012 , 12, 246-50	14
1946	Effect of mass spectrometric parameters on peptide and protein identification rates for shotgun proteomic experiments on an LTQ-orbitrap mass analyzer. 2012 , 12, 21-31	43
1945	Expanding the zebrafish embryo proteome using multiple fractionation approaches and tandem mass spectrometry. 2012 , 12, 1879-82	17
1944	Systematic discovery of structural elements governing stability of mammalian messenger RNAs. 2012 , 485, 264-8	116
1943	Protein-protein interactions in plants. 2012 , 53, 617-25	32
1942	Human proteome analysis by using reversed phase monolithic silica capillary columns with enhanced sensitivity. 2012 , 1228, 292-7	50
1941	Detection and diagnostic value of urine leucine-rich ⊉-glycoprotein in children with suspected acute appendicitis. 2012 , 60, 78-83.e1	44
1940	Synapse-directed delivery of immunomodulators using T-cell-conjugated nanoparticles. 2012 , 33, 5776-87	7.17
· ·	-,··	141
1939	Enhanced performance of pulsed Q collision induced dissociation-based peptide identification on a dual-pressure linear ion trap. 2012 , 23, 186-9	5
	Enhanced performance of pulsed Q collision induced dissociation-based peptide identification on a	
1939	Enhanced performance of pulsed Q collision induced dissociation-based peptide identification on a dual-pressure linear ion trap. 2012 , 23, 186-9 Lowered expression of galectin-2 is associated with lymph node metastasis in gastric cancer. 2012 ,	5
1939	Enhanced performance of pulsed Q collision induced dissociation-based peptide identification on a dual-pressure linear ion trap. 2012, 23, 186-9 Lowered expression of galectin-2 is associated with lymph node metastasis in gastric cancer. 2012, 47, 37-48 Unrestrictive identification of post-translational modifications in the urine proteome without	5
1939 1938 1937	Enhanced performance of pulsed Q collision induced dissociation-based peptide identification on a dual-pressure linear ion trap. 2012, 23, 186-9 Lowered expression of galectin-2 is associated with lymph node metastasis in gastric cancer. 2012, 47, 37-48 Unrestrictive identification of post-translational modifications in the urine proteome without enrichment. 2013, 11, 1 Method for isolation and molecular characterization of extracellular microvesicles released from	5 27 27
1939 1938 1937 1936	Enhanced performance of pulsed Q collision induced dissociation-based peptide identification on a dual-pressure linear ion trap. 2012, 23, 186-9 Lowered expression of galectin-2 is associated with lymph node metastasis in gastric cancer. 2012, 47, 37-48 Unrestrictive identification of post-translational modifications in the urine proteome without enrichment. 2013, 11, 1 Method for isolation and molecular characterization of extracellular microvesicles released from brain endothelial cells. 2013, 10, 4 Mass Spectrometry Investigation of Glycosylation Aberration via De-N-Glycopeptide Analysis. 2013,	5 27 27 135
1939 1938 1937 1936	Enhanced performance of pulsed Q collision induced dissociation-based peptide identification on a dual-pressure linear ion trap. 2012, 23, 186-9 Lowered expression of galectin-2 is associated with lymph node metastasis in gastric cancer. 2012, 47, 37-48 Unrestrictive identification of post-translational modifications in the urine proteome without enrichment. 2013, 11, 1 Method for isolation and molecular characterization of extracellular microvesicles released from brain endothelial cells. 2013, 10, 4 Mass Spectrometry Investigation of Glycosylation Aberration via De-N-Glycopeptide Analysis. 2013, 66, 770 Chicken innate immune response to oral infection with Salmonella enterica serovar Enteritidis.	5 27 27 135

1931	iFASP: combining isobaric mass tagging with filter-aided sample preparation. 2013 , 12, 3809-12	47
1930	Data-independent acquisition strategies for quantitative proteomics. 2013 , 51-54	
1929	Small-molecule modulation of Wnt signaling via modulating the Axin-LRP5/6 interaction. 2013 , 9, 579-85	58
1928	Cdc7-dependent and -independent phosphorylation of Claspin in the induction of the DNA replication checkpoint. 2013 , 12, 1560-8	23
1927	Tissue Sample Preparation for Proteomic Analysis. 2013 , 39-50	3
1926	Characterization of a high field Orbitrap mass spectrometer for proteome analysis. 2013 , 13, 2552-62	9
1925	Whole human genome proteogenomic mapping for ENCODE cell line data: identifying protein-coding regions. 2013 , 14, 141	45
1924	Proteomic analysis indicates massive changes in metabolism prior to the inhibition of growth and photosynthesis of grapevine (Vitis vinifera L.) in response to water deficit. 2013 , 13, 49	96
1923	A reversible gene trap collection empowers haploid genetics in human cells. <i>Nature Methods</i> , 2013 , 10, 965-71	76
1922	DMSO enhances electrospray response, boosting sensitivity of proteomic experiments. <i>Nature Methods</i> , 2013 , 10, 989-91	170
1921	Comparison of bottom-up proteomic approaches for LC-MS analysis of complex proteomes. 2013 , 5,	28
1920	Virus-Host Interactions. 2013,	2
1919	Advances in Proteomic Methods. 2013 , 127-167	
1918	Proteomic analysis of cow, yak, buffalo, goat and camel milk whey proteins: quantitative differential expression patterns. 2013 , 12, 1660-7	75
1917	RAP1 protects from obesity through its extratelomeric role regulating gene expression. 2013 , 3, 2059-74	77
1916	Quantitative proteomic analysis reveals the neuroprotective effects of huperzine A for amyloid beta treated neuroblastoma N2a cells. 2013 , 13, 1314-24	32
1915	Identification of differentially expressed proteins in atherosclerotic aorta and effect of vitamin E. 2013 , 92, 260-73	21
1914	An activity-maintaining sequential protein extraction method for bioactive assay and proteome analysis of velvet antlers. 2013 , 107, 189-94	12

1913	Identification of proteomic biomarkers in M. Longissimus dorsi as potential predictors of pork quality. 2013 , 95, 679-87	31
1912	Combined proteome and transcriptome analyses for the discovery of urinary biomarkers for urothelial carcinoma. 2013 , 108, 1854-61	35
1911	Sample handling and mass spectrometry for microbial metaproteomic analyses. 2013 , 531, 289-303	9
1910	Unifying expression scale for peptide hydrophobicity in proteomic reversed phase high-pressure liquid chromatography experiments. 2013 , 85, 10878-86	8
1909	Dynamics of chloroplast proteome in salt-stressed mangrove Kandelia candel (L.) Druce. 2013 , 12, 5124-36	76
1908	Immune-mediated pore-forming pathways induce cellular hypercitrullination and generate citrullinated autoantigens in rheumatoid arthritis. 2013 , 5, 209ra150	157
1907	Affinity proteomics reveals human host factors implicated in discrete stages of LINE-1 retrotransposition. 2013 , 155, 1034-48	133
1906	Serum biomarkers reveal long-term cardiac injury in isoproterenol-treated African green monkeys. 2013 , 12, 1830-7	6
1905	Quantitative proteomics reveals oxygen-dependent changes in neuronal mitochondria affecting function and sensitivity to rotenone. 2013 , 12, 4599-606	18
1904	The human cap-binding complex is functionally connected to the nuclear RNA exosome. 2013 , 20, 1367-76	157
1903	Multi-peptide nLC-PC-IDMS-SRM-based assay for the quantification of biomarkers in the chicken ovarian cancer model. 2013 , 61, 323-30	12
1902	Label-free quantitative proteomic analysis of right ventricular remodeling in infant Tetralogy of Fallot patients. 2013 , 84, 78-91	13
1901	Comparative study of label and label-free techniques using shotgun proteomics for relative protein quantification. 2013 , 928, 83-92	22
1900	Trypanosomatid Phosphoproteomics. 2013 , 61-78	
1899	A simple integrated system for rapid analysis of sialic-acid-containing N-glycopeptides from human serum. 2013 , 13, 1306-13	28
1898	Global quantitative SILAC phosphoproteomics reveals differential phosphorylation is widespread between the procyclic and bloodstream form lifecycle stages of Trypanosoma brucei. 2013 , 12, 2233-44	139
1897	Physiological adaptations of Saccharomyces cerevisiae evolved for improved butanol tolerance. 2013 , 6, 101	40
1896	Bottom-up proteome analysis of E. coli using capillary zone electrophoresis-tandem mass spectrometry with an electrokinetic sheath-flow electrospray interface. 2013 , 13, 2546-51	35

(2013-2013)

1895	skeletal muscle. 2013 , 12, 4327-39	17
1894	Proteome digestion specificity analysis for rational design of extended bottom-up and middle-down proteomics experiments. 2013 , 12, 5558-69	30
1893	A high-throughput sample preparation method for cellular proteomics using 96-well filter plates. 2013 , 13, 2980-3	26
1892	Evaluation of the combinative application of SDS and sodium deoxycholate to the LC-MS-based shotgun analysis of membrane proteomes. 2013 , 36, 3026-34	7
1891	Leucoagaricus gongylophorus produces diverse enzymes for the degradation of recalcitrant plant polymers in leaf-cutter ant fungus gardens. 2013 , 79, 3770-8	75
1890	Yolk-shell magnetic microspheres with mesoporous yttrium phosphate shells for selective capture and identification of phosphopeptides. 2013 , 1, 3661-3669	22
1889	Proteomics-based methods for discovery, quantification, and validation of protein-protein interactions. 2013 , 85, 749-68	69
1888	Comparative proteomics analysis of selenium responses in selenium-enriched rice grains. 2013 , 12, 808-20	19
1887	The revolution and evolution of shotgun proteomics for large-scale proteome analysis. 2013 , 135, 1629-40	91
1886	In-depth membrane proteomic study of breast cancer tissues for the generation of a chromosome-based protein list. 2013 , 12, 208-13	19
1885	System-wide identification of RNA-binding proteins by interactome capture. 2013 , 8, 491-500	135
1884	Urinary exosomes and diabetic nephropathy: a proteomic approach. 2013 , 9, 1139-46	52
1883	Quantitative mass spectrometry for colorectal cancer proteomics. 2013 , 7, 42-54	15
1882	PLK1 signaling in breast cancer cells cooperates with estrogen receptor-dependent gene transcription. 2013 , 3, 2021-32	45
1881	Efficient retrograde transport of pseudorabies virus within neurons requires local protein synthesis in axons. 2013 , 13, 54-66	54
1880	Retinoic acid-induced protein 3: identification and characterisation of a novel prognostic colon cancer biomarker. 2013 , 49, 531-9	33
1879	Quantitative site-specific reactivity profiling of S-nitrosylation in mouse skeletal muscle using cysteinyl peptide enrichment coupled with mass spectrometry. 2013 , 57, 68-78	53
1878	Quantitative assessment of in-solution digestion efficiency identifies optimal protocols for unbiased protein analysis. 2013 , 12, 2992-3005	168

1877	Discovery and mass spectrometric analysis of novel splice-junction peptides using RNA-Seq. 2013 , 12, 2341-53	96
1876	Rapid and deep human proteome analysis by single-dimension shotgun proteomics. 2013 , 12, 3330-8	107
1875	A proteomic perspective of inbuilt viral protein regulation: pUL46 tegument protein is targeted for degradation by ICP0 during herpes simplex virus type 1 infection. 2013 , 12, 3237-52	29
1874	The SH2 domain interaction landscape. 2013 , 3, 1293-305	89
1873	Prostasomes from four different species are able to produce extracellular adenosine triphosphate (ATP). 2013 , 1830, 4604-10	40
1872	MALDI profiles of proteins and lipids for the rapid characterisation of upper GI-tract cancers. 2013 , 80, 207-15	13
1871	A unique Oct4 interface is crucial for reprogramming to pluripotency. 2013 , 15, 295-301	109
1870	Dynamic readers for 5-(hydroxy)methylcytosine and its oxidized derivatives. 2013 , 152, 1146-59	748
1869	Development of a high-performance liquid chromatography-electrospray ionization-quadrupole-time-of-flight-mass spectrometry methodology for the determination of three highly antihypertensive peptides in maize crops. 2013 , 1285, 69-77	16
1868	Deficiency of terminal ADP-ribose protein glycohydrolase TARG1/C6orf130 in neurodegenerative disease. 2013 , 32, 1225-37	215
1867	Sources of technical variability in quantitative LC-MS proteomics: human brain tissue sample analysis. 2013 , 12, 2128-37	118
1866	The coming age of complete, accurate, and ubiquitous proteomes. 2013 , 49, 583-90	294
1865	Protein analysis by shotgun/bottom-up proteomics. 2013 , 113, 2343-94	902
1864	Protein carbamylation: in vivo modification or in vitro artefact?. 2013 , 13, 941-4	98
1863	Integral membrane proteins and bilayer proteomics. 2013 , 85, 2558-68	66
1862	Label-free quantitative analysis of the membrane proteome of Bace1 protease knock-out zebrafish brains. 2013 , 13, 1519-27	21
1861	Proteomic workflow for analysis of archival formalin-fixed and paraffin-embedded clinical samples to a depth of 10 000 proteins. 2013 , 7, 225-33	117
1860	In vivo SILAC-based proteomics reveals phosphoproteome changes during mouse skin carcinogenesis. 2013 , 3, 552-66	82

Membrane proteomics by high performance liquid chromatography-tandem mass spectrometry: Analytical approaches and challenges. 2013 , 13, 404-23	72
Spatial regulation of VEGF receptor endocytosis in angiogenesis. 2013 , 15, 249-60	190
Target identification for small bioactive molecules: finding the needle in the haystack. 2013 , 52, 2744-92	339
Centrosome isolation and analysis by mass spectrometry-based proteomics. 2013 , 525, 371-93	9
From cells to peptides: "one-stop" integrated proteomic processing using amphipols. 2013, 12, 1512-9	21
Phosphoproteomicsmore than meets the eye. 2013 , 34, 1483-92	32
Using guanidine-hydrochloride for fast and efficient protein digestion and single-step affinity-purification mass spectrometry. 2013 , 12, 1020-30	33
Membrane protein shaving with thermolysin can be used to evaluate topology predictors. 2013 , 13, 1467-80	9
Integrated capillary zone electrophoresis-electrospray ionization tandem mass spectrometry system with an immobilized trypsin microreactor for online digestion and analysis of picogram amounts of RAW 264.7 cell lysate. 2013 , 85, 4187-94	45
Efficient proteolysis strategies based on microchip bioreactors. 2013 , 82, 1-13	17
A decade of plant proteomics and mass spectrometry: translation of technical advancements to food security and safety issues. 2013 , 32, 335-65	59
In-solution digestion of glycoproteins for glycopeptide-based mass analysis. 2013 , 951, 103-11	4
A systematic quantitative proteomic examination of multidrug resistance in Acinetobacter baumannii. 2013 , 84, 17-39	37
Proteomics identifies molecular networks affected by tetradecylthioacetic acid and fish oil supplemented diets. 2013 , 84, 61-77	15
A proteomic characterization of factors enriched at nascent DNA molecules. 2013 , 3, 1105-16	87
Quantitation of Met tyrosine phosphorylation using MRM-MS. 2013 , 1002, 181-93	2
Label-free quantitative shotgun proteomics using normalized spectral abundance factors. 2013 , 1002, 205-22	48
Plant proteogenomics: from protein extraction to improved gene predictions. 2013 , 1002, 267-94	13
	Analytical approaches and challenges. 2013, 13, 404-23 Spatial regulation of VEGF receptor endocytosis in angiogenesis. 2013, 15, 249-60 Target identification for small bioactive molecules: finding the needle in the haystack. 2013, 52, 2744-92 Centrosome isolation and analysis by mass spectrometry-based proteomics. 2013, 525, 371-93 From cells to peptides: "one-stop" integrated proteomic processing using amphipols. 2013, 12, 1512-9 Phosphoproteomics—more than meets the eye. 2013, 34, 1483-92 Using guanidine-hydrochloride for fast and efficient protein digestion and single-step affinity-purification mass spectrometry. 2013, 12, 1020-30 Membrane protein shaving with thermolysin can be used to evaluate topology predictors. 2013, 13, 1467-80 Integrated capillary zone electrophoresis-electrospray ionization tandem mass spectrometry system with an immobilized trypsin microreactor for online digestion and analysis of picogram amounts of RAW 264.7 cell lysate. 2013, 85, 4187-94 Efficient proteolysis strategies based on microchip bioreactors. 2013, 82, 1-13 A decade of plant proteomics and mass spectrometry: translation of technical advancements to food security and safety issues. 2013, 32, 335-65 In-solution digestion of glycoproteins for glycopeptide-based mass analysis. 2013, 951, 103-11 A systematic quantitative proteomic examination of multidrug resistance in Acinetobacter baumannii. 2013, 84, 17-39 Proteomics identifies molecular networks affected by tetradecylthioacetic acid and fish oil supplemented diets. 2013, 84, 61-77 A proteomic characterization of factors enriched at nascent DNA molecules. 2013, 3, 1105-16 Quantitation of Met tyrosine phosphorylation using MRM-MS. 2013, 1002, 181-93 Label-free quantitative shotgun proteomics using normalized spectral abundance factors. 2013, 1002, 205-22

1841	Protein tyrosine phosphatase SHP2/PTPN11 mistargeting as a consequence of SH2-domain point mutations associated with Noonan Syndrome and leukemia. 2013 , 84, 132-47	11
1840	Citric acid-assisted two-step enrichment with TiO2 enhances the separation of multi- and monophosphorylated peptides and increases phosphoprotein profiling. 2013 , 12, 2467-76	27
1839	Target proteomic profiling of frozen pancreatic CD24+ adenocarcinoma tissues by immuno-laser capture microdissection and nano-LC-MS/MS. 2013 , 12, 2791-804	31
1838	Evaluation and optimization of mass spectrometric settings during data-dependent acquisition mode: focus on LTQ-Orbitrap mass analyzers. 2013 , 12, 3071-86	110
1837	□1- and □-class integrins cooperate to regulate myosin II during rigidity sensing of fibronectin-based microenvironments. 2013 , 15, 625-36	307
1836	Proteomic identification of unique photoreceptor disc components reveals the presence of PRCD, a protein linked to retinal degeneration. 2013 , 12, 3010-8	34
1835	MScDB: a mass spectrometry-centric protein sequence database for proteomics. 2013 , 12, 2386-98	9
1834	Deconvolution of mixture spectra and increased throughput of peptide identification by utilization of intensified complementary ions formed in tandem mass spectrometry. 2013 , 12, 3362-71	20
1833	Improved mass spectrometric analysis of membrane proteins based on rapid and versatile sample preparation on nanodiamond particles. 2013 , 85, 6748-55	37
1832	In-depth proteomic analysis of mouse cochlear sensory epithelium by mass spectrometry. 2013 , 12, 3620-30	12
1831	Protein interaction networks in innate immunity. 2013 , 34, 610-9	19
1820		
1030	Label-free quantification in clinical proteomics. 2013 , 1834, 1581-90	134
1829	Label-free quantification in clinical proteomics. 2013 , 1834, 1581-90 Global protein phosphorylation dynamics during deoxynivalenol-induced ribotoxic stress response in the macrophage. 2013 , 268, 201-11	134 37
	Global protein phosphorylation dynamics during deoxynivalenol-induced ribotoxic stress response	
1829	Global protein phosphorylation dynamics during deoxynivalenol-induced ribotoxic stress response in the macrophage. 2013 , 268, 201-11 Dimethyl-labeling-based protein quantification and pathway search: a novel method of spinal cord	37
1829 1828 1827	Global protein phosphorylation dynamics during deoxynivalenol-induced ribotoxic stress response in the macrophage. 2013, 268, 201-11 Dimethyl-labeling-based protein quantification and pathway search: a novel method of spinal cord analysis applicable for neurological studies. 2013, 12, 2245-52 ETheraphotoxin-An1a: primary structure determination and assessment of the pharmacological activity of a promiscuous anti-insect toxin from the venom of the tarantula Acanthoscurria	37
1829 1828 1827	Global protein phosphorylation dynamics during deoxynivalenol-induced ribotoxic stress response in the macrophage. 2013, 268, 201-11 Dimethyl-labeling-based protein quantification and pathway search: a novel method of spinal cord analysis applicable for neurological studies. 2013, 12, 2245-52 ETheraphotoxin-An1a: primary structure determination and assessment of the pharmacological activity of a promiscuous anti-insect toxin from the venom of the tarantula Acanthoscurria natalensis (Mygalomorphae, Theraphosidae). 2013, 70, 123-34	37 14 6

1823	Diagnosis of 🛮 lactam resistance in Acinetobacter baumannii using shotgun proteomics and LC-nano-electrospray ionization ion trap mass spectrometry. 2013 , 85, 2802-8	20
1822	Getting intimate with trypsin, the leading protease in proteomics. 2013 , 32, 453-65	127
1821	Mapping of the N-linked glycoproteome of human spermatozoa. 2013 , 12, 5750-9	44
1820	PTRF/cavin-1 is essential for multidrug resistance in cancer cells. 2013 , 12, 605-14	38
1819	Studies of mucus in mouse stomach, small intestine, and colon. II. Gastrointestinal mucus proteome reveals Muc2 and Muc5ac accompanied by a set of core proteins. 2013 , 305, G348-56	86
1818	Two birds with one stone: doing metabolomics with your proteomics kit. 2013 , 13, 3371-86	19
1817	Coordinated post-translational responses of aquaporins to abiotic and nutritional stimuli in Arabidopsis roots. 2013 , 12, 3886-97	60
1816	SILAC-based phosphoproteomics reveals an inhibitory role of KSR1 in p53 transcriptional activity via modulation of DBC1. 2013 , 109, 2675-84	15
1815	Comparative LC-MS/MS analysis of optimal cutting temperature (OCT) compound removal for the study of mammalian proteomes. 2013 , 138, 6380-4	14
1814	Novel phosphorylation sites in the S. cerevisiae Cdc13 protein reveal new targets for telomere length regulation. 2013 , 12, 316-27	16
1813	Combining filter-aided sample preparation and pseudoshotgun technology to profile the proteome of a low number of early passage human melanoma cells. 2013 , 12, 1040-8	29
1812	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
1811	Quantitative proteome analysis of alveolar type-II cells reveals a connection of integrin receptor subunits beta 2/6 and WNT signaling. 2013 , 12, 5598-608	8
1810	Activated ion negative electron transfer dissociation of multiply charged peptide anions. 2013 , 85, 4721-8	10
1809	Proteome-wide characterization of the RNA-binding protein RALY-interactome using the in vivo-biotinylation-pulldown-quant (iBioPQ) approach. 2013 , 12, 2869-84	34
1808	Hydrogenosomes in the diplomonad Spironucleus salmonicida. 2013 , 4, 2493	41
1807	Human prostasomes express glycolytic enzymes with capacity for ATP production. 2013, 304, E576-82	38
1806	Novel, gel-free proteomics approach identifies RNF5 and JAMP as modulators of GPCR stability. 2013 , 27, 1245-66	25

1805	Modulation of B-cell exosome proteins by gamma herpesvirus infection. 2013 , 110, E2925-33	187
1804	A SILAC-based approach identifies substrates of caspase-dependent cleavage upon TRAIL-induced apoptosis. 2013 , 12, 1436-50	23
1803	Protein composition of bronchoalveolar lavage fluid and airway surface liquid from newborn pigs. 2013 , 305, L256-66	23
1802	Ube2W conjugates ubiquitin to ⊞mino groups of protein N-termini. 2013 , 453, 137-45	69
1801	A potential role for the interaction of Wolbachia surface proteins with the Brugia malayi glycolytic enzymes and cytoskeleton in maintenance of endosymbiosis. 2013 , 7, e2151	28
1800	Functional proteomics of barley and barley chloroplasts - strategies, methods and perspectives. 2013 , 4, 52	16
1799	Kinetics of antigen expression and epitope presentation during virus infection. 2013 , 9, e1003129	108
1798	CaMKII is essential for the proasthmatic effects of oxidation. 2013 , 5, 195ra97	46
1797	Lissencephaly-1 promotes the recruitment of dynein and dynactin to transported mRNAs. 2013 , 202, 479-94	56
1796	Activated cyclin-dependent kinase 5 promotes microglial phagocytosis of fibrillar \(\partial \text{amyloid by up-regulating lipoprotein lipase expression. \(\textbf{2013}, 12, 2833-44 \)	42
1795	Predicting response to bevacizumab in ovarian cancer: a panel of potential biomarkers informing treatment selection. 2013 , 19, 5227-39	54
1794	Distinct XPPX sequence motifs induce ribosome stalling, which is rescued by the translation elongation factor EF-P. 2013 , 110, 15265-70	123
1793	In-depth characterization of the secretome of colorectal cancer metastatic cells identifies key proteins in cell adhesion, migration, and invasion. 2013 , 12, 1602-20	82
1792	Putting the pieces together: high-performance LC-MS/MS provides network-, pathway-, and protein-level perspectives in Populus. 2013 , 12, 106-19	21
1791	Early phosphoproteomic changes in the mouse spleen during deoxynivalenol-induced ribotoxic stress. 2013 , 135, 129-43	21
1790	Temporal analysis of the magnaporthe oryzae proteome during conidial germination and cyclic AMP (cAMP)-mediated appressorium formation. 2013 , 12, 2249-65	34
1789	High precision platelet releasate definition by quantitative reversed protein profilingbrief report. 2013 , 33, 1635-8	69
1788	Human cytomegalovirus pp71 stimulates major histocompatibility complex class i presentation of IE1-derived peptides at immediate early times of infection. 2013 , 87, 5229-38	9

(2013-2013)

1787	The GlycoFilter: a simple and comprehensive sample preparation platform for proteomics, N-glycomics and glycosylation site assignment. 2013 , 12, 2981-91	28
1786	Mast cell-deficient Kit(W-sh) "Sash" mutant mice display aberrant myelopoiesis leading to the accumulation of splenocytes that act as myeloid-derived suppressor cells. 2013 , 190, 5534-44	32
1785	Melanoma-associated mutations in protein phosphatase 6 cause chromosome instability and DNA damage owing to dysregulated Aurora-A. 2013 , 126, 3429-40	54
1784	Interaction between AP-5 and the hereditary spastic paraplegia proteins SPG11 and SPG15. 2013 , 24, 2558-69	77
1783	Integrative analysis of miRNA and mRNA expression profiles in pheochromocytoma and paraganglioma identifies genotype-specific markers and potentially regulated pathways. 2013 , 20, 477-93	40
1782	Quantitative dissection and stoichiometry determination of the human SET1/MLL histone methyltransferase complexes. 2013 , 33, 2067-77	145
1781	QARIP: a web server for quantitative proteomic analysis of regulated intramembrane proteolysis. 2013 , 41, W459-64	17
1780	Prolyl hydroxylase domain protein 2 (PHD2) binds a Pro-Xaa-Leu-Glu motif, linking it to the heat shock protein 90 pathway. 2013 , 288, 9662-9674	40
1779	An Internal Standard-Assisted Synthesis and Degradation Proteomic Approach Reveals the Potential Linkage between VPS4B Depletion and Activation of Fatty Acid I-Oxidation in Breast Cancer Cells. 2013 , 2013, 291415	7
1778	Glycoproteome of elongating cotton fiber cells. 2013 , 12, 3677-89	32
1777	N-linked glycoproteome profiling of human serum using tandem enrichment and multiple fraction concatenation. 2013 , 34, 2440-50	24
1776	Combined phospho- and glycoproteome enrichment in nephrocalcinosis tissues of phytate-fed rats. 2013 , 27, 2767-76	2
1775	In-depth proteomic analysis of mouse microglia using a combination of FASP and StageTip-based, high pH, reversed-phase fractionation. 2013 , 13, 2984-8	27
1774	Comparison of detergent-based sample preparation workflows for LTQ-Orbitrap analysis of the Escherichia coli proteome. 2013 , 13, 2597-607	81
1773	High pH reversed-phase chromatography as a superior fractionation scheme compared to off-gel isoelectric focusing for complex proteome analysis. 2013 , 13, 2956-66	30
1772	Global remodelling of cellular microenvironment due to loss of collagen VII. 2013 , 9, 657	71
1771	A complex of YlbF, YmcA and YaaT regulates sporulation, competence and biofilm formation by accelerating the phosphorylation of Spo0A. 2013 , 88, 283-300	34
1770	Enhanced recovery of lyophilized peptides in shotgun proteomics by using an LC-ESI-MS compatible surfactant. 2013 , 13, 751-5	15

1769	Recent technological developments in proteomics shed new light on translational research on diabetic microangiopathy. 2013 , 280, 5668-81	11
1768	MiR-26b is down-regulated in carcinoma-associated fibroblasts from ER-positive breast cancers leading to enhanced cell migration and invasion. 2013 , 231, 388-99	85
1767	Two-step OFFGEL approach for effective peptide separation compatible with iTRAQ labeling. 2013 , 13, 3261-6	1
1766	Toward improving the proteomic analysis of formalin-fixed, paraffin-embedded tissue. 2013 , 10, 389-400	36
1765	Accessing microenvironment compartments in formalin-fixed paraffin-embedded tissues by protein expression analysis. 2013 , 5, 2647-59	4
1764	Site-specific O-glycosylation on the MUC2 mucin protein inhibits cleavage by the Porphyromonas gingivalis secreted cysteine protease (RgpB). 2013 , 288, 14636-14646	56
1763	RNA-protein analysis using a conditional CRISPR nuclease. 2013 , 110, 5416-21	58
1762	Hyperglycemia mediates a shift from cap-dependent to cap-independent translation via a 4E-BP1-dependent mechanism. 2013 , 62, 2204-14	22
1761	Quantitative mass spectrometry-based proteomics in angiogenesis. 2013 , 7, 464-76	4
1760	Proteomic analysis of formalin-fixed paraffin-embedded renal tissue samples by label-free MS: assessment of overall technical variability and the impact of block age. 2013 , 7, 273-82	39
1759	Proteomic sample preparation from formalin fixed and paraffin embedded tissue. 2013,	34
1758	A combinatorial approach of Proteomics and Systems Biology in unravelling the mechanisms of acute kidney injury (AKI): involvement of NMDA receptor GRIN1 in murine AKI. 2013 , 7, 110	28
1757	Immunohistochemical staining, laser capture microdissection, and filter-aided sample preparation-assisted proteomic analysis of target cell populations within tissue samples. 2013 , 34, 1627-36	11
1756	A sample preparation method for micro-scale membrane proteome analysis. 2013 , 1,	1
1755	Top-down structural analysis of posttranslationally modified proteins by Fourier transform ion cyclotron resonance-MS with hydrogen/deuterium exchange and electron capture dissociation. 2013 , 13, 974-81	30
1754	Identifizierung der Zielproteine bioaktiver Verbindungen: Die Suche nach der Nadel im Heuhaufen. 2013 , 125, 2808-2859	43
1753	Identification of injury specific proteins in a cell culture model of traumatic brain injury. 2013, 8, e55983	28
1752	High yield production of a soluble human interleukin-3 variant from E. coli with wild-type bioactivity and improved radiolabeling properties. 2013 , 8, e74376	11

(2014-2013)

1751	by perturbation of proteostasis with an Hsp90 inhibitor. 2013 , 8, e80423	31
1750	Dynamic impacts of the inhibition of the molecular chaperone Hsp90 on the T-cell proteome have implications for anti-cancer therapy. 2013 , 8, e80425	31
1749	Interaction network of proteins associated with human cytomegalovirus IE2-p86 protein during infection: a proteomic analysis. 2013 , 8, e81583	9
1748	Evaluating the impact of different sequence databases on metaproteome analysis: insights from a lab-assembled microbial mixture. 2013 , 8, e82981	78
1747	Dynamic changes in mucus thickness and ion secretion during Citrobacter rodentium infection and clearance. 2013 , 8, e84430	34
1746	Quantitative proteomic analysis of oral brush biopsies identifies secretory leukocyte protease inhibitor as a promising, mechanism-based oral cancer biomarker. 2014 , 9, e95389	19
1745	Comparative proteomics of milk fat globule membrane proteins from transgenic cloned cattle. 2014 , 9, e105378	13
1744	The cultural divide: exponential growth in classical 2D and metabolic equilibrium in 3D environments. 2014 , 9, e106973	40
1743	Quantitative mass spectrometry of urinary biomarkers. 2014 , 4, 69-78	3
1742	Optimal Concentration of 2,2,2-Trichloroacetic Acid for Protein Precipitation Based on Response Surface Methodology. 2014 , 5,	8
1741	Unveiling novel interactions of histone chaperone Asf1 linked to TREX-2 factors Sus1 and Thp1. 2014 , 5, 247-59	10
1740	Application of clinical proteomics in acute respiratory distress syndrome. 2014 , 3, 34	6
1739	Tomato nuclear proteome reveals the involvement of specific E2 ubiquitin-conjugating enzymes in fruit ripening. 2014 , 15, 548	67
1738	Defective Tibetan PHD2 binding to p23 links high altitude adaption to altered oxygen sensing. 2014 , 289, 14656-65	52
1737	Ultradeep human phosphoproteome reveals a distinct regulatory nature of Tyr and Ser/Thr-based signaling. 2014 , 8, 1583-94	616
1736	A mass spectrometry view of stable and transient protein interactions. 2014 , 806, 263-82	27
1735	The urinary proteome and peptidome of renal cell carcinoma patients: a comparison of different techniques. 2014 , 11, 503-14	9
1734	Chasing Phosphoarginine Proteins: Development of a Selective Enrichment Method Using a Phosphatase Trap. 2014 , 13, 1953-64	40

1733	Quantitative phosphoproteomics reveals the role of protein arginine phosphorylation in the bacterial stress response. 2014 , 13, 537-50	75
1732	Identifying nuclear protein-protein interactions using GFP affinity purification and SILAC-based quantitative mass spectrometry. 2014 , 1188, 207-26	21
1731	Proteomic analysis of the Burkholderia pseudomallei type II secretome reveals hydrolytic enzymes, novel proteins, and the deubiquitinase TssM. 2014 , 82, 3214-26	37
1730	A straightforward and efficient analytical pipeline for metaproteome characterization. 2014 , 2, 49	65
1729	Proteome Cleavage Reveals Iterative Digestion Strategy for High Sequence Coverage. 2014 , 2014,	8
1728	Comparative proteomic profiling of pancreatic ductal adenocarcinoma cell lines. 2014 , 37, 888-98	29
1727	Palmitoylation of gephyrin controls receptor clustering and plasticity of GABAergic synapses. 2014 , 12, e1001908	57
1726	Recoding of the stop codon UGA to glycine by a BD1-5/SN-2 bacterium and niche partitioning between Alpha- and Gammaproteobacteria in a tidal sediment microbial community naturally selected in a laboratory chemostat. 2014 , 5, 231	26
1725	Phosphoinositide metabolism links cGMP-dependent protein kinase G to essential Call+ signals at key decision points in the life cycle of malaria parasites. 2014 , 12, e1001806	136
1724	Bottom-up and shotgun proteomics to identify a comprehensive cochlear proteome. 2014,	5
1723	Differential secretome analysis of Pseudomonas syringae pv tomato using gel-free MS proteomics. 2014 , 5, 242	18
1722	Label-free quantitative proteomics and N-terminal analysis of human metastatic lung cancer cells. 2014 , 37, 457-66	7
1721	Membrane protein profiling of human colon reveals distinct regional differences. 2014 , 13, 2277-87	26
1720	Eliminating Bottlenecks for Efficient Bioanalysis: Practices and Applications in Drug Discovery and Development. 2014 ,	1
1719	Bioanalysis of biomarkers in support of drug discovery and development. 2014 , 182-199	
1718	Diverse and divergent protein post-translational modifications in two growth stages of a natural microbial community. 2014 , 5, 4405	36
1717	Quantitative proteomic analysis of compartmentalized signaling networks. 2014 , 535, 309-25	2
1716	Thiol-free reducing agents in electrophoretic separations and FASP proteolytic digestions for the analysis of metal-binding proteins. 2014 , 1, 175-80	1

1715	Proteome screening of pleural effusions identifies galectin 1 as a diagnostic biomarker and highlights several prognostic biomarkers for malignant mesothelioma. 2014 , 13, 701-15	36
1714	Copy number analysis of the murine platelet proteome spanning the complete abundance range. 2014 , 13, 3435-45	138
1713	Quantitative metaproteomics: functional insights into microbial communities. 2014 , 1096, 231-40	15
1712	A holin and an endopeptidase are essential for chitinolytic protein secretion in Serratia marcescens. 2014 , 207, 615-26	24
1711	The COP9 signalosome is involved in the regulation of lipid metabolism and of transition metals uptake in Saccharomyces Lerevisiae. 2014 , 281, 175-90	13
1710	Evaluating nonpolar surface area and liquid chromatography/mass spectrometry response: an application for site occupancy measurements for enzyme intermediates in polyketide biosynthesis. 2014 , 28, 2511-22	4
1709	Hyaluronan enhances wound repair and increases collagen III in aged dermal wounds. 2014 , 22, 521-6	34
1708	Mass spectrometry-based membrane proteomics in cancer biomarker discovery. 2014 , 14, 549-63	17
1707	The Q Exactive HF, a Benchtop mass spectrometer with a pre-filter, high-performance quadrupole and an ultra-high-field Orbitrap analyzer. 2014 , 13, 3698-708	229
1706	Elevated S-adenosylhomocysteine alters adipocyte functionality with corresponding changes in gene expression and associated epigenetic marks. 2014 , 63, 2273-83	23
1705	Proteomics analysis of adult testis from Bombyx mori. 2014 , 14, 2345-9	5
1704	Comprehensive assessment of proteins regulated by dexamethasone reveals novel effects in primary human peripheral blood mononuclear cells. 2014 , 13, 5989-6000	41
1703	Label-free quantitative urinary proteomics identifies the arginase pathway as a new player in congenital obstructive nephropathy. 2014 , 13, 3421-34	20
1702	Quantitative proteomics for cardiac biomarker discovery using isoproterenol-treated nonhuman primates. 2014 , 13, 5909-17	9
1701	N-capping motifs promote interaction of amphipathic helical peptides with hydrophobic surfaces and drastically alter hydrophobicity values of individual amino acids. 2014 , 86, 11498-502	18
1700	Improvement of a sample preparation method assisted by sodium deoxycholate for mass-spectrometry-based shotgun membrane proteomics. 2014 , 37, 3321-9	17
1699	Tyrosine phosphorylation of HuR by JAK3 triggers dissociation and degradation of HuR target mRNAs. 2014 , 42, 1196-208	35
1698	Automated sample preparation platform for mass spectrometry-based plasma proteomics and biomarker discovery. 2014 , 3, 205-19	8

1697	Proteomic analysis of solid pseudopapillary tumor of the pancreas reveals dysfunction of the endoplasmic reticulum protein processing pathway. 2014 , 13, 2593-603	55
1696	Identification of lipid synthesis and secretion proteins in bovine milk. 2014 , 81, 65-72	20
1695	Harnessing Chinese hamster ovary cell proteomics for biopharmaceutical processing. 2014 , 2, 421-435	3
1694	Global absolute quantification reveals tight regulation of protein expression in single Xenopus eggs. 2014 , 42, 9880-91	47
1693	The CJIE1 prophage of Campylobacter jejuni affects protein expression in growth media with and without bile salts. 2014 , 14, 70	14
1692	The response of porcine monocyte derived macrophages and dendritic cells to Salmonella Typhimurium and lipopolysaccharide. 2014 , 10, 244	13
1691	A targeted proteomics approach for profiling murine cytochrome P450 expression. 2014 , 349, 221-8	24
1690	Altered protein expression profiles in umbilical veins: insights into vascular dysfunctions of the children born after in vitro fertilization. 2014 , 91, 71	8
1689	Translational stalling at polyproline stretches is modulated by the sequence context upstream of the stall site. 2014 , 42, 10711-9	63
1688	The acute transcriptomic and proteomic response of HC-04 hepatoma cells to hepatocyte growth factor and its implications for Plasmodium falciparum sporozoite invasion. 2014 , 13, 1153-64	12
1687	The use of a rapid MS-based method for the quantification of the CYP 3A4 protein directly from hepatocyte cell lysate for CYP induction studies. 2014 , 6, 3271-82	2
1686	Proteomic landscape of the human choroid-retinal pigment epithelial complex. 2014 , 132, 1271-81	31
1685	Evaluation of a method for nitrotyrosine site identification and relative quantitation using a stable isotope-labeled nitrated spike-in standard and high resolution fourier transform MS and MS/MS analysis. 2014 , 15, 6265-85	10
1684	Inhibition of Cyclooxygenase-2 Prevents Chronic and Recurrent Cystitis. 2014 , 1, 46-57	61
1683	Integral proteomic analysis of blastocysts reveals key molecular machinery governing embryonic diapause and reactivation for implantation in mice. 2014 , 90, 52	33
1682	Toward sensitive and accurate analysis of antibody biotherapeutics by liquid chromatography coupled with mass spectrometry. 2014 , 42, 1858-66	38
1681	A comparative quantitative proteomic study identifies new proteins relevant for sulfur oxidation in the purple sulfur bacterium Allochromatium vinosum. 2014 , 80, 2279-92	32
1680	Hepatic uptake of atorvastatin: influence of variability in transporter expression on uptake clearance and drug-drug interactions. 2014 , 42, 1210-8	83

1679	Efficient sample processing for proteomics applicationsare we there yet?. 2014 , 10, 758		3
1678	Time-resolved dissection of early phosphoproteome and ensuing proteome changes in response to TGF- \square 2014 , 7, rs5		32
1677	Probing SH2-domains using Inhibitor Affinity Purification (IAP). 2014 , 12, 41		10
1676	Dynamic changes of urinary proteins in a focal segmental glomerulosclerosis rat model. 2014 , 12, 42		28
1675	Identification and functional characterization of a highly divergent N-acetylglucosaminyltransferase I (TbGnTI) in Trypanosoma brucei. 2014 , 289, 9328-39		17
1674	Jumonji domain containing protein 6 (Jmjd6) modulates splicing and specifically interacts with arginine-serine-rich (RS) domains of SR- and SR-like proteins. 2014 , 42, 7833-50		47
1673	A comprehensive protein-protein interactome for yeast PAS kinase 1 reveals direct inhibition of respiration through the phosphorylation of Cbf1. 2014 , 25, 2199-215		12
1672	Performance comparisons of nano-LC systems, electrospray sources and LC-MS-MS platforms. 2014 , 52, 120-7		13
1671	Proteome-wide identification of SUMO2 modification sites. 2014 , 7, rs2		142
1670	A neuroproteomic and systems biology analysis of rat brain post intracerebral hemorrhagic stroke. 2014 , 102, 46-56		21
1669	Site-specific characterization of cell membrane N-glycosylation with integrated hydrophilic interaction chromatography solid phase extraction and LC-MS/MS. 2014 , 103, 194-203		36
1668	Proteomics of larval hemolymph in Bombyx mori reveals various nutrient-storage and immunity-related proteins. 2014 , 46, 1021-31		34
1667	Immobilization of trypsin onto multifunctional meso-/macroporous core-shell microspheres: a new platform for rapid enzymatic digestion. 2014 , 812, 65-73		25
1666	Proteogenomic analysis of human chromosome 9-encoded genes from human samples and lung cancer tissues. 2014 , 13, 137-46		13
1665	Environmental Microbiology. 2014 ,		5
1664	C9orf72 nucleotide repeat structures initiate molecular cascades of disease. 2014 , 507, 195-200		630
1663	Proteomic analysis of membrane proteins of vero cells: exploration of potential proteins responsible for virus entry. 2014 , 33, 20-8		19
1662	Minimal, encapsulated proteomic-sample processing applied to copy-number estimation in eukaryotic cells. <i>Nature Methods</i> , 2014 , 11, 319-24	21.6	977

1661	Identification of small ORFs in vertebrates using ribosome footprinting and evolutionary conservation. 2014 , 33, 981-93	418
1660	Interplay of acetyltransferase EP300 and the proteasome system in regulating heat shock transcription factor 1. 2014 , 156, 975-85	106
1659	Cleaved and missed sites for trypsin, lys-C, and lys-N can be predicted with high confidence on the basis of sequence context. 2014 , 13, 702-9	37
1658	Proteomic profiles of human lung adeno and squamous cell carcinoma using super-SILAC and label-free quantification approaches. 2014 , 14, 795-803	24
1657	Enhanced FASP (eFASP) to increase proteome coverage and sample recovery for quantitative proteomic experiments. 2014 , 13, 1885-95	202
1656	Effects of three commonly-used diuretics on the urinary proteome. 2014 , 12, 120-6	14
1655	Proteome-based systems biology analysis of the diabetic mouse aorta reveals major changes in fatty acid biosynthesis as potential hallmark in diabetes mellitus-associated vascular disease. 2014 , 7, 161-70	17
1654	CD4(+) T cell lineage integrity is controlled by the histone deacetylases HDAC1 and HDAC2. 2014 , 15, 439-448	56
1653	Magnetic separation techniques in sample preparation for biological analysis: a review. 2014 , 101, 84-101	181
1652	Post-genomics nanotechnology is gaining momentum: nanoproteomics and applications in life sciences. 2014 , 18, 111-31	19
1651	Comparative interactomes of SIRT6 and SIRT7: Implication of functional links to aging. 2014 , 14, 1610-22	59
1650	Monomethylarsonous acid inhibited endogenous cholesterol biosynthesis in human skin fibroblasts. 2014 , 277, 21-9	7
1649	Exosomes as critical agents of cardiac regeneration triggered by cell therapy. 2014 , 2, 606-19	548
1648	Rescue of embryonic stem cells from cellular transformation by proteomic stabilization of mutant p53 and conversion into WT conformation. 2014 , 111, 7006-11	36
1647	A fully automated dual-online multifunctional ultrahigh pressure liquid chromatography system for high-throughput proteomics analysis. 2014 , 1329, 83-9	13
1646	Coordinated activation of PTA-ACS and TCA cycles strongly reduces overflow metabolism of acetate in Escherichia coli. 2014 , 98, 5131-43	26
1645	Suspension trapping (STrap) sample preparation method for bottom-up proteomics analysis. 2014 , 14, 1006-0	157
1644	Urine sample preparation in 96-well filter plates for quantitative clinical proteomics. 2014 , 86, 5470-7	69

1643	Molecular characterization and functional analyses of ZtWor1, a transcriptional regulator of the fungal wheat pathogen Zymoseptoria tritici. 2014 , 15, 394-405	38
1642	A review on preparative and semi-preparative offgel electrophoresis for multidimensional protein/peptide assessment. 2014 , 836, 1-17	25
1641	In situ activity-based protein profiling of serine hydrolases in E. coli. 2014 , 4, 18-24	3
1640	Fine tuning of proteomic technologies to improve biological findings: advancements in 2011-2013. 2014 , 86, 176-95	18
1639	Design and characterization of an injectable tendon hydrogel: a novel scaffold for guided tissue regeneration in the musculoskeletal system. 2014 , 20, 1550-61	71
1638	Thermoanaerobacter thermohydrosulfuricus WC1 shows protein complement stability during fermentation of key lignocellulose-derived substrates. 2014 , 80, 1602-15	22
1637	Guanylate binding protein 1-mediated interaction of T cell antigen receptor signaling with the cytoskeleton. 2014 , 192, 771-81	29
1636	Resolution of the type material of the Asian elephant, Elephas maximus Linnaeus, 1758 (Proboscidea, Elephantidae). 2014 , 170, 222-232	24
1635	Large-scale mass spectrometric detection of variant peptides resulting from nonsynonymous nucleotide differences. 2014 , 13, 228-40	64
1634	Metaproteomics analysis reveals the adaptation process for the chicken gut microbiota. 2014 , 80, 478-85	51
1633	Comprehensive proteomic profiling of outer membrane vesicles from Campylobacter jejuni. 2014 , 98, 90-8	52
1632	Depletion of abundant plasma proteins by poly(N-isopropylacrylamide-acrylic acid) hydrogel particles. 2014 , 86, 1543-50	22
1631	Lifelong exercise training modulates cardiac mitochondrial phosphoproteome in rats. 2014 , 13, 2045-55	15
1630	Validation of N-myristoyltransferase as an antimalarial drug target using an integrated chemical biology approach. 2014 , 6, 112-21	151
1629	Accurate identification of deamidated peptides in global proteomics using a quadrupole orbitrap mass spectrometer. 2014 , 13, 777-85	28
1628	Improvement and simplification of fed-batch bioprocesses with a highly soluble phosphotyrosine sodium salt. 2014 , 186, 110-8	17
1627	Hepatitis B virus e antigen (HBeAg) may have a negative effect on dendritic cell generation. 2014 , 219, 944-9	10
1626	A systems level analysis reveals transcriptomic and proteomic complexity in Ixodes ricinus midgut and salivary glands during early attachment and feeding. 2014 , 13, 2725-35	61

1625	Preparation of mixed lanthanides-immobilized magnetic nanoparticles for selective enrichment and identification of phosphopeptides by MS. 2014 , 35, 3470-8	13
1624	Resolubilization of precipitated intact membrane proteins with cold formic acid for analysis by mass spectrometry. 2014 , 13, 6001-12	35
1623	Quantitative phosphoproteomic analysis of RIP3-dependent protein phosphorylation in the course of TNF-induced necroptosis. 2014 , 14, 713-24	18
1622	Comparative proteomic analysis of outer membrane vesicles from Shigella flexneri under different culture conditions. 2014 , 453, 696-702	12
1621	Quantitative proteomics reveals the dynamics of protein changes during Drosophila oocyte maturation and the oocyte-to-embryo transition. 2014 , 111, 16023-8	42
1620	Exploring intercellular signaling by proteomic approaches. 2014 , 14, 498-512	13
1619	A proteomic perspective of Sirtuin 6 (SIRT6) phosphorylation and interactions and their dependence on its catalytic activity. 2014 , 13, 168-83	37
1618	Proteomic study of the microdissected aortic media in human thoracic aortic aneurysms. 2014 , 13, 5071-80	19
1617	Quantitative proteomics reveals novel therapeutic and diagnostic markers in hypertension. 2014 , 2, 79-87	20
1616	A "proteomic ruler" for protein copy number and concentration estimation without spike-in standards. 2014 , 13, 3497-506	324
1616 1615		324 7
1615	Discovery of novel disease-specific and membrane-associated candidate markers in a mouse model	
1615	Discovery of novel disease-specific and membrane-associated candidate markers in a mouse model of multiple sclerosis. 2014 , 13, 679-700	7
1615 1614	Discovery of novel disease-specific and membrane-associated candidate markers in a mouse model of multiple sclerosis. 2014, 13, 679-700 Ultrasensitive proteome analysis using paramagnetic bead technology. 2014, 10, 757 Cell-specific labeling enzymes for analysis of cell-cell communication in continuous co-culture. 2014	7 497
1615 1614 1613	Discovery of novel disease-specific and membrane-associated candidate markers in a mouse model of multiple sclerosis. 2014, 13, 679-700 Ultrasensitive proteome analysis using paramagnetic bead technology. 2014, 10, 757 Cell-specific labeling enzymes for analysis of cell-cell communication in continuous co-culture. 2014, 13, 1866-76 Comprehensive comparative and semiquantitative proteome of a very low number of native and	7 497 26
1615 1614 1613 1612	Discovery of novel disease-specific and membrane-associated candidate markers in a mouse model of multiple sclerosis. 2014, 13, 679-700 Ultrasensitive proteome analysis using paramagnetic bead technology. 2014, 10, 757 Cell-specific labeling enzymes for analysis of cell-cell communication in continuous co-culture. 2014, 13, 1866-76 Comprehensive comparative and semiquantitative proteome of a very low number of native and matched epstein-barr-virus-transformed B lymphocytes infiltrating human melanoma. 2014, 13, 2830-45 Fis overexpression enhances Pseudomonas putida biofilm formation by regulating the ratio of	7 497 26
1615 1614 1613 1612 1611	Discovery of novel disease-specific and membrane-associated candidate markers in a mouse model of multiple sclerosis. 2014, 13, 679-700 Ultrasensitive proteome analysis using paramagnetic bead technology. 2014, 10, 757 Cell-specific labeling enzymes for analysis of cell-cell communication in continuous co-culture. 2014, 13, 1866-76 Comprehensive comparative and semiquantitative proteome of a very low number of native and matched epstein-barr-virus-transformed B lymphocytes infiltrating human melanoma. 2014, 13, 2830-45 Fis overexpression enhances Pseudomonas putida biofilm formation by regulating the ratio of LapA and LapF. 2014, 160, 2681-2693	7 497 26 12

1607	Protein turnover forms one of the highest maintenance costs in Lactococcus lactis. 2014 , 160, 1501-1512	30
1606	A protein profile of visceral adipose tissues linked to early pathogenesis of type 2 diabetes mellitus. 2014 , 13, 811-22	45
1605	Advancements of Mass Spectrometry in Biomedical Research. 2014,	4
1604	Disclosure of selective advantages in the "modern" sublineage of the Mycobacterium tuberculosis Beijing genotype family by quantitative proteomics. 2014 , 13, 2632-45	23
1603	abFASP-MS: affinity-based filter-aided sample preparation mass spectrometry for quantitative analysis of chemically labeled protein complexes. 2014 , 13, 1147-55	12
1602	Development of a multipoint quantitation method to simultaneously measure enzymatic and structural components of the Clostridium thermocellum cellulosome protein complex. 2014 , 13, 692-701	11
1601	Templated Biomineralization on Self-Assembled Protein Nanofibers Buried in Calcium Oxalate Raphides of Musa spp 2014 , 26, 3862-3869	14
1600	Separation methodology to improve proteome coverage depth. 2014 , 11, 409-14	9
1599	Integration of cell lysis, protein extraction, and digestion into one step for ultrafast sample preparation for phosphoproteome analysis. 2014 , 86, 6786-91	17
1598	Insulin increases phosphorylation of mitochondrial proteins in human skeletal muscle in vivo. 2014 , 13, 2359-69	20
1597	Piezo1 integration of vascular architecture with physiological force. 2014 , 515, 279-282	519
1596	PIM2 kinase is induced by cisplatin in ovarian cancer cells and limits drug efficacy. 2014 , 13, 4970-82	17
1595	Interaction modes and approaches to glycopeptide and glycoprotein enrichment. 2014, 139, 688-704	96
1594	Quantitative proteomics reveals that PEA15 regulates astroglial Allphagocytosis in an Alzheimer's disease mouse model. 2014 , 110, 45-58	26
1593	Mass spectrometry and imaging analysis of nanoparticle-containing vesicles provide a mechanistic insight into cellular trafficking. 2014 , 8, 10077-88	66
1592	Overview of peptide and protein analysis by mass spectrometry. 2014 , 108, 10.21.1-30	20
1591	Biochemical and proteomic analysis of a potential anticancer agent: Palladium(II) Saccharinate complex of terpyridine acting through double strand break formation. 2014 , 13, 5240-9	28
1590	Compartment proteomics analysis of white perch (Morone americana) ovary using support vector machines. 2014 , 13, 1515-26	14

1589	Method Development for the Detection of Human Myostatin by High-Resolution and Targeted Mass Spectrometry. 2014 , 13, 3802-3809	7
1588	Functional amyloids in the mouse sperm acrosome. 2014 , 34, 2624-34	51
1587	Identification and characterization of proteins encoded by chromosome 12 as part of chromosome-centric human proteome project. 2014 , 13, 3166-77	11
1586	Statistical characterization of HCD fragmentation patterns of tryptic peptides on an LTQ Orbitrap Velos mass spectrometer. 2014 , 109, 26-37	12
1585	Multi-enzyme digestion FASP and the 'Total Protein Approach'-based absolute quantification of the Escherichia coli proteome. 2014 , 109, 322-31	121
1584	Proteomic analysis of the mitochondria from embryonic and postnatal rat brains reveals response to developmental changes in energy demands. 2014 , 109, 228-39	18
1583	Estimating influence of cofragmentation on peptide quantification and identification in iTRAQ experiments by simulating multiplexed spectra. 2014 , 13, 3488-97	14
1582	Enhanced identification of zero-length chemical cross-links using label-free quantitation and high-resolution fragment ion spectra. 2014 , 13, 898-914	15
1581	Family-wide analysis of poly(ADP-ribose) polymerase activity. 2014 , 5, 4426	286
1580	Proteomics meets genetics: SILAC labeling of Drosophila melanogaster larvae and cells for in vivo functional studies. 2014 , 1188, 293-311	3
1579	Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC). 2014 ,	1
1578	Protein interactomics based on direct molecular fishing on paramagnetic particles: practical realization and further SPR validation. 2014 , 14, 2261-74	20
1577	Effect of embryonic development on the chicken egg yolk plasma proteome after 12 days of incubation. 2014 , 62, 2531-40	24
1576	Determination of selected reaction monitoring peptide transitions via multiplexed product-ion scan modes. 2014 , 28, 773-80	2
1575	Immunoproteomics using polyclonal antibodies and stable isotope-labeled affinity-purified recombinant proteins. 2014 , 13, 1611-24	22
1574	Phosphorylation dynamics of membrane proteins from Arabidopsis roots submitted to salt stress. 2014 , 14, 1058-70	29
1573	Quantitative phosphoproteomic profiling of fiber differentiation and initiation in a fiberless mutant of cotton. 2014 , 15, 466	31
1572	Comparative transcriptomics of the model mushroom Coprinopsis cinerea reveals tissue-specific armories and a conserved circuitry for sexual development. 2014 , 15, 492	50

1571	Using Galaxy-P to leverage RNA-Seq for the discovery of novel protein variations. 2014 , 15, 703	58
1570	The Lottia gigantea shell matrix proteome: re-analysis including MaxQuant iBAQ quantitation and phosphoproteome analysis. 2014 , 12, 28	44
1569	Critical comparison of sample preparation strategies for shotgun proteomic analysis of formalin-fixed, paraffin-embedded samples: insights from liver tissue. 2014 , 11, 28	41
1568	Reduced catabolic protein expression in Clostridium butyricum DSM 10702 correlate with reduced 1,3-propanediol synthesis at high glycerol loading. 2014 , 4, 63	19
1567	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
1566	The Caenorhabditis elegans pericentriolar material components SPD-2 and SPD-5 are monomeric in the cytoplasm before incorporation into the PCM matrix. 2014 , 25, 2984-92	26
1565	Monodisperse boronate polymeric particles synthesized by a precipitation polymerization strategy: particle formation and glycoprotein response from the standpoint of the Flory-Huggins model. 2014 , 6, 2059-66	22
1564	A cell surface biotinylation assay to reveal membrane-associated neuronal cues: Negr1 regulates dendritic arborization. 2014 , 13, 733-48	40
1563	Assessing the citrullinome in rheumatoid arthritis synovial fluid with and without enrichment of citrullinated peptides. 2014 , 13, 2867-73	58
1562	Influence of the digestion technique, protease, and missed cleavage peptides in protein quantitation. 2014 , 13, 3979-86	39
1561	The quantitative nuclear matrix proteome as a biochemical snapshot of nuclear organization. 2014 , 13, 3940-56	31
1560	De novo identification and quantification of single amino-acid variants in human brain. 2014 , 6, 421-33	9
1559	Shotgun proteomics to unravel the complexity of the Leishmania infantum exoproteome and the relative abundance of its constituents. 2014 , 195, 43-53	15
1558	Exposure to silver nanoparticles induces size- and dose-dependent oxidative stress and cytotoxicity in human colon carcinoma cells. 2014 , 28, 1280-9	116
1557	Quantitative proteomics of synaptic and nonsynaptic mitochondria: insights for synaptic mitochondrial vulnerability. 2014 , 13, 2620-36	59
1556	The emergence of proteome-wide technologies: systematic analysis of proteins comes of age. 2014 , 15, 453-64	67
1555	Evaluation of empirical rule of linearly correlated peptide selection (ERLPS) for proteotypic peptide-based quantitative proteomics. 2014 , 14, 1593-603	О
1554	Comprehensive mapping of protein N-glycosylation in human liver by combining hydrophilic interaction chromatography and hydrazide chemistry. 2014 , 13, 1713-21	61

1553	Proteomics. 2014 , 147-179	5
1552	Multivalent hydrazide-functionalized magnetic nanoparticles for glycopeptide enrichment and identification. 2014 , 139, 603-9	33
1551	Changes of proteins induced by anticoagulants can be more sensitively detected in urine than in plasma. 2014 , 57, 649-56	34
1550	Integrated proteomic and transcriptomic analysis of the Aedes aegypti eggshell. 2014 , 14, 15	38
1549	Comprehensive identification of novel proteins and N-glycosylation sites in royal jelly. 2014 , 15, 135	29
1548	Characterization of the pigmented shell-forming proteome of the common grove snail Cepaea nemoralis. 2014 , 15, 249	62
1547	Characterization of the membrane proteome and N-glycoproteome in BV-2 mouse microglia by liquid chromatography-tandem mass spectrometry. 2014 , 15, 95	14
1546	Quantitative proteomics by SWATH-MS reveals altered expression of nucleic acid binding and regulatory proteins in HIV-1-infected macrophages. 2014 , 13, 2109-19	54
1545	High-confidence glycosome proteome for procyclic form Trypanosoma brucei by epitope-tag organelle enrichment and SILAC proteomics. 2014 , 13, 2796-806	72
1544	The interplay of light and oxygen in the reactive oxygen stress response of Chlamydomonas reinhardtii dissected by quantitative mass spectrometry. 2014 , 13, 969-89	23
1543	Highly specific enrichment of N-linked glycopeptides based on hydrazide functionalized soluble nanopolymers. 2014 , 50, 1027-9	45
1542	In vivo quantitative proteomics for the study of oncometabolism. 2014 , 543, 235-59	2
1541	Towards single-cell LC-MS phosphoproteomics. 2014 , 139, 4733-49	21
1540	Deep proteome mapping of mouse kidney based on OFFGel prefractionation reveals remarkable protein post- translational modifications. 2014 , 13, 1636-46	20
1539	The one hour yeast proteome. 2014 , 13, 339-47	413
1538	From hundreds to thousands: Widening the normal human Urinome. 2014 , 1, 25-8	11
1537	Chromatin enrichment for proteomics. 2014 , 9, 2090-9	53
1536	Proteomic analysis in Giardia duodenalis yields insights into strain virulence and antigenic variation. 2014 , 14, 2523-34	22

1535	N-linked glycosylation enrichment for in-depth cell surface proteomics of diffuse large B-cell lymphoma subtypes. 2014 , 13, 240-51	64
1534	Rapid temporal dynamics of transcription, protein synthesis, and secretion during macrophage activation. 2014 , 13, 792-810	70
1533	mTor is a signaling hub in cell survival: a mass-spectrometry-based proteomics investigation. 2014 , 13, 2433-44	34
1532	DnaJA1/Hsp40 is co-opted by influenza A virus to enhance its viral RNA polymerase activity. 2014 , 88, 14078-89	37
1531	Acute phencyclidine treatment induces extensive and distinct protein phosphorylation in rat frontal cortex. 2014 , 13, 1578-92	11
1530	The genome, proteome and phylogenetic analysis of Sinorhizobium meliloti phage M12, the founder of a new group of T4-superfamily phages. 2014 , 450-451, 84-97	27
1529	iTRAQ-based quantitative proteomics analysis revealed alterations of carbohydrate metabolism pathways and mitochondrial proteins in a male sterile cybrid pummelo. 2014 , 13, 2998-3015	51
1528	Molecular analysis of an alternative N-glycosylation machinery by functional transfer from Actinobacillus pleuropneumoniae to Escherichia coli. 2014 , 289, 2170-9	60
1527	Insights into the cellular response triggered by silver nanoparticles using quantitative proteomics. 2014 , 8, 2161-75	153
1526	Massifquant: open-source Kalman filter-based XC-MS isotope trace feature detection. 2014 , 30, 2636-43	29
1525	Confident and sensitive phosphoproteomics using combinations of collision induced dissociation and electron transfer dissociation. 2014 , 103, 1-14	28
1524	Combining TBP-based rOFFGEL-IEF with FASP and nLC-ESI-LTQ-MS/MS for the analysis of cisplatin-binding proteins in rat kidney. 2014 , 120, 433-42	15
1523	A synthetic lethal interaction between APC/C and topoisomerase poisons uncovered by proteomic screens. 2014 , 6, 670-83	38
1522	An amino acid depleted cell-free protein synthesis system for the incorporation of non-canonical amino acid analogs into proteins. 2014 , 178, 12-22	23
1521	Acetyl coenzyme A synthetase is acetylated on multiple lysine residues by a protein acetyltransferase with a single Gcn5-type N-acetyltransferase (GNAT) domain in Saccharopolyspora erythraea. 2014 , 196, 3169-78	32
1520	Global protein expression profiling of zebrafish organs based on in vivo incorporation of stable isotopes. 2014 , 13, 2162-74	21
1519	Generating a detailed protein profile of Fasciola hepatica during the chronic stage of infection in cattle. 2014 , 14, 1519-30	19
1518	Recent advances in proteomics: towards the human proteome. 2014 , 28, 848-57	20

1517	Drift time-specific collision energies enable deep-coverage data-independent acquisition proteomics. <i>Nature Methods</i> , 2014 , 11, 167-70	21.6	284
1516	Functional proteomic discovery of Slr0110 as a central regulator of carbohydrate metabolism in Synechocystis species PCC6803. 2014 , 13, 204-19		18
1515	A common atopy-associated variant in the Th2 cytokine locus control region impacts transcriptional regulation and alters SMAD3 and SP1 binding. 2014 , 69, 632-42		9
1514	Extracellular vesicles modulate the glioblastoma microenvironment via a tumor suppression signaling network directed by miR-1. 2014 , 74, 738-750		170
1513	Functional links between Snail-1 and Cx43 account for the recruitment of Cx43-positive cells into the invasive front of prostate cancer. 2014 , 35, 1920-30		33
1512	Pluronic modified leptin with increased systemic circulation, brain uptake and efficacy for treatment of obesity. 2014 , 191, 34-46		31
1511	Widespread changes in the posttranscriptional landscape at the Drosophila oocyte-to-embryo transition. 2014 , 7, 1495-1508		81
1510	Secreted major Venus flytrap chitinase enables digestion of Arthropod prey. 2014 , 1844, 374-83		28
1509	Mass spectrometry-based proteomics in Chest Medicine, Gerontology, and Nephrology: subgroups omics for personalized medicine. 2014 , 4, 25		11
1508	Quantitative phosphoproteomics unveils temporal dynamics of thrombin signaling in human endothelial cells. 2014 , 123, e22-36		27
1507	Resolution of the type material of the Asian elephant, Elephas maximus Linnaeus, 1758 (Proboscidea, Elephantidae). 2014 , 170, 222-232		18
1506	A new approach for the comparative analysis of multiprotein complexes based on 15N metabolic labeling and quantitative mass spectrometry. 2014 ,		2
1505	New perspectives on bioactivity of olive oil: evidence from animal models, human interventions and the use of urinary proteomic biomarkers. 2015 , 74, 268-81		13
1504	Food Traceability. 2015 , 289-296		
1503	RBM7 subunit of the NEXT complex binds U-rich sequences and targets 3'-end extended forms of snRNAs. 2015 , 43, 4236-48		38
1502	Extensive differential protein phosphorylation as intraerythrocytic Plasmodium falciparum schizonts develop into extracellular invasive merozoites. 2015 , 15, 2716-29		46
1501	Gel-aided sample preparation (GASP)a simplified method for gel-assisted proteomic sample generation from protein extracts and intact cells. 2015 , 15, 1224-9		73
1500	Belinostat, a potent HDACi, exerts antileukaemic effect in human acute promyelocytic leukaemia cells via chromatin remodelling. 2015 , 19, 1742-55		22

1499	Label-free Quantitative Analysis of Changes in Broiler Liver Proteins under Heat Stress using SWATH-MS Technology. 2015 , 5, 15119	28
1498	Digestion, Purification, and Enrichment of Protein Samples for Mass Spectrometry. 2015 , 7, 201-222	10
1497	Urinary candidate biomarker discovery in a rat unilateral ureteral obstruction model. 2015 , 5, 9314	32
1496	Palmitoylation and palmitoyl-transferases in Plasmodium parasites. 2015 , 43, 240-5	13
1495	Minimal amounts of kindlin-3 suffice for basal platelet and leukocyte functions in mice. 2015 , 126, 2592-600	36
1494	The NHERF2 sequence adjacent and upstream of the ERM-binding domain affects NHERF2-ezrin binding and dexamethasone stimulated NHE3 activity. 2015 , 470, 77-90	7
1493	The external PASTA domain of the essential serine/threonine protein kinase PknB regulates mycobacterial growth. 2015 , 5, 150025	20
1492	Soil restoration with organic amendments: linking cellular functionality and ecosystem processes. 2015 , 5, 15550	88
1491	Dimethyl adipimidate/Thin film Sample processing (DTS); A simple, low-cost, and versatile nucleic acid extraction assay for downstream analysis. 2015 , 5, 14127	15
1490	Integrated analysis of global proteome, phosphoproteome, and glycoproteome enables complementary interpretation of disease-related protein networks. 2015 , 5, 18189	23
1489	Comparative proteomic analysis of compartmentalised Ras signalling. 2015 , 5, 17307	8
1488	A comprehensive analysis of the chorion locus in silkmoth. 2015 , 5, 16424	18
1487	Systems-wide analysis of BCR signalosomes and downstream phosphorylation and ubiquitylation. 2015 , 11, 810	82
1486	Alteration of intracellular protein expressions as a key mechanism of the deterioration of bacterial denitrification caused by copper oxide nanoparticles. 2015 , 5, 15824	64
1485	Proteomic analysis of tylosin-resistant Mycoplasma gallisepticum reveals enzymatic activities associated with resistance. 2015 , 5, 17077	6
1484	Combined Analyses of the VHL and Hypoxia Signaling Axes in an Isogenic Pairing of Renal Clear Cell Carcinoma Cells. 2015 , 14, 5263-72	10
1483	Differential urinary glycoproteome analysis of type 2 diabetic nephropathy using 2D-LC-MS/MS and iTRAQ quantification. 2015 , 13, 371	23
1482	Phosphoproteomic analysis reveals Smarcb1 dependent EGFR signaling in Malignant Rhabdoid tumor cells. 2015 , 14, 167	11

1481	Evaluation of the accuracy of protein quantification using isotope TMPP-labeled peptides. 2015 , 15, 2903-9	5
1480	Gel-free mass spectrometry analysis of Drosophila melanogaster heads. 2015 , 15, 3356-60	36
1479	Five omic technologies are concordant in differentiating the biochemical characteristics of the berries of five grapevine (Vitis vinifera L.) cultivars. 2015 , 16, 946	30
1478	High-level secretion of native recombinant human calreticulin in yeast. 2015 , 14, 165	16
1477	Lipopolysaccharide challenge significantly influences lipid metabolism and proteome of white adipose tissue in growing pigs. 2015 , 14, 68	15
1476	The calcified eggshell matrix proteome of a songbird, the zebra finch (Taeniopygia guttata). 2015 , 13, 29	23
1475	White matter injury restoration after stem cell administration in subcortical ischemic stroke. 2015 , 6, 121	45
1474	Local Joint inflammation and histone citrullination in a murine model of the transition from preclinical autoimmunity to inflammatory arthritis. 2015 , 67, 2877-87	72
1473	Development of an Automated, High-throughput Sample Preparation Protocol for Proteomics Analysis. 2015 , 36, 1791-1798	10
1472	Unrestricted modification search reveals lysine methylation as major modification induced by tissue formalin fixation and paraffin embedding. 2015 , 15, 2568-79	35
1471	Quantitative proteomic analysis of cabernet sauvignon grape cells exposed to thermal stresses reveals alterations in sugar and phenylpropanoid metabolism. 2015 , 15, 3048-60	26
1470	Machine learning reveals sex-specific 17I-estradiol-responsive expression patterns in white perch (Morone americana) plasma proteins. 2015 , 15, 2678-90	10
1469	An Integrated Multiomics Approach to Identify Candidate Antigens for Serodiagnosis of Human Onchocerciasis. 2015 , 14, 3224-33	9
1468	Membrane protein isolation and identification by covalent binding for proteome research. 2015 , 15, 3892-900	3
1467	Shotgun analysis of the marine mussel Mytilus edulis hemolymph proteome and mapping the innate immunity elements. 2015 , 15, 4021-9	30
1466	Integrated approach using multistep enzyme digestion, TiO2 enrichment, and database search for in-depth phosphoproteomic profiling. 2015 , 15, 618-23	4
1465	Proteomic and bioinformatics profile of paired human alveolar macrophages and peripheral blood monocytes. 2015 , 15, 3797-805	11
1464	A quantitative proteomics analysis of MCF7 breast cancer stem and progenitor cell populations. 2015 , 15, 3772-83	20

1463	LymPHOS 2.0: an update of a phosphosite database of primary human T cells. 2015 , 2015,	9
1462	Acylated monogalactosyl diacylglycerol: prevalence in the plant kingdom and identification of an enzyme catalyzing galactolipid head group acylation in Arabidopsis thaliana. 2015 , 84, 1152-66	23
1461	Large-scale identification of membrane proteins with properties favorable for crystallization. 2015 , 24, 1756-63	2
1460	Protein Corona Influences Cell-Biomaterial Interactions in Nanostructured Tissue Engineering Scaffolds. 2015 , 25, 4379-4389	40
1459	Urinary Biomarkers for Detection of Early and Advanced Chronic Kidney Disease - A Pilot Study. 2015 , 5,	1
1458	Quantitative Analysis of Staphylococcal Enterotoxins A and B in Food Matrices Using Ultra High-Performance Liquid Chromatography Tandem Mass Spectrometry (UPLC-MS/MS). 2015 , 7, 3637-56	29
1457	Incomplete LPS Core-Specific Felix01-Like Virus vB_EcoM_VpaE1. 2015 , 7, 6163-81	10
1456	Affinity proteomics to study endogenous protein complexes: pointers, pitfalls, preferences and perspectives. 2015 , 58, 103-19	39
1455	Proteomics Analysis of Cellular Proteins Co-Immunoprecipitated with Nucleoprotein of Influenza A Virus (H7N9). 2015 , 16, 25982-98	27
1454	A Proteomic Study of Subsp. Culture Supernatants. 2015 , 3, 411-423	5
1453	Changes in protein abundance are observed in bacterial isolates from a natural host. 2015 , 5, 71	4
1452	iTRAQ protein profile analysis of neuroblastoma (NA) cells infected with the rabies viruses rHep-Flury and Hep-dG. 2015 , 6, 691	7
1451	An ancient Pygo-dependent Wnt enhanceosome integrated by Chip/LDB-SSDP. 2015 , 4,	37
1450	Retinal glia promote dorsal root ganglion axon regeneration. 2015 , 10, e0115996	8
1449	Quantitative proteomics reveal distinct protein regulations caused by Aggregatibacter actinomycetemcomitans within subgingival biofilms. 2015 , 10, e0119222	31
1448	Quantitative proteomic analysis reveals that anti-cancer effects of selenium-binding protein 1 in vivo are associated with metabolic pathways. 2015 , 10, e0126285	18
1447	The Successful Diagnosis and Typing of Systemic Amyloidosis Using A Microwave-Assisted Filter-Aided Fast Sample Preparation Method and LC/MS/MS Analysis. 2015 , 10, e0127180	11
1446	Proteomic insight into the molecular function of the vitreous. 2015 , 10, e0127567	58

1445	Ineffective degradation of immunogenic gluten epitopes by currently available digestive enzyme supplements. 2015 , 10, e0128065	31
1444	The Goblet Cell Protein Clca1 (Alias mClca3 or Gob-5) Is Not Required for Intestinal Mucus Synthesis, Structure and Barrier Function in Naive or DSS-Challenged Mice. 2015 , 10, e0131991	14
1443	A Proteomic Analysis of Individual and Gender Variations in Normal Human Urine and Cerebrospinal Fluid Using iTRAQ Quantification. 2015 , 10, e0133270	44
1442	Differential Proteomic Analysis Using iTRAQ Reveals Alterations in Hull Development in Rice (Oryza sativa L.). 2015 , 10, e0133696	9
1441	Monocyte Chemoattractant Protein-Induced Protein 1 (MCPIP1) Enhances Angiogenic and Cardiomyogenic Potential of Murine Bone Marrow-Derived Mesenchymal Stem Cells. 2015 , 10, e0133746	21
1440	Detailed Functional and Proteomic Characterization of Fludarabine Resistance in Mantle Cell Lymphoma Cells. 2015 , 10, e0135314	8
1439	Proteins with Intrinsically Disordered Domains Are Preferentially Recruited to Polyglutamine Aggregates. 2015 , 10, e0136362	24
1438	Comparative Analysis of Label-Free and 8-Plex iTRAQ Approach for Quantitative Tissue Proteomic Analysis. 2015 , 10, e0137048	74
1437	Identification and Characterization of Anaplasma phagocytophilum Proteins Involved in Infection of the Tick Vector, Ixodes scapularis. 2015 , 10, e0137237	22
1436	Accuracy and Reproducibility in Quantification of Plasma Protein Concentrations by Mass Spectrometry without the Use of Isotopic Standards. 2015 , 10, e0140097	16
1435	The Skeleton Forming Proteome of an Early Branching Metazoan: A Molecular Survey of the Biomineralization Components Employed by the Coralline Sponge Vaceletia Sp. 2015 , 10, e0140100	19
1434	Comparison of the Cowpox Virus and Vaccinia Virus Mature Virion Proteome: Analysis of the Species- and Strain-Specific Proteome. 2015 , 10, e0141527	16
1433	Quantitative Proteomics Analysis of the Hepatitis C Virus Replicon High-Permissive and Low-Permissive Cell Lines. 2015 , 10, e0142082	10
1432	ABCE1 is a highly conserved RNA silencing suppressor. 2015 , 10, e0116702	9
1431	Spaceflight Effects on Cytochrome P450 Content in Mouse Liver. 2015 , 10, e0142374	22
1430	Phosphoproteomic analysis of the response of maize leaves to drought, heat and their combination stress. 2015 , 6, 298	91
1429	Global Cell Proteome Profiling, Phospho-signaling and Quantitative Proteomics for Identification of New Biomarkers in Acute Myeloid Leukemia Patients. 2016 , 17, 52-70	20
1428	Human Urine Proteomics: Analytical Techniques and Clinical Applications in Renal Diseases. 2015 , 2015, 782798	39

1427	Human Amniotic Fluid Mesenchymal Stem Cells from Second- and Third-Trimester Amniocentesis: Differentiation Potential, Molecular Signature, and Proteome Analysis. 2015 , 2015, 319238	54
1426	Dramatic improvement of proteomic analysis of zebrafish liver tumor by effective protein extraction with sodium deoxycholate and heat denaturation. 2015 , 2015, 763969	8
1425	The GARP complex is required for cellular sphingolipid homeostasis. 2015 , 4,	53
1424	Mx2 expression is associated with reduced susceptibility to HIV infection in highly exposed HIV seronegative Kenyan sex workers. 2015 , 29, 35-41	7
1423	Label-free proteomics uncovers energy metabolism and focal adhesion regulations responsive for endometrium receptivity. 2015 , 14, 1831-42	28
1422	Discovery and Longitudinal Evaluation of Candidate Protein Biomarkers for Disease Recurrence in Prostate Cancer. 2015 , 14, 2769-83	8
1421	Enterococcus faecalis Gelatinase Mediates Intestinal Permeability via Protease-Activated Receptor 2. 2015 , 83, 2762-70	45
1420	Current strategies and findings in clinically relevant post-translational modification-specific proteomics. 2015 , 12, 235-53	123
1419	Understanding the Mechanism of Thermotolerance Distinct From Heat Shock Response Through Proteomic Analysis of Industrial Strains of Saccharomyces cerevisiae. 2015 , 14, 1885-97	41
1418	A Comprehensive Transcriptomic and Proteomic Analysis of Hydra Head Regeneration. 2015 , 32, 1928-47	78
1417	A Comprehensive Analysis of Chromoplast Differentiation Reveals Complex Protein Changes Associated with Plastoglobule Biogenesis and Remodeling of Protein Systems in Sweet Orange Flesh. 2015 , 168, 1648-65	30
1416	Analysis of protein expression changes of the Vero E6 cells infected with classic PEDV strain CV777 by using quantitative proteomic technique. 2015 , 218, 27-39	30
1415	Development of a highly automated and multiplexed targeted proteome pipeline and assay for 112 rat brain synaptic proteins. 2015 , 15, 1202-14	11
1414	Effect of transient blood glucose increases after oral glucose intake on the human urinary proteome. 2015 , 9, 618-22	4
1413	Plant Mitochondria. 2015 ,	1
1412	Proteomic responses to a methyl viologen-induced oxidative stress in the wild type and FerB mutant strains of Paracoccus denitrificans. 2015 , 125, 68-75	11
1411	The functional interactome of PYHIN immune regulators reveals IFIX is a sensor of viral DNA. 2015 , 11, 787	59
1410	Effect of the DGAT1 K232A genotype of dairy cows on the milk metabolome and proteome. 2015 , 98, 3460-9	23

1409	The central nervous system transcriptome of the weakly electric brown ghost knifefish (Apteronotus leptorhynchus): de novo assembly, annotation, and proteomics validation. 2015 , 16, 166	14
1408	Chromatographic behavior of peptides containing oxidized methionine residues in proteomic LC-MS experiments: Complex tale of a simple modification. 2015 , 125, 131-9	14
1407	An Integrated Metagenomics/Metaproteomics Investigation of the Microbial Communities and Enzymes in Solid-state Fermentation of Pu-erh tea. 2015 , 5, 10117	65
1406	Vascular smooth muscle LRP6 limits arteriosclerotic calcification in diabetic LDLR-/- mice by restraining noncanonical Wnt signals. 2015 , 117, 142-56	61
1405	Neutrophil Extracellular Traps in Ulcerative Colitis: A Proteome Analysis of Intestinal Biopsies. 2015 , 21, 2052-67	88
1404	Changes in the repertoire of bovine milk proteins during mammary involution. 2015 , 9, 65-75	11
1403	Protein degradation and dynamic tRNA thiolation fine-tune translation at elevated temperatures. 2015 , 43, 4701-12	29
1402	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
1401	Novel Molecular Insights into Classical and Alternative Activation States of Microglia as Revealed by Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC)-based Proteomics. 2015 , 14, 3173-84	36
1400	Cdc42-dependent actin dynamics controls maturation and secretory activity of dendritic cells. 2015 , 211, 553-67	20
1399	Proteomics of Primary Cilia by Proximity Labeling. 2015 , 35, 497-512	225
1398	Automated, Online Sample Preparation for LC-MS Analyses: Affinity Capture, Digestion, and Clean-Up. 2015 , 335-356	1
1397	Structural Basis for Oxygen Activation at a Heterodinuclear Manganese/Iron Cofactor. 2015 , 290, 25254-72	26
1396	SWATH-MS in proteomics: current status. 2015 , 8, 192	3
1395	Neutrophil extracellular traps in sheep mastitis. 2015 , 46, 59	38
1394	Pacemaker-induced transient asynchrony suppresses heart failure progression. 2015 , 7, 319ra207	22
1393	Delineating the glycoproteome of elongating cotton fiber cells. 2015 , 5, 717-25	3
1392	Finding Missing Proteins from the Epigenetically Manipulated Human Cell with Stringent Quality Criteria. 2015 , 14, 3645-57	18

1391	Necroptosis signalling is tuned by phosphorylation of MLKL residues outside the pseudokinase domain activation loop. 2015 , 471, 255-65	76
1390	Poster Abstracts. 2015 , 47, 41-297	1
1389	Differential proteomic profiling of primary and recurrent chordomas. 2015 , 33, 2207-18	6
1388	Identification of oxidoreductases from the petroleum strain. 2015 , 8, 152-159	14
1387	Differential Proteomic Analysis of Syncytiotrophoblast Extracellular Vesicles from Early-Onset Severe Preeclampsia, using 8-Plex iTRAQ Labeling Coupled with 2D Nano LC-MS/MS. 2015 , 36, 1116-30	30
1386	In-depth evaluation of software tools for data-independent acquisition based label-free quantification. 2015 , 15, 3140-51	40
1385	Proteomic analysis and functional characterization of mouse brain mitochondria during aging reveal alterations in energy metabolism. 2015 , 15, 1574-86	32
1384	Quantitation of 47 human tear proteins using high resolution multiple reaction monitoring (HR-MRM) based-mass spectrometry. 2015 , 115, 36-48	38
1383	DIGESTIF: a universal quality standard for the control of bottom-up proteomics experiments. 2015 , 14, 787-803	20
1382	Quantitative glycome analysis of N-glycan patterns in bladder cancer vs normal bladder cells using an integrated strategy. 2015 , 14, 639-53	47
1381	Proteomics of skin proteins in psoriasis: from discovery and verification in a mouse model to confirmation in humans. 2015 , 14, 109-19	33
1380	Comparative phosphoproteome analysis of Magnaporthe oryzae-responsive proteins in susceptible and resistant rice cultivars. 2015 , 115, 66-80	25
1379	Nanostructured microfluidic digestion system for rapid high-performance proteolysis. 2015, 15, 650-4	12
1378	Inactivation of myeloperoxidase by benzoic acid hydrazide. 2015 , 570, 14-22	10
1377	Data from proteomic characterization and comparison of mammalian milk fat globule proteomes by iTRAQ analysis. 2015 , 3, 12-5	О
1376	Data set from the phosphoproteomic analysis of Magnaporthe oryzae-responsive proteins in susceptible and resistant rice cultivars. 2015 , 3, 7-11	1
1375	PAS kinase is activated by direct SNF1-dependent phosphorylation and mediates inhibition of TORC1 through the phosphorylation and activation of Pbp1. 2015 , 26, 569-82	41
1374	Comparative reevaluation of FASP and enhanced FASP methods by LC-MS/MS. 2015 , 14, 1637-42	39

1373	Dosage and temporal thresholds in microRNA proteomics. 2015 , 14, 289-302	9
1372	An integrated workflow for multiplex CSF proteomics and peptidomics-identification of candidate cerebrospinal fluid biomarkers of Alzheimer's disease. 2015 , 14, 654-63	65
1371	Quantitative proteomic analysis of sub-MIC erythromycin inhibiting biofilm formation of S. suis in vitro. 2015 , 116, 1-14	35
1370	Glycerol-3-phosphate O-acyltransferase is required for PBAN-induced sex pheromone biosynthesis in Bombyx mori. 2015 , 5, 8110	12
1369	A comprehensive map and functional annotation of the normal human cerebrospinal fluid proteome. 2015 , 119, 90-9	47
1368	Targeted mass spectrometry for the analysis of nutritive modulation of catalase and heme oxygenase-1 expression. 2015 , 117, 58-69	6
1367	Sample preparation for phosphoproteomic analysis of circadian time series in Arabidopsis thaliana. 2015 , 551, 405-31	7
1366	Rapid analyses of proteomes and interactomes using an integrated solid-phase extraction-liquid chromatography-MS/MS system. 2015 , 14, 977-85	5
1365	Plasmodium vivax trophozoite-stage proteomes. 2015 , 115, 157-76	28
1364	Profiling global kinome signatures of the radioresistant MCF-7/C6 breast cancer cells using MRM-based targeted proteomics. 2015 , 14, 193-201	27
1363	N-linked glycoproteome profiling of seedling leaf in Brachypodium distachyon L. 2015 , 14, 1727-38	19
1362	Integrative analysis of genomics and proteomics data on clinical breast cancer tissue specimens extracted with acid guanidinium thiocyanate-phenol-chloroform. 2015 , 14, 1627-36	12
1361	A quantitative proteomics tool to identify DNA-protein interactions in primary cells or blood. 2015 , 14, 1315-29	26
1360	High-resolution mass spectrometry-based background subtraction for identifying protein modifications in a complex biological system: detection of acetaminophen-bound microsomal proteins including argininosuccinate synthetase. 2015 , 28, 775-81	8
1359	High-sensitivity N-glycoproteomic analysis of mouse brain tissue by protein extraction with a mild detergent of N-dodecyl [-]D-maltoside. 2015 , 87, 2054-7	20
1358	New mass-spectrometry-compatible degradable surfactant for tissue proteomics. 2015 , 14, 1587-99	48
1357	High-antibody-producing Chinese hamster ovary cells up-regulate intracellular protein transport and glutathione synthesis. 2015 , 14, 609-18	45
1356	Functional and phylogenetic characterization of proteins detected in various nematode intestinal compartments. 2015 , 14, 812-27	15

1355	detrusor muscle. 2015 , 14, 635-45	12
1354	Interactome analysis of AMP-activated protein kinase (AMPK)- and - 11 in INS-1 pancreatic beta-cells by affinity purification-mass spectrometry. 2014 , 4, 4376	32
1353	Proprotein convertase 5/6 cleaves platelet-derived growth factor A in the human endometrium in preparation for embryo implantation. 2015 , 21, 262-70	8
1352	Sample preparation strategies for targeted proteomics via proteotypic peptides in human blood using liquid chromatography tandem mass spectrometry. 2015 , 9, 5-16	35
1351	Salivary proteomics in bisphosphonate-related osteonecrosis of the jaw. 2015 , 21, 46-56	13
1350	Chinese hamster ovary (CHO) host cell engineering to increase sialylation of recombinant therapeutic proteins by modulating sialyltransferase expression. 2015 , 31, 334-46	54
1349	Xylem sap in cotton contains proteins that contribute to environmental stress response and cell wall development. 2015 , 15, 17-26	29
1348	TRPC3 channels critically regulate hippocampal excitability and contextual fear memory. 2015 , 281, 69-77	37
1347	Single muscle fiber proteomics reveals unexpected mitochondrial specialization. 2015 , 16, 387-95	124
1346	Proteomic biomarkers in kidney disease: issues in development and implementation. 2015 , 11, 221-32	82
1345	Early markers of Fabry disease revealed by proteomics. 2015 , 11, 1543-51	
	Early markers of Fabry disease revealed by processmes. 2015, 11, 1515-51	36
1344	Deep proteomics of mouse skeletal muscle enables quantitation of protein isoforms, metabolic pathways, and transcription factors. 2015 , 14, 841-53	162
1344	Deep proteomics of mouse skeletal muscle enables quantitation of protein isoforms, metabolic	
	Deep proteomics of mouse skeletal muscle enables quantitation of protein isoforms, metabolic pathways, and transcription factors. 2015 , 14, 841-53 Mycobacterial proteomics: analysis of expressed proteomes and post-translational modifications to	162
1343	Deep proteomics of mouse skeletal muscle enables quantitation of protein isoforms, metabolic pathways, and transcription factors. 2015 , 14, 841-53 Mycobacterial proteomics: analysis of expressed proteomes and post-translational modifications to identify candidate virulence factors. 2015 , 12, 21-35 Fast profiling of protease specificity reveals similar substrate specificities for cathepsins K, L and S.	162
1343 1342	Deep proteomics of mouse skeletal muscle enables quantitation of protein isoforms, metabolic pathways, and transcription factors. 2015 , 14, 841-53 Mycobacterial proteomics: analysis of expressed proteomes and post-translational modifications to identify candidate virulence factors. 2015 , 12, 21-35 Fast profiling of protease specificity reveals similar substrate specificities for cathepsins K, L and S. 2015 , 15, 2479-90	162
1343 1342 1341	Deep proteomics of mouse skeletal muscle enables quantitation of protein isoforms, metabolic pathways, and transcription factors. 2015, 14, 841-53 Mycobacterial proteomics: analysis of expressed proteomes and post-translational modifications to identify candidate virulence factors. 2015, 12, 21-35 Fast profiling of protease specificity reveals similar substrate specificities for cathepsins K, L and S. 2015, 15, 2479-90 Global analysis of bacterial membrane proteins and their modifications. 2015, 305, 203-8 Dihydrolipoyl dehydrogenase as a potential UVB target in skin epidermis; using an integrated	162 10 33

1337	Proteomics-based metabolic modeling reveals that fatty acid oxidation (FAO) controls endothelial cell (EC) permeability. 2015 , 14, 621-34	63
1336	An optimized platform for hydrophilic interaction chromatography-immobilized metal affinity chromatography enables deep coverage of the rat liver phosphoproteome. 2015 , 14, 997-1009	19
1335	Characterization of quinoa seed proteome combining different protein precipitation techniques: Improvement of knowledge of nonmodel plant proteomics. 2015 , 38, 1017-25	21
1334	Terminal epidermal differentiation is regulated by the interaction of Fra-2/AP-1 with Ezh2 and ERK1/2. 2015 , 29, 144-56	37
1333	Differential reprogramming of isogenic colorectal cancer cells by distinct activating KRAS mutations. 2015 , 14, 1535-46	42
1332	Mass spectrometry of human leukocyte antigen class I peptidomes reveals strong effects of protein abundance and turnover on antigen presentation. 2015 , 14, 658-73	267
1331	Discovery of novel candidate urinary protein biomarkers for prostate cancer in a multiethnic cohort of South African patients via label-free mass spectrometry. 2015 , 9, 597-609	17
1330	Enrichment or depletion? The impact of stool pretreatment on metaproteomic characterization of the human gut microbiota. 2015 , 15, 3474-85	52
1329	PHOTOSYSTEM II SUBUNIT R is required for efficient binding of LIGHT-HARVESTING COMPLEX STRESS-RELATED PROTEIN3 to photosystem II-light-harvesting supercomplexes in Chlamydomonas reinhardtii. 2015 , 167, 1566-78	40
1328	Proteome reallocation in Escherichia coli with increasing specific growth rate. 2015 , 11, 1184-93	75
1327	A two-stage spin cartridge for integrated protein precipitation, digestion and SDS removal in a comparative bottom-up proteomics workflow. 2015 , 118, 140-50	17
1326	Glycosylation profiles determine extravasation and disease-targeting properties of armed antibodies. 2015 , 112, 2000-5	30
1325	Quantitative phosphoproteomics of the ataxia telangiectasia-mutated (ATM) and ataxia telangiectasia-mutated and rad3-related (ATR) dependent DNA damage response in Arabidopsis thaliana. 2015 , 14, 556-71	133
1324	Quantitative proteomic analyses of Schistosoma japonicum in response to artesunate. 2015 , 11, 1400-9	6
1323	Comprehensive proteome analysis of fresh frozen and optimal cutting temperature (OCT) embedded primary non-small cell lung carcinoma by LC-MS/MS. 2015 , 81, 50-5	22
1322	Phosphoproteomics analysis of a clinical Mycobacterium tuberculosis Beijing isolate: expanding the mycobacterial phosphoproteome catalog. 2015 , 6, 6	57
1321	Phosphoproteome of the cyanobacterium Synechocystis sp. PCC 6803 and its dynamics during nitrogen starvation. 2015 , 6, 248	59
1320	Biomarker Discovery and Verification of Esophageal Squamous Cell Carcinoma Using Integration of SWATH/MRM. 2015 , 14, 3793-803	35

1319	protein abundances between spiral and coccoid forms of the gastric pathogen Helicobacter pylori. 2015 , 126, 34-45	10
1318	Klebsiella pneumoniae O antigen loss alters the outer membrane protein composition and the selective packaging of proteins into secreted outer membrane vesicles. 2015 , 180, 1-10	29
1317	Analysis of site-specific N-glycan remodeling in the endoplasmic reticulum and the Golgi. 2015 , 25, 1335-49	48
1316	Isolation of acetylated and free N-terminal peptides from proteomic samples based on tresyl-functionalized microspheres. 2015 , 144, 122-8	7
1315	Subtle Regulation of Potato Acid Invertase Activity by a Protein Complex of Invertase, Invertase Inhibitor, and SUCROSE NONFERMENTING1-RELATED PROTEIN KINASE. 2015 , 168, 1807-19	31
1314	Structure and Functional Characterization of the Conserved JAK Interaction Region in the Intrinsically Disordered N-Terminus of SOCS5. 2015 , 54, 4672-82	11
1313	The generation gap: Proteome changes and strain variation during encystation in Giardia duodenalis. 2015 , 201, 47-56	14
1312	Extracellular protein analysis of activated sludge and their functions in wastewater treatment plant by shotgun proteomics. 2015 , 5, 12041	35
1311	Characterization of anti-theft devices directly from the surface of banknotes via easy ambient sonic spray ionization mass spectrometry. 2015 , 55, 285-90	10
1310	The effects of endogenous non-peptide molecule isatin and hydrogen peroxide on proteomic profiling of rat brain amyloid-□binding proteins: relevance to Alzheimer's disease?. 2014 , 16, 476-95	21
1309	A Phosphoproteomic Comparison of B-RAFV600E and MKK1/2 Inhibitors in Melanoma Cells. 2015 , 14, 1599-615	62
1308	Advances in proteomics for production strain analysis. 2015 , 35, 111-7	6
1307	Carbamidomethylation Side Reactions May Lead to Glycan Misassignments in Glycopeptide Analysis. 2015 , 87, 6297-302	22
1306	Definitive Screening Design Optimization of Mass Spectrometry Parameters for Sensitive Comparison of Filter and Solid Phase Extraction Purified, INLIGHT Plasma N-Glycans. 2015 , 87, 7305-12	30
1305	Functionally and morphologically distinct populations of extracellular vesicles produced by human neutrophilic granulocytes. 2015 , 98, 583-9	25
1304	Polarized cell motility induces hydrogen peroxide to inhibit cofilin via cysteine oxidation. 2015 , 25, 1520-5	44
1303	Quantitative Glycoproteomic Analysis Identifies Platelet-Induced Increase of Monocyte Adhesion via the Up-Regulation of Very Late Antigen 5. 2015 , 14, 3015-26	3
1302	Data-independent-acquisition mass spectrometry for identification of targeted-peptide site-specific modifications. 2015 , 407, 6627-35	15

1301	Applying SWATH Mass Spectrometry to Investigate Human Cervicovaginal Fluid During the Menstrual Cycle. 2015 , 93, 39	11
1300	Rescuing Those Left Behind: Recovering and Characterizing Underdigested Membrane and Hydrophobic Proteins To Enhance Proteome Measurement Depth. 2015 , 87, 7720-8	10
1299	Proteomic identification of novel cytoskeletal proteins associated with TbPLK, an essential regulator of cell morphogenesis in Trypanosoma brucei. 2015 , 26, 3013-29	53
1298	Convenient and Precise Strategy for Mapping N-Glycosylation Sites Using Microwave-Assisted Acid Hydrolysis and Characteristic Ions Recognition. 2015 , 87, 7833-9	19
1297	Proteomic Comparison and MRM-Based Comparative Analysis of Metabolites Reveal Metabolic Shift in Human Prostate Cancer Cell Lines. 2015 , 14, 3390-402	7
1296	Comparative Proteomic Analysis of Human Liver Tissue and Isolated Hepatocytes with a Focus on Proteins Determining Drug Exposure. 2015 , 14, 3305-14	74
1295	Binding of STIL to Plk4 activates kinase activity to promote centriole assembly. 2015 , 209, 863-78	126
1294	An Augmented Multiple-Protease-Based Human Phosphopeptide Atlas. 2015 , 11, 1834-43	78
1293	Protomer Roles in Chloroplast Chaperonin Assembly and Function. 2015 , 8, 1478-92	23
1292	Comparative Study of Three Methods of Sample Preparation for Proteomics Research. 2015, 43, 808-813	4
1291	mRNA 3'-UTR shortening is a molecular signature of mTORC1 activation. 2015 , 6, 7218	37
1290	Systems biology of tissue-specific response to Anaplasma phagocytophilum reveals differentiated apoptosis in the tick vector Ixodes scapularis. 2015 , 11, e1005120	88
1289	Proteomic challenges: sample preparation techniques for microgram-quantity protein analysis from biological samples. 2015 , 16, 3537-63	174
1288	Why phosphoproteomics is still a challenge. 2015 , 11, 1487-93	63
1287	A proteomic perspective on the changes in milk proteins due to high somatic cell count. 2015 , 98, 5339-51	21
1286	Comparative membrane proteomics: a technical advancement in the search of renal cell carcinoma biomarkers. 2015 , 11, 1708-16	16
1285	Proteomic analysis of the palmitoyl protein thioesterase 1 interactome in SH-SY5Y human	38
	neuroblastoma cells. 2015 , 123, 42-53	

1283	Microbial communities, extracellular proteomics and polysaccharides: A comparative investigation on biofilm and suspended sludge. 2015 , 190, 21-8	51
1282	Shotgun analysis of plasma fibrin clot-bound proteins in patients with acute myocardial infarction. 2015 , 135, 754-9	9
1281	Quantification of proteins by flow cytometry: Quantification of human hepatic transporter P-gp and OATP1B1 using flow cytometry and mass spectrometry. 2015 , 82, 38-46	11
1280	Mitochondrial Lon regulates apoptosis through the association with Hsp60-mtHsp70 complex. 2015 , 6, e1642	46
1279	Integrated systems for exosome investigation. 2015 , 87, 31-45	134
1278	Integrated SDS removal and protein digestion by hollow fiber membrane based device for SDS-assisted proteome analysis. 2015 , 141, 235-8	6
1277	Proteome-wide identification and quantification of S-glutathionylation targets in mouse liver. 2015 , 469, 25-32	21
1276	Simultaneous Quantification of Viral Antigen Expression Kinetics Using Data-Independent (DIA) Mass Spectrometry. 2015 , 14, 1361-72	18
1275	STATE TRANSITION7-Dependent Phosphorylation Is Modulated by Changing Environmental Conditions, and Its Absence Triggers Remodeling of Photosynthetic Protein Complexes. 2015 , 168, 615-34	53
1274	Dairy manure protein analysis using UV-vis based on the Bradford method. 2015 , 7, 2645-2652	17
1273	A multi-pronged investigation into the effect of glucose starvation and culture duration on fed-batch CHO cell culture. 2015 , 112, 2172-84	46
1272	Quantitative urinary proteomics using stable isotope labelling by peptide dimethylation in patients with prostate cancer. 2015 , 407, 3393-404	9
1271	A Commensal Strain of Staphylococcus epidermidis Overexpresses Membrane Proteins Associated with Pathogenesis When Grown in Biofilms. 2015 , 248, 431-42	10
1270	Targeting metabolic plasticity in breast cancer cells via mitochondrial complex I modulation. 2015 , 150, 43-56	15
1269	Large-Scale Examination of Factors Influencing Phosphopeptide Neutral Loss during Collision Induced Dissociation. 2015 , 26, 1128-42	7
1268	Human cytomegalovirus pUL97 kinase induces global changes in the infected cell phosphoproteome. 2015 , 15, 2006-22	35
1267	A preliminary quantitative proteomic analysis of glioblastoma pseudoprogression. 2015 , 13, 12	12
1266	Towards further defining the proteome of mouse saliva. 2015 , 13, 10	10

1265	Diagnosing inflammation and infection in the urinary system via proteomics. 2015, 13, 111	32
1264	Zinc regulates a switch between primary and alternative S18 ribosomal proteins in Mycobacterium tuberculosis. 2015 , 97, 263-80	30
1263	Toward the complete proteome of Synechocystis sp. PCC 6803. 2015 , 126, 203-19	24
1262	Sample preparation strategies for improving the identification of membrane proteins by mass spectrometry. 2015 , 407, 4893-905	12
1261	Natural alleles of a proteasome ₹ subunit gene contribute to thermotolerance and adaptation of African rice. 2015 , 47, 827-33	159
1260	Systematically ranking the tightness of membrane association for peripheral membrane proteins (PMPs). 2015 , 14, 340-53	12
1259	iTRAQ-based quantitative analysis of hippocampal postsynaptic density-associated proteins in a rat chronic mild stress model of depression. 2015 , 298, 220-92	46
1258	Quantitative proteomic analysis of the cellulolytic system of Clostridium termitidis CT1112 reveals distinct protein expression profiles upon growth on Eellulose and cellobiose. 2015 , 125, 41-53	12
1257	iTRAQ-based quantitative subcellular proteomic analysis of Avibirnavirus-infected cells. 2015 , 36, 1596-611	6
1256	Mass-spectrometry-based molecular characterization of extracellular vesicles: lipidomics and proteomics. 2015 , 14, 2367-84	148
1256 1255		148
1255	proteomics. 2015 , 14, 2367-84	148 333
1255	proteomics. 2015, 14, 2367-84 Effects of diuretics on urinary proteins. 2015, 845, 133-42	
1255 1254	Effects of diuretics on urinary proteins. 2015, 845, 133-42 Widespread Proteome Remodeling and Aggregation in Aging C. elegans. 2015, 161, 919-32 Dodecyl maltopyranoside enabled purification of active human GABA type A receptors for deep	333
1255 1254 1253	Effects of diuretics on urinary proteins. 2015, 845, 133-42 Widespread Proteome Remodeling and Aggregation in Aging C. elegans. 2015, 161, 919-32 Dodecyl maltopyranoside enabled purification of active human GABA type A receptors for deep and direct proteomic sequencing. 2015, 14, 724-38 Discovery and targeted proteomics on cutaneous biopsies infected by borrelia to investigate lyme	333
1255 1254 1253 1252	Effects of diuretics on urinary proteins. 2015, 845, 133-42 Widespread Proteome Remodeling and Aggregation in Aging C. elegans. 2015, 161, 919-32 Dodecyl maltopyranoside enabled purification of active human GABA type A receptors for deep and direct proteomic sequencing. 2015, 14, 724-38 Discovery and targeted proteomics on cutaneous biopsies infected by borrelia to investigate lyme disease. 2015, 14, 1254-64 A versatile reversed phase-strong cation exchange-reversed phase (RP-SCX-RP) multidimensional	333 14 16
1255 1254 1253 1252 1251	Effects of diuretics on urinary proteins. 2015, 845, 133-42 Widespread Proteome Remodeling and Aggregation in Aging C. elegans. 2015, 161, 919-32 Dodecyl maltopyranoside enabled purification of active human GABA type A receptors for deep and direct proteomic sequencing. 2015, 14, 724-38 Discovery and targeted proteomics on cutaneous biopsies infected by borrelia to investigate lyme disease. 2015, 14, 1254-64 A versatile reversed phase-strong cation exchange-reversed phase (RP-SCX-RP) multidimensional liquid chromatography platform for qualitative and quantitative shotgun proteomics. 2015, 140, 1237-52 Network-based proteomic approaches reveal the neurodegenerative, neuroprotective and	333 14 16

1247	Protein corona of nanoparticles: distinct proteins regulate the cellular uptake. 2015 , 16, 1311-21	388
1246	A novel cysteine cathepsin inhibitor yields macrophage cell death and mammary tumor regression. 2015 , 34, 6066-78	41
1245	A proteomic analysis reveals that Snail regulates the expression of the nuclear orphan receptor Nuclear Receptor Subfamily 2 Group F Member 6 (Nr2f6) and interleukin 17 (IL-17) to inhibit adipocyte differentiation. 2015 , 14, 303-15	22
1244	Basal and exercise induced label-free quantitative protein profiling of m. vastus lateralis in trained and untrained individuals. 2015 , 122, 119-32	42
1243	Rat liver sinusoidal surface N-linked glycoproteomic analysis by affinity enrichment and mass spectrometric identification. 2015 , 80, 260-75	2
1242	Elucidation of the CHO Super-Ome (CHO-SO) by Proteoinformatics. 2015 , 14, 4687-703	29
1241	Differential effects of acellular embryonic matrices on pluripotent stem cell expansion and neural differentiation. 2015 , 73, 231-42	54
1240	Comparison of sodium dodecyl sulfate depletion techniques for proteome analysis by mass spectrometry. 2015 , 1418, 158-166	41
1239	Machine Learning-based Classification of Diffuse Large B-cell Lymphoma Patients by Their Protein Expression Profiles. 2015 , 14, 2947-60	58
1238	Exosome enrichment of human serum using multiple cycles of centrifugation. 2015 , 36, 2017-26	43
1238	Exosome enrichment of human serum using multiple cycles of centrifugation. 2015 , 36, 2017-26 Cell type- and brain region-resolved mouse brain proteome. 2015 , 18, 1819-31	43
	Cell type- and brain region-resolved mouse brain proteome. 2015 , 18, 1819-31	
1237	Cell type- and brain region-resolved mouse brain proteome. 2015 , 18, 1819-31 Performing protein crosslinking using gas-phase cleavable chemical crosslinkers and liquid	418
1237	Cell type- and brain region-resolved mouse brain proteome. 2015 , 18, 1819-31 Performing protein crosslinking using gas-phase cleavable chemical crosslinkers and liquid chromatography-tandem mass spectrometry. 2015 , 89, 64-73 Quantitative Differences in the Urinary Proteome of Siblings Discordant for Type 1 Diabetes	418
1237 1236 1235	Cell type- and brain region-resolved mouse brain proteome. 2015 , 18, 1819-31 Performing protein crosslinking using gas-phase cleavable chemical crosslinkers and liquid chromatography-tandem mass spectrometry. 2015 , 89, 64-73 Quantitative Differences in the Urinary Proteome of Siblings Discordant for Type 1 Diabetes Include Lysosomal Enzymes. 2015 , 14, 3123-35 A lectin-based isolation/enrichment strategy for improved coverage of N-glycan analysis. 2015 ,	418 3 19
1237 1236 1235	Cell type- and brain region-resolved mouse brain proteome. 2015, 18, 1819-31 Performing protein crosslinking using gas-phase cleavable chemical crosslinkers and liquid chromatography-tandem mass spectrometry. 2015, 89, 64-73 Quantitative Differences in the Urinary Proteome of Siblings Discordant for Type 1 Diabetes Include Lysosomal Enzymes. 2015, 14, 3123-35 A lectin-based isolation/enrichment strategy for improved coverage of N-glycan analysis. 2015, 416, 7-13 Molecular control of irreversible bistability during trypanosome developmental commitment. 2015,	418 3 19
1237 1236 1235 1234	Cell type- and brain region-resolved mouse brain proteome. 2015, 18, 1819-31 Performing protein crosslinking using gas-phase cleavable chemical crosslinkers and liquid chromatography-tandem mass spectrometry. 2015, 89, 64-73 Quantitative Differences in the Urinary Proteome of Siblings Discordant for Type 1 Diabetes Include Lysosomal Enzymes. 2015, 14, 3123-35 A lectin-based isolation/enrichment strategy for improved coverage of N-glycan analysis. 2015, 416, 7-13 Molecular control of irreversible bistability during trypanosome developmental commitment. 2015, 211, 455-68	418 3 19 9

1229	The Magellania venosa Biomineralizing Proteome: A Window into Brachiopod Shell Evolution. 2015 , 7, 1349-62	40
1228	Widespread somatic L1 retrotransposition occurs early during gastrointestinal cancer evolution. 2015 , 25, 1536-45	92
1227	Prediction of Recurrence and Survival for Triple-Negative Breast Cancer (TNBC) by a Protein Signature in Tissue Samples. 2015 , 14, 2936-46	33
1226	Lack of presynaptic interaction between glucocorticoid and CB1 cannabinoid receptors in GABA-and glutamatergic terminals in the frontal cortex of laboratory rodents. 2015 , 90, 72-84	9
1225	Accumulation of non-outer segment proteins in the outer segment underlies photoreceptor degeneration in Bardet-Biedl syndrome. 2015 , 112, E4400-9	84
1224	Data for a comprehensive map and functional annotation of the human cerebrospinal fluid proteome. 2015 , 3, 103-7	6
1223	Label-free Quantitative Proteomics of Mouse Cerebrospinal Fluid Detects I-Site APP Cleaving Enzyme (BACE1) Protease Substrates In Vivo. 2015 , 14, 2550-63	52
1222	Global Proteomic Analysis of Functional Compartments in Immature Avian Follicles Using Laser Microdissection Coupled to LC-MS/MS. 2015 , 14, 3912-23	6
1221	Control of Homeostasis and Dendritic Cell Survival by the GTPase RhoA. 2015 , 195, 4244-56	3
1220	Temporal SILAC-based quantitative proteomics identifies host factors involved in chikungunya virus replication. 2015 , 15, 2267-80	12
1219	Integration-independent Transgenic Huntington Disease Fragment Mouse Models Reveal Distinct Phenotypes and Life Span in Vivo. 2015 , 290, 19287-306	13
1218	Quantitative Phosphoproteomics Revealed Glucose-Stimulated Responses of Islet Associated with Insulin Secretion. 2015 , 14, 4635-46	17
1217	Identification and quantitative analysis of cellular proteins affected by treatment with withaferin a using a SILAC-based proteomics approach. 2015 , 175, 86-92	15
1216	Highly Pathogenic H5N1 and Novel H7N9 Influenza A Viruses Induce More Profound Proteomic Host Responses than Seasonal and Pandemic H1N1 Strains. 2015 , 14, 4511-23	35
1215	Comparison of Influenza Virus Particle Purification Using Magnetic Sulfated Cellulose Particles with an Established Centrifugation Method for Analytics. 2015 , 87, 10708-11	3
1214	SERBP1 Is a Component of the Liver Receptor Homologue-1 Transcriptional Complex. 2015 , 14, 4571-80	6
1213	Comparison of Different Sample Preparation Protocols Reveals Lysis Buffer-Specific Extraction Biases in Gram-Negative Bacteria and Human Cells. 2015 , 14, 4472-85	40
1212	Data for mitochondrial proteomic alterations in the aging mouse brain. 2015 , 4, 127-9	5

1211	Secretome Analysis of Lipid-Induced Insulin Resistance in Skeletal Muscle Cells by a Combined Experimental and Bioinformatics Workflow. 2015 , 14, 4885-95	47
1210	Multifunctional nanoreactor for comprehensive characterization of membrane proteins based on surface functionalized mesoporous foams. 2015 , 87, 9360-7	12
1209	Minimizing technical variation during sample preparation prior tollabel-free quantitative mass spectrometry. 2015 , 490, 14-9	36
1208	RNAi-mediated downregulation of poplar plasma membrane intrinsic proteins (PIPs) changes plasma membrane proteome composition and affects leaf physiology. 2015 , 128, 321-32	17
1207	Proteomic Profiling of Detergent Resistant Membranes (Lipid Rafts) of Prostasomes. 2015 , 14, 3015-22	31
1206	Generation of a synthetic GlcNAcylated nucleosome reveals regulation of stability by H2A-Thr101 GlcNAcylation. 2015 , 6, 7978	40
1205	Less is More: Membrane Protein Digestion Beyond Urea-Trypsin Solution for Next-level Proteomics. 2015 , 14, 2441-53	35
1204	Proteome analysis of the triton-insoluble erythrocyte membrane skeleton. 2015 , 128, 298-305	15
1203	Body fluid peptide and protein signatures in diabetic kidney diseases. 2015 , 30 Suppl 4, iv43-53	5
1202	Development and application of wide-range gradient gel electrophoresis to proteome analysis. 2015 , 7, 8109-8115	6
1201	Comparative proteomic analysis of silkworm fat body after knocking out fibroin heavy chain gene: a novel insight into cross-talk between tissues. 2015 , 15, 611-37	9
1200	MStern Blotting-High Throughput Polyvinylidene Fluoride (PVDF) Membrane-Based Proteomic Sample Preparation for 96-Well Plates. 2015 , 14, 2814-23	40
1199	Enhanced SDC-assisted digestion coupled with lipid chromatography-tandem mass spectrometry for shotgun analysis of membrane proteome. 2015 , 1002, 144-51	9
1198	Reversible, Specific, Active Aggregates of Endogenous Proteins Assemble upon Heat Stress. 2015 , 162, 1286-98	264
1197	Global Identification of Protein Post-translational Modifications in a Single-Pass Database Search. 2015 , 14, 4714-20	34
1196	Elucidation of Xylem-Specific Transcription Factors and Absolute Quantification of Enzymes Regulating Cellulose Biosynthesis in Populus trichocarpa. 2015 , 14, 4158-68	12
1195	The application of systems biology to biomanufacturing. 2015 , 3, 341-355	1
1194	Fully automated multidimensional reversed-phase liquid chromatography with tandem anion/cation exchange columns for simultaneous global endogenous tyrosine nitration detection, integral membrane protein characterization, and quantitative proteomics mapping in cerebral	7

1193	Proteomic analysis of early-stage embryos: implications for egg quality in hapuku (Polyprion oxygeneios). 2015 , 41, 1403-17	8
1192	Methods of processing mass spectrometry data to identify peptides and proteins. 2015 , 70, 211-222	
1191	Proteome-wide dataset generated by iTRAQ-3DLCMS/MS technique for studying the role of FerB protein in oxidative stress in Paracoccus denitrificans. 2015 , 4, 390-4	
1190	A human gut metaproteomic dataset from stool samples pretreated or not by differential centrifugation. 2015 , 4, 559-62	5
1189	Data from proteomic characterization of the role of Snail1 in murine mesenchymal stem cells and 3T3-L1 fibroblasts differentiation. 2015 , 4, 606-13	5
1188	Quantitative analysis of glycans, related genes, and proteins in two human bone marrow stromal cell lines using an integrated strategy. 2015 , 43, 760-9.e7	5
1187	Bioengineered vocal fold mucosa for voice restoration. 2015 , 7, 314ra187	46
1186	Supervised multi-view canonical correlation analysis (sMVCCA): integrating histologic and proteomic features for predicting recurrent prostate cancer. 2015 , 34, 284-97	61
1185	The role of protein and peptide separation before mass spectrometry analysis in clinical proteomics. 2015 , 1381, 1-12	51
1184	endoProteoFASP: a novel FASP approach to profile salivary peptidome and disclose salivary proteases. 2015 , 132, 486-93	9
1183	Current approaches and challenges in targeted absolute quantification of membrane proteins. 2015 , 15, 915-29	10
1182	Phosphoproteomic analysis of the resistant and susceptible genotypes of maize infected with sugarcane mosaic virus. 2015 , 47, 483-96	18
1181	Intact stable isotope labeled plasma proteins from the SILAC-labeled HepG2 secretome. 2015 , 15, 3104-15	7
1180	Proteomic identification of differentially expressed proteins in vascular wall of patients with ruptured intracranial aneurysms. 2015 , 238, 201-6	9
1179	Profiling the RNA editomes of wild-type C. elegans and ADAR mutants. 2015 , 25, 66-75	53
1178	Proteomic analysis of rat plasma with experimental autoimmune uveitis based on label-free liquid chromatography-tandem mass spectrometry (LC-MS/MS). 2015 , 976-977, 84-90	8
1177	The cellular and proteomic response of primary and immortalized murine Kupffer cells following immune stimulation diverges from that of monocyte-derived macrophages. 2015 , 15, 545-53	3
1176	Quantitative comparison of a human cancer cell surface proteome between interphase and mitosis. 2015 , 34, 251-65	27

1175	Protein quantification using a cleavable reporter peptide. 2015 , 14, 728-37	6
1174	Identification of prolyl hydroxylation modifications in mammalian cell proteins. 2015 , 15, 1259-67	14
1173	Construction of a high-performance magnetic enzyme nanosystem for rapid tryptic digestion. 2014 , 4, 6947	64
1172	Hg-responsive proteins identified in wheat seedlings using iTRAQ analysis and the role of ABA in Hg stress. 2015 , 14, 249-67	29
1171	Temporal proteomic analysis and label-free quantification of viral proteins of an invertebrate iridovirus. 2015 , 96, 196-205	7
1170	Comparative proteomic analysis revealing the complex network associated with waterlogging stress in maize (Zea mays L.) seedling root cells. 2015 , 15, 135-47	34
1169	Proteome sequencing goes deep. 2015 , 24, 11-7	77
1168	The impact of high-fat diet on metabolism and immune defense in small intestine mucosa. 2015 , 14, 353-65	41
1167	Whole cell, label free protein quantitation with data independent acquisition: quantitation at the MS2 level. 2015 , 15, 16-24	15
1166	State of the art of 2D DIGE. 2015 , 9, 277-88	79
1165	Integration of conventional quantitative and phospho-proteomics reveals new elements in activated Jurkat T-cell receptor pathway maintenance. 2015 , 15, 25-33	9
1164	Mass spectrometry in natural product structure elucidation. 2015 , 100, 77-221	8
1163	A generic approach for "shotgun" analysis of the soluble proteome of plant cell suspension cultures. 2015 , 974, 48-56	1
1162	The calcium-dependent protein kinase CPK7 acts on root hydraulic conductivity. 2015 , 38, 1312-20	20
1161	Urine Proteomics in Kidney Disease Biomarker Discovery. 2015 ,	3
1160	A proteomic analysis of p53-independent induction of apoptosis by bortezomib in 4T1 breast cancer cell line. 2015 , 113, 315-25	17
1159	Making proteomics data accessible and reusable: current state of proteomics databases and repositories. 2015 , 15, 930-49	138
1158	Elevated temperature alters proteomic responses of individual organisms within a biofilm community. 2015 , 9, 180-94	42

1157	From hundreds to thousands: Widening the normal human Urinome (1). 2015 , 112, 53-62	35
1156	Comparative proteomic analysis of Arthrobacter phenanthrenivorans Sphe3 on phenanthrene, phthalate and glucose. 2015 , 113, 73-89	44
1155	Glucagon-like peptide-1 receptor agonists increase pancreatic mass by induction of protein synthesis. 2015 , 64, 1046-56	37
1154	The hand eczema proteome: imbalance of epidermal barrier proteins. 2015 , 172, 994-1001	31
1153	Mass spectrometry based quantitative proteomics and integrative network analysis accentuates modulating roles of annexin-1 in mammary tumorigenesis. 2015 , 15, 408-18	13
1152	Robotics-assisted mass spectrometry assay platform enabled by open-source electronics. 2015 , 64, 260-8	34
1151	Differential proteomic analysis of umbilical artery tissue from preeclampsia patients, using iTRAQ isobaric tags and 2D nano LC-MS/MS. 2015 , 112, 262-73	16
1150	Proteomic developments in the analysis of formalin-fixed tissue. 2015 , 1854, 559-80	74
1149	Astrocyte-neuron crosstalk regulates the expression and subcellular localization of carbohydrate metabolism enzymes. 2015 , 63, 328-40	45
1148	Fungi Contribute Critical but Spatially Varying Roles in Nitrogen and Carbon Cycling in Acid Mine Drainage. 2016 , 7, 238	40
1147	Proteomic Upregulation of Fatty Acid Synthase and Fatty Acid Binding Protein 5 and Identification of Cancer- and Race-Specific Pathway Associations in Human Prostate Cancer Tissues. 2016 , 7, 1452-64	27
1146	Identification of low potassium stress-responsive proteins in tobacco (Nicotiana tabacum) seedling roots using an iTRAQ-based analysis. 2016 , 15,	3
1145	AminoxyTMT: A novel multi-functional reagent for characterization of protein carbonylation. 2016 , 60, 186-8, 190, 192-6	13
1144	Proteomic and Clinical Analysis of a Fine-Needle Aspirate Biopsy from a Single Cold Thyroid Nodule: A Case Study. 2016 , 06,	1
1143	The Brain Proteome of the Ubiquitin Ligase Peli1 Knock-Out Mouse during Experimental Autoimmune Encephalomyelitis. 2016 , 9, 209-219	7
1142	Changes in the Expression of Biofilm-Associated Surface Proteins in Food-Environmental Isolates Subjected to Sublethal Concentrations of Disinfectants. 2016 , 2016, 4034517	13
1141	Dynamic Proteomic Analysis of Pancreatic Mesenchyme Reveals Novel Factors That Enhance Human Embryonic Stem Cell to Pancreatic Cell Differentiation. 2016 , 2016, 6183562	18
1140	Set7 mediated Gli3 methylation plays a positive role in the activation of Sonic Hedgehog pathway in mammals. 2016 , 5,	30

(2016-2016)

1139	tabel-Free Proteomics Assisted by Affinity Enrichment for Elucidating the Chemical Reactivity of the Liver Mitochondrial Proteome toward Adduction by the Lipid Electrophile 4-hydroxy-2-nonenal (HNE). 2016 , 4, 2	18
1138	Degradation of Swainsonine by the NADP-Dependent Alcohol Dehydrogenase A1R6C3 in Arthrobacter sp. HW08. 2016 , 8,	3
1137	Phosphoproteome Analysis Reveals the Molecular Mechanisms Underlying Deoxynivalenol-Induced Intestinal Toxicity in IPEC-J2 Cells. 2016 , 8,	19
1136	Complement Regulator FHR-3 Is Elevated either Locally or Systemically in a Selection of Autoimmune Diseases. 2016 , 7, 542	16
1135	Comparative Proteomic Analysis of Desulfotomaculum reducens MI-1: Insights into the Metabolic Versatility of a Gram-Positive Sulfate- and Metal-Reducing Bacterium. 2016 , 7, 191	10
1134	Sub-MIC Tylosin Inhibits Streptococcus suis Biofilm Formation and Results in Differential Protein Expression. 2016 , 7, 384	19
1133	Plasma Membrane Profiling Reveals Upregulation of ABCA1 by Infected Macrophages Leading to Restriction of Mycobacterial Growth. 2016 , 7, 1086	13
1132	Proteomics Analysis Reveals Novel RASSF2 Interaction Partners. 2016 , 8,	6
1131	Proteomics-Based Analysis of Protein Complexes in Pluripotent Stem Cells and Cancer Biology. 2016 , 17, 432	2
1130	Antibacterial Activity of Juglone against Staphylococcus aureus: From Apparent to Proteomic. 2016 , 17,	33
1129	Identification of New Epididymal Luminal Fluid Proteins Involved in Sperm Maturation in Infertile Rats Treated by Dutasteride Using iTRAQ. 2016 , 21,	9
1128	Laccase Gene Family in Cerrena sp. HYB07: Sequences, Heterologous Expression and Transcriptional Analysis. 2016 , 21,	13
1127	Proteomics of Skeletal Muscle: Focus on Insulin Resistance and Exercise Biology. 2016 , 4,	22
1126	Global Proteome Changes in Liver Tissue 6 Weeks after FOLFOX Treatment of Colorectal Cancer Liver Metastases. 2016 , 4,	Ο
1125	The intracellular bacterium Anaplasma phagocytophilum selectively manipulates the levels of vertebrate host proteins in the tick vector Ixodes scapularis. 2016 , 9, 467	19
1124	iTRAQ-Based Quantitative Proteomics Analysis of Black Rice Grain Development Reveals Metabolic Pathways Associated with Anthocyanin Biosynthesis. 2016 , 11, e0159238	17
1123	The EARP Complex and Its Interactor EIPR-1 Are Required for Cargo Sorting to Dense-Core Vesicles. 2016 , 12, e1006074	29
1122	Endogenous Mouse Dicer Is an Exclusively Cytoplasmic Protein. 2016 , 12, e1006095	20

1121	The Presence of Pretreated Lignocellulosic Solids from Birch during Saccharomyces cerevisiae Fermentations Leads to Increased Tolerance to InhibitorsA Proteomic Study of the Effects. 2016 , 11, e0148635	6
1120	Lamellipodia and Membrane Blebs Drive Efficient Electrotactic Migration of Rat Walker Carcinosarcoma Cells WC 256. 2016 , 11, e0149133	8
1119	DegP Chaperone Suppresses Toxic Inner Membrane Translocation Intermediates. 2016 , 11, e0162922	11
1118	Use of Filter-Aided Capture and Elution Protocol for Concurrent Preparation of N-glycan and O-glycopeptides for LC-MS/MS Analysis. 2016 , 13, 48-54	1
1117	Selecting Sample Preparation Workflows for Mass Spectrometry-Based Proteomic and Phosphoproteomic Analysis of Patient Samples with Acute Myeloid Leukemia. 2016 , 4,	16
1116	Deep Phosphoproteomic Measurements Pinpointing Drug Induced Protective Mechanisms in Neuronal Cells. 2016 , 7, 635	4
1115	Comparative Proteomic Analysis of the Response of Maize (Zea mays L.) Leaves to Long Photoperiod Condition. 2016 , 7, 752	13
1114	Shotgun Proteomics of Tomato Fruits: Evaluation, Optimization and Validation of Sample Preparation Methods and Mass Spectrometric Parameters. 2016 , 7, 969	16
1113	Shotgun Label-free Proteomic Analysis of Clubroot (Plasmodiophora brassicae) Resistance Conferred by the Gene Rcr1 in Brassica rapa. 2016 , 7, 1013	26
1112	Metabolic Reconstruction of Setaria italica: A Systems Biology Approach for Integrating Tissue-Specific Omics and Pathway Analysis of Bioenergy Grasses. 2016 , 7, 1138	14
1111	The Difference of Physiological and Proteomic Changes in Maize Leaves Adaptation to Drought, Heat, and Combined Both Stresses. 2016 , 7, 1471	70
1110	Mass spectrometry methods for predicting antibiotic resistance. 2016 , 10, 964-981	27
1109	Proteomic analysis of Rhodotorula mucilaginosa: dealing with the issues of a non-conventional yeast. 2016 , 33, 433-49	8
1108	Comprehensive Proteomic Analysis of Nitrogen-Starved Mycobacterium smegmatis pup Reveals the Impact of Pupylation on Nitrogen Stress Response. 2016 , 15, 2812-25	20
1107	Three-Dimensional Adult Cardiac Extracellular Matrix Promotes Maturation of Human Induced Pluripotent Stem Cell-Derived Cardiomyocytes. 2016 , 22, 1016-25	92
1106	Mass spectrometry insights into a tandem ubiquitin-binding domain hybrid engineered for the selective recognition of unanchored polyubiquitin. 2016 , 16, 1961-9	8
1105	Recombinant acetylated trypsin demonstrates superior stability and higher activity than commercial products in quantitative proteomics studies. 2016 , 30, 1059-66	10
1104	Common errors in mass spectrometry-based analysis of post-translational modifications. 2016 , 16, 700-14	75

(2016-2016)

1103	Human aqueous humor proteome in cataract, glaucoma, and pseudoexfoliation syndrome. 2016 , 16, 1938-46	39
1102	Comparative proteomics analysis of silkworm hemolymph during the stages of metamorphosis via liquid chromatography and mass spectrometry. 2016 , 16, 1421-31	8
1101	Sensitivity of mass spectrometry analysis depends on the shape of the filtration unit used for filter aided sample preparation (FASP). 2016 , 16, 1852-7	33
1100	Laser ablation sample transfer for localized LC-MS/MS proteomic analysis of tissue. 2016 , 51, 261-8	21
1099	Oral secretions from Mythimna separata insects specifically induce defence responses in maize as revealed by high-dimensional biological data. 2016 , 39, 1749-1766	40
1098	Supernatant protein biomarkers of red blood cell storage hemolysis as determined through an absolute quantification proteomics technology. 2016 , 56, 1329-39	31
1097	Endurance Exercise Improves Molecular Pathways of Aerobic Metabolism in Patients With Myositis. 2016 , 68, 1738-50	48
1096	A Critical Evaluation of the PAXgene Tissue Fixation System: Morphology, Immunohistochemistry, Molecular Biology, and Proteomics. 2016 , 146, 25-40	28
1095	Rearrangement of mitochondrial pyruvate dehydrogenase subunit dihydrolipoamide dehydrogenase protein-protein interactions by the MDM2 ligand nutlin-3. 2016 , 16, 2327-44	12
1094	Quantitative Phosphoproteomic Study Reveals that Protein Kinase A Regulates Neural Stem Cell Differentiation Through Phosphorylation of Catenin Beta-1 and Glycogen Synthase Kinase $3\square$ 2016 , 34, 2090-101	12
1093	Improved 6-Plex Tandem Mass Tags Quantification Throughput Using a Linear Ion Trap-High-Energy Collision Induced Dissociation MS(3) Scan. 2016 , 88, 7471-5	14
1092	Automated SDS Depletion for Mass Spectrometry of Intact Membrane Proteins though Transmembrane Electrophoresis. 2016 , 15, 2634-42	18
1091	Extracellular matrix protein expression is brain region dependent. 2016 , 524, 1309-36	65
1090	Comparison of commercial nanoliquid chromatography columns for fast, targeted mass spectrometry-based proteomics. 2016 , 2, FSO119	11
1089	Identification of Apo B48 and other novel biomarkers in amyotrophic lateral sclerosis patient fibroblasts. 2016 , 10, 453-62	9
1088	Human promyelocytic leukemia protein is targeted to distinct subnuclear domains in plant nuclei and colocalizes with nucleolar constituents in a SUMO-dependent manner. 2016 , 6, 1141-1154	2
1087	Mortalin-mediated and ERK-controlled targeting of HIF-14 mitochondria confers resistance to apoptosis under hypoxia. 2017 , 130, 466-479	40
1086	Phosphoribosylation of Ubiquitin Promotes Serine Ubiquitination and Impairs Conventional Ubiquitination. 2016 , 167, 1636-1649.e13	157

1085	New insights into functional regulation in MS-based drug profiling. 2016 , 6, 18826	7
1084	Combinatory annotation of cell membrane receptors and signalling pathways of Bombyx mori prothoracic glands. 2016 , 3, 160073	4
1083	A proteomic approach to the development of DIVA ELISA distinguishing pigs infected with Salmonella Typhimurium and pigs vaccinated with a Salmonella Typhimurium-based inactivated vaccine. 2016 , 12, 252	2
1082	Proteome quantification of cotton xylem sap suggests the mechanisms of potassium-deficiency-induced changes in plant resistance to environmental stresses. 2016 , 6, 21060	20
1081	Insight On Colorectal Carcinoma Infiltration by Studying Perilesional Extracellular Matrix. 2016 , 6, 22522	43
1080	An interactomics overview of the human and bovine milk proteome over lactation. 2016 , 15, 1	27
1079	Gene-specific correlation of RNA and protein levels in human cells and tissues. 2016 , 12, 883	230
1078	Spatially-Resolved Proteomics: Rapid Quantitative Analysis of Laser Capture Microdissected Alveolar Tissue Samples. 2016 , 6, 39223	51
1077	Understanding of Networks In Vitro and/or In Vivo. 2016 , 141-152	
1076	A proteomic evaluation of urinary changes associated with cardiopulmonary bypass. 2016 , 13, 17	6
1076 1075	A proteomic evaluation of urinary changes associated with cardiopulmonary bypass. 2016, 13, 17 Protocol: a fast, comprehensive and reproducible one-step extraction method for the rapid preparation of polar and semi-polar metabolites, lipids, proteins, starch and cell wall polymers from a single sample. 2016, 12, 45	86
ĺ	Protocol: a fast, comprehensive and reproducible one-step extraction method for the rapid preparation of polar and semi-polar metabolites, lipids, proteins, starch and cell wall polymers from	
1075	Protocol: a fast, comprehensive and reproducible one-step extraction method for the rapid preparation of polar and semi-polar metabolites, lipids, proteins, starch and cell wall polymers from a single sample. 2016 , 12, 45 Data for iTRAQ-based quantitative proteomics analysis of different biotypes in with multi-herbicide	86
1075	Protocol: a fast, comprehensive and reproducible one-step extraction method for the rapid preparation of polar and semi-polar metabolites, lipids, proteins, starch and cell wall polymers from a single sample. 2016 , 12, 45 Data for iTRAQ-based quantitative proteomics analysis of different biotypes in with multi-herbicide treatment. 2016 , 9, 741-745 Highly Selective Enrichment of Glycopeptides Based on Zwitterionically Functionalized Soluble	86
1075 1074 1073	Protocol: a fast, comprehensive and reproducible one-step extraction method for the rapid preparation of polar and semi-polar metabolites, lipids, proteins, starch and cell wall polymers from a single sample. 2016, 12, 45 Data for iTRAQ-based quantitative proteomics analysis of different biotypes in with multi-herbicide treatment. 2016, 9, 741-745 Highly Selective Enrichment of Glycopeptides Based on Zwitterionically Functionalized Soluble Nanopolymers. 2016, 6, 29776	86
1075 1074 1073	Protocol: a fast, comprehensive and reproducible one-step extraction method for the rapid preparation of polar and semi-polar metabolites, lipids, proteins, starch and cell wall polymers from a single sample. 2016, 12, 45 Data for iTRAQ-based quantitative proteomics analysis of different biotypes in with multi-herbicide treatment. 2016, 9, 741-745 Highly Selective Enrichment of Glycopeptides Based on Zwitterionically Functionalized Soluble Nanopolymers. 2016, 6, 29776 Proteomics in Human Reproduction. 2016, Interactomic analysis of REST/NRSF and implications of its functional links with the transcription	86 4 21
1075 1074 1073 1072	Protocol: a fast, comprehensive and reproducible one-step extraction method for the rapid preparation of polar and semi-polar metabolites, lipids, proteins, starch and cell wall polymers from a single sample. 2016, 12, 45 Data for iTRAQ-based quantitative proteomics analysis of different biotypes in with multi-herbicide treatment. 2016, 9, 741-745 Highly Selective Enrichment of Glycopeptides Based on Zwitterionically Functionalized Soluble Nanopolymers. 2016, 6, 29776 Proteomics in Human Reproduction. 2016, Interactomic analysis of REST/NRSF and implications of its functional links with the transcription suppressor TRIM28 during neuronal differentiation. 2016, 6, 39049 The impact of sequence database choice on metaproteomic results in gut microbiota studies. 2016,	86 4 21 1

1067 Evolution of a mass spectrometry-grade protease with PTM-directed specificity. 2016 , 113, 14686-1469	l 16
1066 Modern Proteomics Bample Preparation, Analysis and Practical Applications. 2016,	10
1065 Protein Structural Analysis via Mass Spectrometry-Based Proteomics. 2016 , 919, 397-431	21
1064 JUN dependency in distinct early and late BRAF inhibition adaptation states of melanoma. 2016 , 2, 1602	8 42
Rational engineering of a virulence gene from Mycobacterium tuberculosis facilitates proteomic analysis of a natural protein N-terminus. 2016 , 6, 33265	4
Proteomic analysis of scallop hepatopancreatic extract provides insights into marine polysaccharide digestion. 2016 , 6, 34866	10
1061 Pro-inflammatory effects of a litchi protein extract in murine RAW264.7 macrophages. 2016 , 3, 16017	8
Data file of a deep proteome analysis of the prefrontal cortex in aged mice with progranulin deficiency or neuronal overexpression of progranulin. 2016 , 9, 1070-1073	1
Targeted histidine-peptide enrichment improved the accuracy of isobaric-based quantitative proteomics. 2016 , 8, 5255-5261	5
Protein, peptide, amino acid composition, and potential functional properties of existing and novel dietary protein sources for monogastrics1,2. 2016 , 94, 30-39	13
Comparative proteomic analysis reveals alterations in development and photosynthesis-related proteins in diploid and triploid rice. 2016 , 16, 199	17
S-nitrosation of proteins relevant to Alzheimer's disease during early stages of neurodegeneration. 2016 , 113, 4152-7	53
1055 Proteomic analysis of exosomal cargo: the challenge of high purity vesicle isolation. 2016 , 12, 1407-19	119
1054 Application of Clinical Bioinformatics. 2016 ,	8
1053 Proteomic Profiling: Data Mining and Analyses. 2016 , 133-173	
In-Depth Proteomic Quantification of Cell Secretome in Serum-Containing Conditioned Medium. 2016 , 88, 4971-8	27
1051 Chemoenzymatic method for glycomics: Isolation, identification, and quantitation. 2016 , 16, 241-56	19
Data from SILAC-based quantitative analysis of lysates from mouse microglial cells treated with Withaferin A (WA). 2016 , 7, 747-50	

1049	Comparative fatty acid transcriptomic test and iTRAQ-based proteomic analysis in Haematococcus pluvialis upon salicylic acid (SA) and jasmonic acid (JA) inductions. 2016 , 17, 277-284	16
1048	Physicochemical characterization of biopharmaceuticals. 2016 , 130, 366-389	40
1047	CIS is a potent checkpoint in NK cell-mediated tumor immunity. 2016 , 17, 816-24	185
1046	Mechanisms of Phenotypic Rifampicin Tolerance in Mycobacterium tuberculosis Beijing Genotype Strain B0/W148 Revealed by Proteomics. 2016 , 15, 1194-204	18
1045	Compensating the Fitness Costs of Synonymous Mutations. 2016 , 33, 1461-77	28
1044	Plasmodiumfalciparum infection induces dynamic changes in the erythrocyte phospho-proteome. 2016 , 58, 35-44	12
1043	Oncogenic KRAS Regulates Tumor Cell Signaling via Stromal Reciprocation. 2016 , 165, 910-20	169
1042	The goat (Capra hircus) mammary gland secretory tissue proteome as influenced by weight loss: A study using label free proteomics. 2016 , 145, 60-69	30
1041	STAGE-diging: A novel in-gel digestion processing for proteomics samples. 2016 , 140, 48-54	12
1040	Simple and Integrated Spintip-Based Technology Applied for Deep Proteome Profiling. 2016 , 88, 4864-71	74
1039	Mass spectrometry analysis of adipose-derived stem cells reveals a significant effect of hypoxia on pathways regulating extracellular matrix. 2016 , 7, 52	33
1038	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
1037	Nucleolar Enrichment of Brain Proteins with Critical Roles in Human Neurodevelopment. 2016 , 15, 2055-75	13
1036	Dissecting the proteome dynamics of the early heat stress response leading to plant survival or death in Arabidopsis. 2016 , 39, 1264-78	53
1035	A proteomics-based identification of putative biomarkers for disease in bovine milk. 2016 , 174, 11-8	14
1034	Human papillomavirus type 16 viral load is decreased following a therapeutic vaccination. 2016 , 65, 563-73	34
1033	Screening and Functional Analyses of Nilaparvata lugens Salivary Proteome. 2016 , 15, 1883-96	55
1032	An RNA matchmaker protein regulates the activity of the long noncoding RNA HOTAIR. 2016 , 22, 995-1010	37

1031	Optimizing the SWATH-MS-workflow for label-free proteomics. 2016 , 145, 137-140	18
1030	Six alternative proteases for mass spectrometry-based proteomics beyond trypsin. 2016 , 11, 993-1006	245
1029	Freezing effects on the acute myeloid leukemia cell proteome and phosphoproteome revealed using optimal quantitative workflows. 2016 , 145, 214-225	32
1028	Quantitative Evaluation of Filter Aided Sample Preparation (FASP) and Multienzyme Digestion FASP Protocols. 2016 , 88, 5438-43	109
1027	Discovery of serum protein biomarkers in drug-free patients with major depressive disorder. 2016 , 69, 60-8	43
1026	Protein identification and in vitro digestion of fractions from Tenebrio molitor. 2016 , 242, 1285-1297	47
1025	The omic approach to parasitic trematode research-a review of techniques and developments within the past 5 years. 2016 , 115, 2523-43	7
1024	Multilayered proteomics reveals molecular switches dictating ligand-dependent EGFR trafficking. 2016 , 23, 608-18	66
1023	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
1022	Molecular Signatures of Membrane Protein Complexes Underlying Muscular Dystrophy. 2016 , 15, 2169-85	15
1021	Vaccinomics Approach to Tick Vaccine Development. 2016 , 1404, 275-286	14
1020	The global regulatory effect of Edwardsiella tarda Fur on iron acquisition, stress resistance, and host infection: A proteomics-based interpretation. 2016 , 140, 100-10	18
1019	Glycan Moieties as Bait to Fish Plasma Membrane Proteins. 2016 , 88, 5065-71	6
1018	Dissecting SUMO Dynamics by Mass Spectrometry. 2016 , 1449, 291-8	1
1017	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
1016	Loss of Pink1 modulates synaptic mitochondrial bioenergetics in the rat striatum prior to motor symptoms: concomitant complex I respiratory defects and increased complex II-mediated respiration. 2016 , 10, 1205-1217	17
1015	Deletion of the hypothetical protein SCO2127 of Streptomyces coelicolor allowed identification of a new regulator of actinorhodin production. 2016 , 100, 9229-9237	6
1014	Direct molecular fishing in molecular partners investigation in proteinprotein and proteinpeptide interactions. 2016 , 42, 14-21	10

1013	Label-free quantitative proteomic analysis of the inhibitory activities of juglone against translation and energy metabolism in Escherichia coli. 2016 , 18, 55-58	3
1012	Global MS-Based Proteomics Drug Profiling. 2016 , 1449, 469-79	1
1011	Human fallopian tube proteome shows high coverage of mesenchymal stem cells associated proteins. 2016 , 36, e00297	6
1010	Comprehensive Proteome Profiling of Platelet Identified a Protein Profile Predictive of Responses to An Antiplatelet Agent Sarpogrelate. 2016 , 15, 3461-3472	14
1009	Xanthine oxidoreductase mediates membrane docking of milk-fat droplets but is not essential for apocrine lipid secretion. 2016 , 594, 5899-5921	28
1008	SWATH-MS proteome profiling data comparison of DJ-1, Parkin, and PINK1 knockout rat striatal mitochondria. 2016 , 9, 589-593	8
1007	Proteomic dataset of Paracentrotus lividus gonads of different sexes and at different maturation stages. 2016 , 8, 824-7	2
1006	Novel Syntrophic Populations Dominate an Ammonia-Tolerant Methanogenic Microbiome. 2016 , 1,	22
1005	Transcriptomic and proteomic analyses of core metabolism in Clostridium termitidis CT1112 during growth on <code>Etellulose</code> , xylan, cellobiose and xylose. 2016 , 16, 91	18
1004	Tetanus toxin production is triggered by the transition from amino acid consumption to peptides. 2016 , 41, 113-124	13
1003	Identification of TRA2B-DNAH5 fusion as a novel oncogenic driver in human lung squamous cell carcinoma. 2016 , 26, 1149-1164	19
1002	Ionic liquid-based method for direct proteome characterization of velvet antler cartilage. 2016 , 161, 541-546	11
1001	Human DNA Ligase I Interacts with and Is Targeted for Degradation by the DCAF7 Specificity Factor of the Cul4-DDB1 Ubiquitin Ligase Complex. 2016 , 291, 21893-21902	11
1000	Discovery Proteomics Identifies a Molecular Link between the Coatomer Protein Complex I and Androgen Receptor-dependent Transcription. 2016 , 291, 18818-42	15
999	Bottom-up proteomics suggests an association between differential expression of mitochondrial proteins and chronic fatigue syndrome. 2016 , 6, e904	15
998	A Tomato Vacuolar Invertase Inhibitor Mediates Sucrose Metabolism and Influences Fruit Ripening. 2016 , 172, 1596-1611	91
997	A multicenter study benchmarks software tools for label-free proteome quantification. 2016 , 34, 1130-1136	202
996	A comparative cell wall proteomic analysis of cucumber leaves under Sphaerotheca fuliginea stress. 2016 , 38, 1	7

995	Arginine phosphorylation marks proteins for degradation by a Clp protease. 2016 , 539, 48-53	108
994	Subcellular proteomics analysis of different stages of colorectal cancer cell lines. 2016 , 16, 3009-3018	9
993	Serine is a new target residue for endogenous ADP-ribosylation on histones. 2016 , 12, 998-1000	138
992	Posttranslational mutagenesis: A chemical strategy for exploring protein side-chain diversity. 2016 , 354,	182
991	Detection of Carbofuran-Protein Adducts in Serum of Occupationally Exposed Pesticide Factory Workers in Pakistan. 2016 , 29, 1720-1728	8
990	Evaluation of Different N-Glycopeptide Enrichment Methods for N-Glycosylation Sites Mapping in Mouse Brain. 2016 , 15, 2960-8	35
989	Genomic, transcriptomic and proteomic analyses of Dehalobacter UNSWDHB in response to chloroform. 2016 , 8, 814-824	14
988	The Power of Human Protective Modifiers: PLS3 and CORO1C Unravel Impaired Endocytosis in Spinal Muscular Atrophy and Rescue SMA Phenotype. 2016 , 99, 647-665	102
987	Supercharging Reagent for Enhanced Liquid Chromatographic Separation and Charging of Sialylated and High-Molecular-Weight Glycopeptides for NanoHPLC-ESI-MS/MS Analysis. 2016 , 88, 8484-94	9
986	Characterization of a heat-resistant extracellular protease from Pseudomonas fluorescens 07A shows that low temperature treatments are more effective in deactivating its proteolytic activity. 2016 , 99, 7842-7851	23
985	Searching Missing Proteins Based on the Optimization of Membrane Protein Enrichment and Digestion Process. 2016 , 15, 4020-4029	14
984	A detailed proteomic profiling of plasma membrane from zebrafish brain. 2016 , 10, 1264-1268	7
983	Comprehensive Proteomic Analysis of Mesenchymal Stem Cell Exosomes Reveals Modulation of Angiogenesis via Nuclear Factor-KappaB Signaling. 2016 , 34, 601-13	304
982	Biomarker discovery in mass spectrometry-based urinary proteomics. 2016 , 10, 358-70	85
981	Toward Biomarker Development in Large Clinical Cohorts: An Integrated High-Throughput 96-Well-Plate-Based Sample Preparation Workflow for Versatile Downstream Proteomic Analyses. 2016 , 88, 8518-25	8
980	Targeted Quantitative Screening of Chromosome 18 Encoded Proteome in Plasma Samples of Astronaut Candidates. 2016 , 15, 4039-4046	24
979	Examining ubiquitinated peptide enrichment efficiency through an lepitope labeled protein. 2016 , 512, 114-119	
978	Target profiling analyses of bile acids in the evaluation of hepatoprotective effect of gentiopicroside on ANIT-induced cholestatic liver injury in mice. 2016 , 194, 63-71	36

977	Progressive Rod-Cone Degeneration (PRCD) Protein Requires N-Terminal S-Acylation and Rhodopsin Binding for Photoreceptor Outer Segment Localization and Maintaining Intracellular Stability. 2016 , 55, 5028-37	20
976	Oxidant Sensing by TRPM2 Inhibits Neutrophil Migration and Mitigates Inflammation. 2016 , 38, 453-62	34
975	Proteomics and transcriptomics of peripheral nerve tissue and cells unravel new aspects of the human Schwann cell repair phenotype. 2016 , 64, 2133-2153	44
974	Holistic Sequencing: Moving Forward from Plant Microbial Proteomics to Metaproteomics. 2016 , 87-103	2
973	The arginylation branch of the N-end rule pathway positively regulates cellular autophagic flux and clearance of proteotoxic proteins. 2016 , 12, 2197-2212	20
972	A Synonymous Mutation Upstream of the Gene Encoding a Weak-Link Enzyme Causes an Ultrasensitive Response in Growth Rate. 2016 , 198, 2853-63	14
971	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
970	N-terminal acetylation promotes synaptonemal complex assembly in C. elegans. 2016 , 30, 2404-2416	20
969	The variant Polycomb Repressor Complex 1 component PCGF1 interacts with a pluripotency sub-network that includes DPPA4, a regulator of embryogenesis. 2015 , 5, 18388	27
968	Removal of SDS from biological protein digests for proteomic analysis by mass spectrometry. 2016 , 14, 11	9
967	Quantitative proteomics analysis of zebrafish exposed to sub-lethal dosages of Imethyl-amino-L-alanine (BMAA). 2016 , 6, 29631	22
966	An oligotrophic deep-subsurface community dependent on syntrophy is dominated by sulfur-driven autotrophic denitrifiers. 2016 , 113, E7927-E7936	108
965	Altered intestinal microbiota-host mitochondria crosstalk in new onset Crohn's disease. 2016 , 7, 13419	189
964	High-throughput proteomics reveal alarmins as amplifiers of tissue pathology and inflammation after spinal cord injury. 2016 , 6, 21607	58
963	Integrative analysis of extracellular and intracellular bladder cancer cell line proteome with transcriptome: improving coverage and validity of -omics findings. 2016 , 6, 25619	11
962	Quantitative secretomic analysis of pancreatic cancer cells in serum-containing conditioned medium. 2016 , 6, 37606	25
961	Disruption of Macrodomain Protein SCO6735 Increases Antibiotic Production in Streptomyces coelicolor. 2016 , 291, 23175-23187	14
960	Autophagy induction stabilizes microtubules and promotes axon regeneration after spinal cord injury. 2016 , 113, 11324-11329	102

(2016-2016)

959	A Comprehensive Proteomics Analysis of the Human Iris Tissue: Ready to Embrace Postgenomics Precision Medicine in Ophthalmology?. 2016 , 20, 510-9	11
958	Biochemical Foundations of Health and Energy Conservation in Hibernating Free-ranging Subadult Brown Bear Ursus arctos. 2016 , 291, 22509-22523	25
957	Novel Aquaporin Regulatory Mechanisms Revealed by Interactomics. 2016 , 15, 3473-3487	57
956	Group 1 metabotropic glutamate receptors 1 and 5 form a protein complex in mouse hippocampus and cortex. 2016 , 16, 2698-2705	39
955	Developmental alcohol exposure leads to a persistent change on astrocyte secretome. 2016 , 137, 730-43	16
954	DnaJ/Hsc70 chaperone complexes control the extracellular release of neurodegenerative-associated proteins. 2016 , 35, 1537-49	116
953	Comprehensive Proteomic Analysis of Human Erythropoiesis. 2016 , 16, 1470-1484	124
952	Carnivorous Nutrition in Pitcher Plants (Nepenthes spp.) via an Unusual Complement of Endogenous Enzymes. 2016 , 15, 3108-17	31
951	Abundant cysteine side reactions in traditional buffers interfere with the analysis of posttranslational modifications and protein quantification - How to compromise. 2016 , 30, 1823-8	8
950	Involvement of exosomes in lung inflammation associated with experimental acute pancreatitis. 2016 , 240, 235-45	37
949	Advancing clinicopathologic diagnosis of high-risk neuroblastoma using computerized image analysis and proteomic profiling. 2016 ,	
948	On the Statistical Significance of Compressed Ratios in Isobaric Labeling: A Cross-Platform Comparison. 2016 , 15, 3029-38	11
947	Abstract. 2016 , 48, 28-157	2
946	Lysine acetylation regulates the activity of Escherichia coli S-adenosylmethionine synthase. 2016 , 48, 723-31	10
945	Recognition of enzymes lacking bound cofactor by protein quality control. 2016 , 113, 12156-12161	42
944	A peptide for targeted, systemic delivery of imaging and therapeutic compounds into acute brain injuries. 2016 , 7, 11980	97
943	Improving the Production of L-Phenylalanine by Identifying Key Enzymes Through Multi-Enzyme Reaction System in Vitro. 2016 , 6, 32208	26
942	Proteome-wide analysis reveals widespread lysine acetylation of major protein complexes in the malaria parasite. 2016 , 6, 19722	54

941	Soil metaproteomics reveals an inter-kingdom stress response to the presence of black truffles. 2016 , 6, 25773	45
940	Rapamycin regulates autophagy and cell adhesion in induced pluripotent stem cells. 2016 , 7, 166	44
939	Tailored Dual PEGylation of Inorganic Porous Nanocarriers for Extremely Long Blood Circulation in Vivo. 2016 , 8, 32723-32731	32
938	Automated Affinity Capture and On-Tip Digestion to Accurately Quantitate in Vivo Deamidation of Therapeutic Antibodies. 2016 , 88, 11521-11526	21
937	Quantitative Persulfide Site Identification (qPerS-SID) Reveals Protein Targets of H2S Releasing Donors in Mammalian Cells. 2016 , 6, 29808	56
936	Proteomic and phosphoproteomic analysis of renal cortex in a salt-load rat model of advanced kidney damage. 2016 , 6, 35906	3
935	Mesoporous metal oxide nanoparticles for selective enrichment of phosphopeptides from complex sample matrices. 2016 , 8, 7747-7754	6
934	Differential expression analysis of the broiler tracheal proteins responsible for the immune response and muscle contraction induced by high concentration of ammonia using iTRAQ-coupled 2D LC-MS/MS. 2016 , 59, 1166-1176	22
933	Mechanism of Arachidonic Acid Accumulation during Aging in Mortierella alpina: A Large-Scale Label-Free Comparative Proteomics Study. 2016 , 64, 9124-9134	25
932	Calredoxin represents a novel type of calcium-dependent sensor-responder connected to redox regulation in the chloroplast. 2016 , 7, 11847	36
931	Quantitative analysis of changes in the phosphoproteome of maize induced by the plant hormone salicylic acid. 2015 , 5, 18155	6
930	Interplay between hepatic mitochondria-associated membranes, lipid metabolism and caveolin-1 in mice. 2016 , 6, 27351	102
929	Comparative proteomic analysis of the shoot apical meristem in maize between a ZmCCT-associated near-isogenic line and its recurrent parent. 2016 , 6, 30641	4
928	Systems-level analysis of mechanisms regulating yeast metabolic flux. 2016 , 354,	157
927	Large-scale mass spectrometry-based analysis of Euplotes octocarinatus supports the high frequency of +1 programmed ribosomal frameshift. 2016 , 6, 33020	7
926	A Novel Role for Pyruvate Kinase M2 as a Corepressor for P53 during the DNA Damage Response in Human Tumor Cells. 2016 , 291, 26138-26150	22
925	Twenty-six circulating antigens and two novel diagnostic candidate molecules identified in the serum of canines with experimental acute toxoplasmosis. 2016 , 9, 374	6
924	Transcriptome and proteome characterization of surface ectoderm cells differentiated from human iPSCs. 2016 , 6, 32007	18

923	cells might control maternal responses to pregnancy. 2016 , 6, 30632	13
922	Addressing proteolytic efficiency in enzymatic degradation therapy for celiac disease. 2016 , 6, 30980	38
921	Identification and Analysis of Protein Phosphorylation by Mass Spectrometry. 2016 , 17-87	1
920	A novel protocol for enzymatic digestion based on covalent binding by protein immobilization. 2016 , 408, 8437-8445	1
919	A novel TP53 pathway influences the HGS-mediated exosome formation in colorectal cancer. 2016 , 6, 28083	38
918	Mass spectrometric analysis of synaptosomal membrane preparations for the determination of brain receptors, transporters and channels. 2016 , 16, 2911-2920	14
917	Quantitative Proteomics Illuminates a Functional Interaction between mDia2 and the Proteasome. 2016 , 15, 4624-4637	8
916	Quantitative proteomics study of the neuroprotective effects of B12 on hydrogen peroxide-induced apoptosis in SH-SY5Y cells. 2016 , 6, 22635	22
915	Mass Spectrometry-Based Bottom-Up Proteomics: Sample Preparation, LC-MS/MS Analysis, and Database Query Strategies. 2016 , 86, 16.4.1-16.4.20	13
914	Efficient Exploitation of Separation Space in Two-Dimensional Liquid Chromatography System for Comprehensive and Efficient Proteomic Analyses. 2016 , 88, 11734-11741	11
913	Apolipoprotein E*4 (APOE*4) Genotype Is Associated with Altered Levels of Glutamate Signaling Proteins and Synaptic Coexpression Networks in the Prefrontal Cortex in Mild to Moderate Alzheimer Disease. 2016 , 15, 2252-62	17
912	Protein turnover measurement using selected reaction monitoring-mass spectrometry (SRM-MS). 2016 , 374,	8
911	FOXE3 contributes to Peters anomaly through transcriptional regulation of an autophagy-associated protein termed DNAJB1. 2016 , 7, 10953	29
910	Characterisation of the circulating acellular proteome of healthy sheep using LC-MS/MS-based proteomics analysis of serum. 2016 , 15, 11	5
909	A Quantitative Glycomics and Proteomics Combined Purification Strategy. 2016,	10
908	Analysis of dynamic protein carbonylation in rice embryo during germination through AP-SWATH. 2016 , 16, 989-1000	25
907	Spatially-resolved protein surface microsampling from tissue sections using liquid extraction surface analysis. 2016 , 16, 1622-32	37
906	Fractionation-dependent improvements in proteome resolution in the mouse hippocampus by IEF LC-MS/MS. 2016 , 37, 2054-62	3

905	In Vitro Characteristics of Porcine Tendon Hydrogel for Tendon Regeneration. 2016, 77, 47-53	5
904	Proteomic Stable Isotope Probing Reveals Taxonomically Distinct Patterns in Amino Acid Assimilation by Coastal Marine Bacterioplankton. 2016 , 1,	22
903	Approaches for Studying the Subcellular Localization, Interactions, and Regulation of Histone Deacetylase 5 (HDAC5). 2016 , 1436, 47-84	3
902	Proteomic changes occurring along gonad maturation in the edible sea urchin Paracentrotus lividus. 2016 , 144, 63-72	14
901	In-Depth Proteomics Identifies a Role for Autophagy in Controlling Reactive Oxygen Species Mediated Endothelial Permeability. 2016 , 15, 2187-97	18
900	Recombinant expression, refolding, purification and characterization of Pseudomonas aeruginosa protease IV in Escherichia coli. 2016 , 126, 69-76	12
899	N-Myristoyltransferase Inhibition Induces ER-Stress, Cell Cycle Arrest, and Apoptosis in Cancer Cells. 2016 , 11, 2165-76	41
898	Progress in Top-Down Proteomics and the Analysis of Proteoforms. 2016 , 9, 499-519	322
897	Trypanosoma cruzi contains two galactokinases; molecular and biochemical characterization. 2016 , 65, 472-82	6
896	Quantitative Proteomics Reveals ¹² Integrin-mediated Cytoskeletal Rearrangement in Vascular Endothelial Growth Factor (VEGF)-induced Retinal Vascular Hyperpermeability. 2016 , 15, 1681-91	13
895	Single Cell Proteomics Using Frog (Xenopus laevis) Blastomeres Isolated from Early Stage Embryos, Which Form a Geometric Progression in Protein Content. 2016 , 88, 6653-7	69
894	Target Identification and Polypharmacology of Nutraceuticals. 2016 , 263-286	7
893	RNAi induced knockdown of a cadherin-like protein (EF531715) does not affect toxicity of Cry34/35Ab1 or Cry3Aa to Diabrotica virgifera virgifera larvae (Coleoptera: Chrysomelidae). 2016 , 75, 117-24	12
892	The blister fluid proteome of paediatric burns. 2016 , 146, 122-32	7
891	Quantitative proteomics of the tobacco pollen tube secretome identifies novel pollen tube guidance proteins important for fertilization. 2016 , 17, 81	25
890	Proteome stability analysis of snap frozen, RNAlater preserved, and formalin-fixed paraffin-embedded human colon mucosal biopsies. 2016 , 6, 942-7	20
889	Environmental Breviatea harbour mutualistic Arcobacter epibionts. 2016 , 534, 254-8	47
888	Quantitative proteomics analysis of the liver reveals immune regulation and lipid metabolism dysregulation in a mouse model of depression. 2016 , 311, 330-339	35

887	Bistability in the Rac1, PAK, and RhoA Signaling Network Drives Actin Cytoskeleton Dynamics and Cell Motility Switches. 2016 , 2, 38-48	106
886	Comparing the proteome of snap frozen, RNAlater preserved, and formalin-fixed paraffin-embedded human tissue samples. 2016 , 10, 9-18	26
885	Cytoskeletal binding proteins distinguish cultured dental follicle cells and periodontal ligament cells. 2016 , 345, 6-16	11
884	Proteomics Unveils Fibroblast-Cardiomyocyte Lactate Shuttle and Hexokinase Paradox in Mouse Muscles. 2016 , 15, 2479-90	10
883	FASIL-MS: An Integrated Proteomic and Bioinformatic Workflow To Universally Quantitate In Vivo-Acetylated Positional Isomers. 2016 , 15, 2579-94	5
882	Illuminating structural proteins in viral "dark matter" with metaproteomics. 2016 , 113, 2436-41	49
881	Antibiotic Resistance, Core-Genome and Protein Expression in IncHI1 Plasmids in Salmonella Typhimurium. 2016 , 8, 1661-71	16
880	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
879	Increased peri-ductal collagen micro-organization may contribute to raised mammographic density. 2016 , 18, 5	70
878	Optimization and comparison of bottom-up proteomic sample preparation for early-stage Xenopus laevis embryos. 2016 , 408, 4743-9	20
877	Effects of peptide acetylation and dimethylation on electrospray ionization efficiency. 2016, 51, 105-10	11
876	Characterization of a SILAC method for proteomic analysis of primary rat microglia. 2016 , 16, 1341-6	7
875	A label-free differential proteomics analysis reveals the effect of melatonin on promoting fruit ripening and anthocyanin accumulation upon postharvest in tomato. 2016 , 61, 138-53	105
874	HD2C histone deacetylase and a SWI/SNF chromatin remodelling complex interact and both are involved in mediating the heat stress response in Arabidopsis. 2016 , 39, 2108-22	62
873	Comparative proteomic analysis of Phalaenopsis leaves in the vegetative and flowering phase. 2016 , 38, 1	3
872	Reliable FASP-based procedures for optimal quantitative proteomic and phosphoproteomic analysis on samples from acute myeloid leukemia patients. 2016 , 18, 13	39
871	Human islets and dendritic cells generate post-translationally modified islet autoantigens. 2016 , 185, 133-40	22
870	Global discovery of protein kinases and other nucleotide-binding proteins by mass spectrometry. 2016 , 35, 601-19	17

869	Trans-Omics: How To Reconstruct Biochemical Networks Across Multiple 'Omic' Layers. 2016 , 34, 276-290	162
868	An NGS-Independent Strategy for Proteome-Wide Identification of Single Amino Acid Polymorphisms by Mass Spectrometry. 2016 , 88, 2784-91	2
867	Presence of Undeclared Food Allergens in Cumin: The Need for Multiplex Methods. 2016 , 64, 1202-11	42
866	Bottom-Up Proteomics Methods for Strain-Level Typing and Identification of Bacteria. 2016 , 83-146	2
865	Testing Suitability of Cell Cultures for SILAC-Experiments Using SWATH-Mass Spectrometry. 2016 , 1394, 101-108	5
864	Quantitative proteomic analysis of the effects of a GalNAc/Man-specific lectin CSL on yeast cells by label-free LC-MS. 2016 , 85, 530-8	2
863	Integrative Proteomics and Metabolomics Analysis of Insect Larva Brain: Novel Insights into the Molecular Mechanism of Insect Wandering Behavior. 2016 , 15, 193-204	17
862	Label-free quantitative proteomic analysis of benzo(a)pyrene-transformed 16HBE cells serum-free culture supernatant and xenografted nude mice sera. 2016 , 245, 39-49	7
861	Label-Free, In-Solution Screening of Peptide Libraries for Binding to Protein Targets Using Hydrogen Exchange Mass Spectrometry. 2016 , 138, 1335-43	10
860	Universal Solid-Phase Reversible Sample-Prep for Concurrent Proteome and N-Glycome Characterization. 2016 , 15, 891-9	5
859	Quantitative phosphoproteomics reveals genistein as a modulator of cell cycle and DNA damage response pathways in triple-negative breast cancer cells. 2016 , 48, 1016-28	32
858	Protein turnover during in vitro tissue engineering. 2016 , 81, 104-113	20
857	Applications of Mass Spectrometry in Microbiology. 2016 ,	8
856	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
855	Mechanisms of Soybean Roots' Tolerances to Salinity Revealed by Proteomic and Phosphoproteomic Comparisons Between Two Cultivars. 2016 , 15, 266-88	50
854	Peroxiredoxin 6 Is a Crucial Factor in the Initial Step of Mitochondrial Clearance and Is Upstream of the PINK1-Parkin Pathway. 2016 , 24, 486-501	47
853	Transgelin is upregulated in stromal cells of lymph node positive breast cancer. 2016 , 132, 103-11	16
852	Metal ion-immobilized magnetic nanoparticles for global enrichment and identification of phosphopeptides by mass spectrometry. 2016 , 6, 1670-1677	21

851	Integrative Network Analysis Combined with Quantitative Phosphoproteomics Reveals Transforming Growth Factor-beta Receptor type-2 (TGFBR2) as a Novel Regulator of Glioblastoma Stem Cell Properties. 2016 , 15, 1017-31	13
850	Shotgun proteomics of bacterial pathogens: advances, challenges and clinical implications. 2016 , 13, 139-56	20
849	Fast and easy phosphopeptide fractionation by combinatorial ERLIC-SCX solid-phase extraction for in-depth phosphoproteome analysis. 2016 , 11, 37-45	21
848	Identification and Characterization of Novel Chitin-Binding Proteins from the Larval Cuticle of Silkworm, Bombyx mori. 2016 , 15, 1435-45	32
847	Extracellular thermostable proteolytic activity of the milk spoilage bacterium Pseudomonas fluorescens PS19 on bovine caseins. 2016 , 99, 4188-4195	19
846	Extraction, Enrichment, Solubilization, and Digestion Techniques for Membrane Proteomics. 2016 , 15, 1243-52	30
845	iTRAQ-based proteomic analysis reveals the mechanisms of silicon-mediated cadmium tolerance in rice (Oryza sativa) cells. 2016 , 104, 71-80	28
844	Label-free quantification in ion mobility-enhanced data-independent acquisition proteomics. 2016 , 11, 795-812	160
843	Personalized evaluation based on quantitative proteomics for drug-treated patients with chronic kidney disease. 2016 , 8, 184-94	5
842	Plasma proteome coverage is increased by unique peptide recovery from sodium deoxycholate precipitate. 2016 , 408, 1963-73	15
841	The RNA-Binding Chaperone Hfq Is an Important Global Regulator of Gene Expression in Pasteurella multocida and Plays a Crucial Role in Production of a Number of Virulence Factors, Including Hyaluronic Acid Capsule. 2016 , 84, 1361-1370	16
840	Changes over lactation in breast milk serum proteins involved in the maturation of immune and digestive system of the infant. 2016 , 147, 40-47	26
839	Qualitative and Quantitative Proteomics Methods for the Analysis of the Anopheles gambiae Mosquito Proteome. 2016 , 37-62	1
838	Pan-proteomics, a concept for unifying quantitative proteome measurements when comparing closely-related bacterial strains. 2016 , 13, 355-65	14
837	3D HPLC-MS with Reversed-Phase Separation Functionality in All Three Dimensions for Large-Scale Bottom-Up Proteomics and Peptide Retention Data Collection. 2016 , 88, 2847-55	35
836	Phosphoproteomic analysis of interacting tumor and endothelial cells identifies regulatory mechanisms of transendothelial migration. 2016 , 9, ra15	27
835	Modulation of Protein S-Nitrosylation by Isoprene Emission in Poplar. 2016 , 170, 1945-61	28
834	Identification of beer spoilage microorganisms using the MALDI Biotyper platform. 2016 , 100, 2761-73	21

833	Sample preparation protocol for bottom-up proteomic analysis of the secretome of the islets of Langerhans. 2016 , 141, 1700-6	11
832	The phosphoproteome of human Jurkat T cell clones upon costimulation with anti-CD3/anti-CD28 antibodies. 2016 , 131, 190-198	16
831	Proteome Profiling and Ultrastructural Characterization of the Human RCMH Cell Line: Myoblastic Properties and Suitability for Myopathological Studies. 2016 , 15, 945-55	9
830	Shotgun proteomics to unravel marine mussel (Mytilus edulis) response to long-term exposure to low salinity and propranolol in a Baltic Sea microcosm. 2016 , 137, 97-106	28
829	Proteomic study on the stability of proteins in bovine, camel, and caprine milk sera after processing. 2016 , 82, 104-111	45
828	Simultaneous Metabolite, Protein, Lipid Extraction (SIMPLEX): A Combinatorial Multimolecular Omics Approach for Systems Biology. 2016 , 15, 1453-66	65
827	Identification of Haloferax volcanii Pilin N-Glycans with Diverse Roles in Pilus Biosynthesis, Adhesion, and Microcolony Formation. 2016 , 291, 10602-14	39
826	The challenge of identifying tuberculosis proteins in archaeological tissues. 2016 , 66, 146-153	28
825	imFASP: An integrated approach combining in-situ filter-aided sample pretreatment with microwave-assisted protein digestion for fast and efficient proteome sample preparation. 2016 , 912, 58-64	11
824	Global Protein Oxidation Profiling Suggests Efficient Mitochondrial Proteome Homeostasis During Aging. 2016 , 15, 1692-709	8
823	Integrated system for extraction, purification, and digestion of membrane proteins. 2016, 408, 3495-502	1
822	Label-free proteomic methodology for the analysis of human kidney stone matrix composition. 2016 , 14, 4	17
821	Dendritic Cells Guide Islet Autoimmunity through a Restricted and Uniquely Processed Peptidome Presented by High-Risk HLA-DR. 2016 , 196, 3253-63	18
820	Surface proteome analysis identifies platelet derived growth factor receptor-alpha as a critical mediator of transforming growth factor-beta-induced collagen secretion. 2016 , 74, 44-59	12
819	Proteomic Profiling Suggests Central Role Of STAT Signaling during Retinal Degeneration in the rd10 Mouse Model. 2016 , 15, 1350-9	13
818	USP7 is a SUMO deubiquitinase essential for DNA replication. 2016 , 23, 270-7	82
817	iTRAQ-based quantitative proteomic analysis of cultivated Pseudostellaria heterophylla and its wild-type. 2016 , 139, 13-25	28
816	Protein species-specific characterization of conformational change induced by multisite phosphorylation. 2016 , 134, 138-143	11

815	The mixed lineage kinase-3 inhibitor URMC-099 improves therapeutic outcomes for long-acting antiretroviral therapy. 2016 , 12, 109-22	24
814	Proteomic profiling of epileptogenesis in a rat model: Focus on inflammation. 2016 , 53, 138-158	46
813	Discovery of a Selective Islet Peptidome Presented by the Highest-Risk HLA-DQ8trans Molecule. 2016 , 65, 732-41	28
812	Quantitative Proteomic Analysis Reveals Molecular Adaptations in the Hippocampal Synaptic Active Zone of Chronic Mild Stress-Unsusceptible Rats. 2015 , 19,	21
811	Proteomic maps of breast cancer subtypes. 2016 , 7, 10259	178
810	Quantitative proteomics reveals protein kinases and phosphatases in the individual phases of contextual fear conditioning in the C57BL/6J mouse. 2016 , 303, 208-17	7
809	From Phosphoproteome to Modeling of Plant Signaling Pathways. 2016 , 1394, 245-259	
808	Ursgal, Universal Python Module Combining Common Bottom-Up Proteomics Tools for Large-Scale Analysis. 2016 , 15, 788-94	31
807	Proteins in Art, Archaeology, and Paleontology: From Detection to Identification. 2016 , 116, 2-79	97
806	Important Metabolic Pathways and Biological Processes Expressed by Chicken Cecal Microbiota. 2015 , 82, 1569-76	153
806 805		153
	2015 , 82, 1569-76	153
805	2015, 82, 1569-76 HIV Protocols. 2016,	
805 804	2015, 82, 1569-76 HIV Protocols. 2016, A Systems Approach to Understand Antigen Presentation and the Immune Response. 2016, 1394, 189-209	20
805 804 803	2015, 82, 1569-76 HIV Protocols. 2016, A Systems Approach to Understand Antigen Presentation and the Immune Response. 2016, 1394, 189-209 A Targeted MRM Approach for Tempo-Spatial Proteomics Analyses. 2016, 1394, 75-85 A Surface Biotinylation Strategy for Reproducible Plasma Membrane Protein Purification and	20
805 804 803	2015, 82, 1569-76 HIV Protocols. 2016, A Systems Approach to Understand Antigen Presentation and the Immune Response. 2016, 1394, 189-209 A Targeted MRM Approach for Tempo-Spatial Proteomics Analyses. 2016, 1394, 75-85 A Surface Biotinylation Strategy for Reproducible Plasma Membrane Protein Purification and Tracking of Genetic and Drug-Induced Alterations. 2016, 15, 647-58 Comparative analysis of Brassica napus plasma membrane proteins under phosphorus deficiency	20 4
805 804 803 802	HIV Protocols. 2016, A Systems Approach to Understand Antigen Presentation and the Immune Response. 2016, 1394, 189-209 A Targeted MRM Approach for Tempo-Spatial Proteomics Analyses. 2016, 1394, 75-85 A Surface Biotinylation Strategy for Reproducible Plasma Membrane Protein Purification and Tracking of Genetic and Drug-Induced Alterations. 2016, 15, 647-58 Comparative analysis of Brassica napus plasma membrane proteins under phosphorus deficiency using label-free and MaxQuant-based proteomics approaches. 2016, 133, 144-152	20 4 23

797	Quantitative proteomic analysis of anticancer drug RH1 resistance in liver carcinoma. 2016 , 1864, 219-32	13
796	An optimization of the LC-MS/MS workflow for deep proteome profiling on an Orbitrap Fusion. 2016 , 8, 425-434	7
795	The biochemistry of blister fluid from pediatric burn injuries: proteomics and metabolomics aspects. 2016 , 13, 35-53	11
794	Isolation and characterization of an antibacterial peptide from protein hydrolysates of Spirulina platensis. 2016 , 242, 685-692	34
793	The Proteome of Native Adult Mler Glial Cells From Murine Retina. 2016 , 15, 462-80	78
792	Label-Free Quantitative Proteomics in Yeast. 2016 , 1361, 289-307	5
791	Proteomics of reproductive systems: Towards a molecular understanding of postmating, prezygotic reproductive barriers. 2016 , 135, 26-37	22
790	Yeast Functional Genomics. 2016 ,	1
789	Proteomic analysis of naturally-sourced biological scaffolds. 2016 , 75, 37-46	85
788	Proteomic and bioinformatic analysis of a nuclear intrinsically disordered proteome. 2016 , 130, 76-84	17
787	Novel Gefitinib Formulation with Improved Oral Bioavailability in Treatment of A431 Skin Carcinoma. 2016 , 33, 137-54	16
786	Hippocampal proteomics defines pathways associated with memory decline and resilience in normal aging and Alzheimer's disease mouse models. 2017 , 322, 288-298	40
785	Identification of differentially expressed reproductive and metabolic proteins in the female abalone (Haliotis laevigata) gonad following artificial induction of spawning. 2017 , 24, 127-138	3
784	Neutrophil proteomic analysis reveals the participation of antioxidant enzymes, motility and ribosomal proteins in the prevention of ischemic effects by preconditioning. 2017 , 151, 162-173	7
783	Nuclear trafficking of the anti-apoptotic Coxiella burnetii effector protein AnkG requires binding to p32 and Importin-4. 2017 , 19, e12634	27
782	Qualitative and quantitative characterization of protein biotherapeutics with liquid chromatography mass spectrometry. 2017 , 36, 734-754	42
781	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
780	Quantitative iTRAQ-based proteomic analysis of rice grains to assess high night temperature stress. 2017 , 17, 1600365	40

779	Characterization of the Molecular Mechanisms Underlying the Chronic Phase of Stroke in a Cynomolgus Monkey Model of Induced Cerebral Ischemia. 2017 , 16, 1150-1166	10
778	Oxidative cleavage and hydrolytic boosting of cellulose in soybean spent flakes by Trichoderma reesei Cel61A lytic polysaccharide monooxygenase. 2017 , 98, 58-66	20
777	Normal human cell proteins that interact with the adenovirus type 5 E1B 55kDa protein. 2017 , 504, 12-24	11
776	Proteolysis of chloroplast proteins is responsible for accumulation of free amino acids in dark-treated tea (Camellia sinensis) leaves. 2017 , 157, 10-17	69
775	A paralogous decoy protects apoplastic effector PsXEG1 from a host inhibitor. 2017, 355, 710-714	117
774	ArtA-Dependent Processing of a Tat Substrate Containing a Conserved Tripartite Structure That Is Not Localized at the C Terminus. 2017 , 199,	8
773	Classical Galactosemia: Insight into Molecular Pathomechanisms by Differential Membrane Proteomics of Fibroblasts under Galactose Stress. 2017 , 16, 516-527	9
772	Human Antiviral Protein IFIX Suppresses Viral Gene Expression during Herpes Simplex Virus 1 (HSV-1) Infection and Is Counteracted by Virus-induced Proteasomal Degradation. 2017 , 16, S200-S214	19
771	Neurons derived from different brain regions are inherently different in vitro: a novel multiregional brain-on-a-chip. 2017 , 117, 1320-1341	61
770	Mass Spectrometry of Intact Proteins Reveals +98 u Chemical Artifacts Following Precipitation in Acetone. 2017 , 16, 889-897	16
769	Mass spectrometric identification of phenol-soluble modulins in the ATCC 43300 standard strain of methicillin-resistant Staphylococcus aureus harboring two distinct phenotypes. 2017 , 36, 1151-1157	8
768	Label-free deep shotgun proteomics reveals protein dynamics during tomato fruit tissues development. 2017 , 90, 396-417	45
767	Tissue Proteomics in Vascular Disease. 2017 , 1527, 53-60	1
766	SPIONs as Nano-Theranostics Agents. 2017 , 1-44	1
765	Quantitative proteomics analysis of Caenorhabditis elegans upon germ cell loss. 2017, 156, 85-93	3
764	SWATH-based proteomics identified carbonic anhydrase 2 as a potential diagnosis biomarker for nasopharyngeal carcinoma. 2017 , 7, 41191	22
763	A Robust Protocol for Protein Extraction and Digestion. 2017 , 1550, 1-10	4
762	TB-IRIS: Proteomic analysis of in vitro PBMC responses to Mycobacterium tuberculosis and response modulation by dexamethasone. 2017 , 102, 237-246	3

761	A Venom Serpin Splicing Isoform of the Endoparasitoid Wasp Pteromalus puparum Suppresses Host Prophenoloxidase Cascade by Forming Complexes with Host Hemolymph Proteinases. 2017 , 292, 1038-1051	26
760	The PeptideAtlas of the Domestic Laying Hen. 2017 , 16, 1352-1363	6
759	Quantitative changes in the protein and miRNA cargo of plasma exosome-like vesicles after exposure to ionizing radiation. 2017 , 93, 569-580	48
758	Strain improvement of Pichia kudriavzevii TY13 for raised phytase production and reduced phosphate repression. 2017 , 10, 341-353	9
757	Mitochondria. 2017,	1
756	The Role of Lipid Droplets in Mortierella alpina Aging Revealed by Integrative Subcellular and Whole-Cell Proteome Analysis. 2017 , 7, 43896	16
755	Temperature-Induced Remodeling of the Photosynthetic Machinery Tunes Photosynthesis in the Thermophilic Alga. 2017 , 174, 35-46	15
754	iTRAQ-based quantitative proteomic analysis reveals potential virulence factors of Erysipelothrix rhusiopathiae. 2017 , 160, 28-37	6
753	Post-transcriptional regulation of fruit ripening and disease resistance in tomato by the vacuolar protease SlVPE3. 2017 , 18, 47	34
752	Label-Free Quantitative Analysis of Mitochondrial Proteomes Using the Multienzyme Digestion-Filter Aided Sample Preparation (MED-FASP) and "Total Protein Approach". 2017 , 1567, 69-77	1
751	Missing Value Monitoring Enhances the Robustness in Proteomics Quantitation. 2017 , 16, 1719-1727	8
750	iTRAQ-based quantitative proteomic analysis of Microcystis aeruginosa exposed to spiramycin at different nutrient levels. 2017 , 185, 193-200	15
749	Quantitative Proteomic Analysis of Serum Exosomes from Patients with Locally Advanced Pancreatic Cancer Undergoing Chemoradiotherapy. 2017 , 16, 1763-1772	64
748	Proteomic analysis and cross species comparison of casein fractions from the milk of dairy animals. 2017 , 7, 43020	19
747	Synergistic effects of citrulline supplementation and exercise on performance in male rats: evidence for implication of protein and energy metabolisms. 2017 , 131, 775-790	12
746	Cellular proteomic analysis of porcine circovirus type 2 and classical swine fever virus coinfection in porcine kidney-15 cells using isobaric tags for relative and absolute quantitation-coupled LC-MS/MS. 2017 , 38, 1276-1291	9
745	A Comprehensive Analytical Strategy To Identify Malondialdehyde-Modified Proteins and Peptides. 2017 , 89, 3847-3852	4
744	Control of Amino Acid Homeostasis by a Ubiquitin Ligase-Coactivator Protein Complex. 2017 , 292, 3827-3840	6

743	The T cell IFT20 interactome reveals new players in immune synapse assembly. 2017, 130, 1110-1121	19
742	Comprehensive Metaboproteomics of Burkitt's and Diffuse Large B-Cell Lymphoma Cell Lines and Primary Tumor Tissues Reveals Distinct Differences in Pyruvate Content and Metabolism. 2017 , 16, 1105-1120	15
74 ¹	A cytoplasmic role of Wnt/II-catenin transcriptional cofactors Bcl9, Bcl9l, and Pygopus in tooth enamel formation. 2017 , 10,	32
74º	Diversity and functions of the sheep faecal microbiota: a multi-omic characterization. 2017 , 10, 541-554	26
739	Quantitative phosphoproteomic analysis reveals system-wide signaling pathways regulated by site-specific phosphorylation of Keratin-8 in skin squamous cell carcinoma derived cell line. 2017 , 17, 1600254	12
738	Bronchoalveolar Lavage Proteomics in Patients with Suspected Lung Cancer. 2017 , 7, 42190	35
737	Comparative proteomics of paired vocal fold and oral mucosa fibroblasts. 2017 , 155, 11-21	13
736	An Interaction Landscape of Ubiquitin Signaling. 2017 , 65, 941-955.e8	75
735	Large-Scale Filter-Aided Sample Preparation Method for the Analysis of the Ubiquitinome. 2017 , 89, 3840-3846	10
734	Quantitative mapping of microtubule-associated protein 2c (MAP2c) phosphorylation and regulatory protein 14-3-3 binding sites reveals key differences between MAP2c and its homolog Tau. 2017 , 292, 6715-6727	11
733	Targeted label-free quantification of interleukin-8 in PMA-activated U937 cell secretome by nanoLC-ESI-MS/MS-sSRM. 2017 , 17, 1600455	2
732	Sample Clean-up Strategies for ESI Mass Spectrometry Applications in Bottom-up Proteomics: Trends from 2012 to 2016. 2017 , 17, 1700011	40
731	The N-linking glycosylation system from Actinobacillus pleuropneumoniae is required for adhesion and has potential use in glycoengineering. 2017 , 7,	22
730	iTRAQ-based quantitative proteomic analysis of wheat roots in response to salt stress. 2017 , 17, 1600265	26
729	Optimized solubilization of TRIzol-precipitated protein permits Western blotting analysis to maximize data available from brain tissue. 2017 , 280, 64-76	48
728	Toward Postgenomics Ophthalmology: A Proteomic Map of the Human Choroid-Retinal Pigment Epithelium Tissue. 2017 , 21, 114-122	8
727	3D-SISPROT: A simple and integrated spintip-based protein digestion and three-dimensional peptide fractionation technology for deep proteome profiling. 2017 , 1498, 207-214	17
726	Antibiotic-dependent perturbations of extended spectrum beta-lactamase producing Klebsiella pneumoniae proteome. 2017 , 17, 1700003	6

725	Proteomic Profiling Analysis Reveals a Link between Experimental Autoimmune Uveitis and Complement Activation in Rats. 2017 , 85, 331-342	8
724	Phosphoproteomics of Fibroblast Growth Factor 1 (FGF1) Signaling in Chondrocytes: Identifying the Signature of Inhibitory Response. 2017 , 16, 1126-1137	14
723	A Method for Microalgae Proteomics Analysis Based on Modified Filter-Aided Sample Preparation. 2017 , 183, 923-930	9
722	miR-132/212 Modulates Seasonal Adaptation and Dendritic Morphology of the Central Circadian Clock. 2017 , 19, 505-520	32
721	Galectin-1 inhibition attenuates profibrotic signaling in hypoxia-induced pulmonary fibrosis. 2017 , 3, 17010	23
720	Comparative proteome analysis of the hepatopancreas from the Pacific white shrimp Litopenaeus vannamei under long-term low salinity stress. 2017 , 162, 1-10	38
719	In-Depth Proteome Coverage by Improving Efficiency for Membrane Proteome Analysis. 2017 , 89, 5179-5185	17
718	Systematic Synergy of Glucose and GLP-1 to Stimulate Insulin Secretion Revealed by Quantitative Phosphoproteomics. 2017 , 7, 1018	5
717	Plant Genomics. 2017,	2
716	Selective degradation of splicing factor CAPER by anticancer sulfonamides. 2017 , 13, 675-680	195
716 715	Selective degradation of splicing factor CAPER® anticancer sulfonamides. 2017, 13, 675-680 Filter-Aided Sample Preparation: The Versatile and Efficient Method for Proteomic Analysis. 2017, 585, 15-27	195 50
<u> </u>	Filter-Aided Sample Preparation: The Versatile and Efficient Method for Proteomic Analysis. 2017 ,	
715	Filter-Aided Sample Preparation: The Versatile and Efficient Method for Proteomic Analysis. 2017 , 585, 15-27	50
715 714	Filter-Aided Sample Preparation: The Versatile and Efficient Method for Proteomic Analysis. 2017, 585, 15-27 An Overview of Advanced SILAC-Labeling Strategies for Quantitative Proteomics. 2017, 585, 29-47 Targeted In-Depth Quantification of Signaling Using Label-Free Mass Spectrometry. 2017, 585, 245-268 Proteomic analysis reveals a role of melatonin in promoting cucumber seed germination under high	50
715 714 713	Filter-Aided Sample Preparation: The Versatile and Efficient Method for Proteomic Analysis. 2017, 585, 15-27 An Overview of Advanced SILAC-Labeling Strategies for Quantitative Proteomics. 2017, 585, 29-47 Targeted In-Depth Quantification of Signaling Using Label-Free Mass Spectrometry. 2017, 585, 245-268 Proteomic analysis reveals a role of melatonin in promoting cucumber seed germination under high	50 8 11
715 714 713 712	Filter-Aided Sample Preparation: The Versatile and Efficient Method for Proteomic Analysis. 2017, 585, 15-27 An Overview of Advanced SILAC-Labeling Strategies for Quantitative Proteomics. 2017, 585, 29-47 Targeted In-Depth Quantification of Signaling Using Label-Free Mass Spectrometry. 2017, 585, 245-268 Proteomic analysis reveals a role of melatonin in promoting cucumber seed germination under high salinity by regulating energy production. 2017, 7, 503 Western Diet Deregulates Bile Acid Homeostasis, Cell Proliferation, and Tumorigenesis in Colon.	50 8 11 71
715 714 713 712 711	Filter-Aided Sample Preparation: The Versatile and Efficient Method for Proteomic Analysis. 2017, 585, 15-27 An Overview of Advanced SILAC-Labeling Strategies for Quantitative Proteomics. 2017, 585, 29-47 Targeted In-Depth Quantification of Signaling Using Label-Free Mass Spectrometry. 2017, 585, 245-268 Proteomic analysis reveals a role of melatonin in promoting cucumber seed germination under high salinity by regulating energy production. 2017, 7, 503 Western Diet Deregulates Bile Acid Homeostasis, Cell Proliferation, and Tumorigenesis in Colon. 2017, 77, 3352-3363 Modifications in acute phase and complement systems predict shifts in cognitive status of	50 8 11 71 44

707	Proteomics Provides Insight into the Interaction between Mulberry and Silkworm. 2017, 16, 2472-2480	10
706	Hydrophobic Interaction Chromatography for Bottom-Up Proteomics Analysis of Single Proteins and Protein Complexes. 2017 , 16, 2318-2323	3
7°5	A survey of proteomic biomarkers for heterotopic ossification in blood serum. 2017 , 12, 69	8
704	Physiological and quantitative phosphoproteome analyses of drought stress-induced mechanisms in Malus baccata (L.) Borkh 2017 , 72, 47-55	1
703	Studies on diagnostic biomarkers and therapeutic mechanism of Alzheimer's disease through metabolomics and hippocampal proteomics. 2017 , 105, 119-126	28
702	Heterologous Protein Production in CHO Cells. 2017,	2
701	Engineer Medium and Feed for Modulating N-Glycosylation of Recombinant Protein Production in CHO Cell Culture. 2017 , 1603, 209-226	2
700	Label-Free Quantitative Proteomics Unravel the Impacts of Salt Stress on Dendrobium huoshanense. 2022 , 13,	О
699	FIP-fve Stimulates Cell Proliferation and Enhances IL-2 Release by Activating MAP2K3/p38- (MAPK14) Signaling Pathway in Jurkat E6-1 Cells. 2022 , 9,	О
698	Proteomic quantification of perturbation to pharmacokinetic target proteins in liver disease 2022 , 104601	О
697	In search of the universal method: a comparative survey of bottom-up proteomics sample preparation methods.	
696	Systematic evaluation and optimization of protein extraction parameters in diagnostic FFPE specimens 2022 , 19, 10	1
695	Endogenous retroviruses promote prion-like spreading of proteopathic seeds.	1
694	The structure and molecular dynamics of prolyl oligopeptidase from Microbulbifer arenaceous provide insights into catalytic and regulatory mechanisms. 2022 , 78,	1
693	Identification of proteins and N-glycosylation sites of knee cartilage in Kashin-Beck disease compared with osteoarthritis 2022 , 210, 128-138	О
692	A proteomic analysis of Arabidopsis ribosomal phosphoprotein P1A mutant 2022 , 262, 104594	O
691	The crosstalk signals of Sodium Tanshinone IIA Sulfonate in rats with cerebral ischemic stroke: Insights from proteomics 2022 , 151, 113059	О
690	Protein sequence databases generated from metagenomics and public databases produced similar soil metaproteomic results of microbial taxonomic and functional changes. 2022 , 32, 507-520	

689	Fasciola hepatica Gastrodermal Cells Selectively Release Extracellular Vesicles via a Novel Atypical Secretory Mechanism. 2022 , 23, 5525	1
688	Melanopsin (Opn4) is an oncogene in cutaneous melanoma 2022 , 5, 461	O
687	Analysis of protein components in blackberry wine and haze. 2022 , 113547	0
686	Zwitter-ionic Monolith-based Spintip Column Coupled with Evosep One Liquid Chromatography for High-throughput Proteomic Analysis. 2022 , 463122	
685	Comparative proteomic analysis identifies differentially expressed proteins and reveals potential mechanisms of traumatic heterotopic ossification progression. 2022 , 34, 42-59	
684	Optimized sample preparation and data analysis for TMT proteomic analysis of cerebrospinal fluid applied to the identification of Alzheimer's disease biomarkers 2022 , 19, 13	1
683	Sample Preparation Matters for Peptide Mapping to Evaluate Deamidation of Adeno-Associated Virus (AAV) Capsid Proteins using LC-MS/MS 2022 ,	0
682	iTRAQ proteomic analysis of the inhibitory effect of 1,6-O,O-diacetylbritannilactone on the plant pathogenic oomycete Phytophthora capsici. 2022 , 105125	1
681	The acetylome of adult mouse sciatic nerve 2022,	0
680	Glycopeptide-Centric Approaches for the Characterization of Microbial Glycoproteomes. 2022 , 153-171	
680 679	Glycopeptide-Centric Approaches for the Characterization of Microbial Glycoproteomes. 2022 , 153-171 Protein Purification and Digestion Methods for Bacterial Proteomic Analyses. 2022 , 63-70	
		1
679	Protein Purification and Digestion Methods for Bacterial Proteomic Analyses. 2022 , 63-70	1
679 678	Protein Purification and Digestion Methods for Bacterial Proteomic Analyses. 2022, 63-70 Comprehensive comparison of sample preparation workflows for proteomics. Affinity Enrichment of Salmonella-Modified Membranes from Murine Macrophages for Proteomic Analyses. 2022, 263-273 Loss of Myosin-1e biases MMTV-PyMT induced breast cancer towards a differentiated and secretory state.	1
679 678 677	Protein Purification and Digestion Methods for Bacterial Proteomic Analyses. 2022, 63-70 Comprehensive comparison of sample preparation workflows for proteomics. Affinity Enrichment of Salmonella-Modified Membranes from Murine Macrophages for Proteomic Analyses. 2022, 263-273 Loss of Myosin-1e biases MMTV-PyMT induced breast cancer towards a differentiated and	2
679 678 677	Protein Purification and Digestion Methods for Bacterial Proteomic Analyses. 2022, 63-70 Comprehensive comparison of sample preparation workflows for proteomics. Affinity Enrichment of Salmonella-Modified Membranes from Murine Macrophages for Proteomic Analyses. 2022, 263-273 Loss of Myosin-1e biases MMTV-PyMT induced breast cancer towards a differentiated and secretory state. A comprehensive study of the differences in protein expression and chemical constituents in tea leaves (Camellia sinensis var. sinensis) with different maturity using a combined proteomics and	
679 678 677 676	Protein Purification and Digestion Methods for Bacterial Proteomic Analyses. 2022, 63-70 Comprehensive comparison of sample preparation workflows for proteomics. Affinity Enrichment of Salmonella-Modified Membranes from Murine Macrophages for Proteomic Analyses. 2022, 263-273 Loss of Myosin-1e biases MMTV-PyMT induced breast cancer towards a differentiated and secretory state. A comprehensive study of the differences in protein expression and chemical constituents in tea leaves (Camellia sinensis var. sinensis) with different maturity using a combined proteomics and metabolomics method. 2022, 111397 Comparing Efficiency of Lysis Buffer Solutions and Sample Preparation Methods for Liquid	2

671	Comparative Proteomic Analysis Reveals the Effect of Selenoprotein W Deficiency on Oligodendrogenesis in Fear Memory. 2022 , 11, 999	Ο
670	Mouse primary T cell phosphotyrosine proteomics enabled by BOOST.	O
669	Characteristics of honey bee physiological proteins extracted from faba bean (Vicia faba L.) honey. 1-12	
668	Protein glycosylation changes during systemic acquired resistance in Arabidopsis thaliana. 2022 , 212, 381-392	O
667	Photoprotective Carbon Redistribution in Mixotrophic Haematococcus Pluvialis Under High Light Stress.	
666	Novel Non-Targeted Proteomics Reveals Altered Immune Response in Geographically Distinct Populations of Green Sea Turtles (Chelonia Mydas).	
665	Membrane Ultrafiltration-Based Sample Preparation Method and Sheath-Flow CZE-MS/MS for Top-Down Proteomics. 2022 , 5-14	
664	Energy homeostasis mediated by the LcSnRK1⊞LcbZIP1 /3 signaling pathway modulates litchi fruit senescence.	O
663	The Combined Partial Knockdown of CBS and MPST Genes Induces Inflammation, Impairs Adipocyte Function-Related Gene Expression and Disrupts Protein Persulfidation in Human Adipocytes. 2022 , 11, 1095	1
662	Protein profiling of hemolymph in Haemaphysalis flava ticks. 2022 , 15,	O
661	Ageing- and AAA-associated differentially expressed proteins identified by proteomic analysis in mice. 10, e13129	
660	Hexokinase 2 is a transcriptional target and a positive modulator of AHR signalling.	1
659	A phospho-switch provided by LRR receptor-like kinase, ALK1/QSK1/KIN7, prioritizes ABCG36/PEN3/PDR8 transport toward defense.	0
658	Quantitative Proteomics Reveals That ADAM15 Can Have Proteolytic-Independent Functions in the Steady State. 2022 , 12, 578	O
657	Cardiac fibroblasts regulate cardiomyocyte hypertrophy through dynamic regulation of type I collagen.	1
656	Role of the Two-Component System CiaRH in the Regulation of Efflux Pump SatAB and Its Correlation with Fluoroquinolone Susceptibility.	O
655	Differences in Vitreous Protein Profiles in Patients With Proliferative Diabetic Retinopathy Before and After Ranibizumab Treatment. 2022 , 9,	
654	Functional Characterization and Whole-Genome Analysis of an Aflatoxin-Degrading Rhodococcus pyridinivorans Strain. 2022 , 11, 774	O

653	A New Strategy for High-Efficient Tandem Enrichment and Simultaneous Profiling of N-Glycopeptides and Phosphopeptides in Lung Cancer Tissue. 2022 , 9,	
652	The RNA-bound proteome of MRSA reveals post-transcriptional roles for helix-turn-helix DNA-binding and Rossmann-fold proteins. 2022 , 13,	1
651	Proteomic Profiling of Cryoglobulinemia. 2022 , 13,	
650	Biomarker Candidates for Tumors Identified from Deep-Profiled Plasma Stem Predominantly from the Low Abundant Area.	2
649	A Comparison of Blood Plasma Small Extracellular Vesicle Enrichment Strategies for Proteomic Analysis. 2022 , 10, 19	0
648	Efficient Detection of the Alternative Spliced Human Proteome Using Translatome Sequencing. 2022 , 9,	O
647	The orphan GPR50 receptor interacting with TIRI induces G1/S-phase cell cycle arrest via Smad3-p27/p21 in BRL-3A cells. 2022 , 115117	
646	Multiomics Analyses Reveal High Temperature-induced Molecular Regulation of Ascorbic acid and Capsaicin Biosynthesis in Pepper Fruits. 2022 , 104941	1
645	Micro-pillar array columns (pPAC): an efficient tool for comparing tissue and cultured cells of glioblastoma. 2022 , 100047	
644	TMT-based comparative proteomics reveals the role of acyl-CoA oxidase 4 in enhancing the drought stress tolerance in common buckwheat (Fagopyrum esculentum). 2022,	
643	Integrative transcriptome and proteome analyses of Trichoderma longibrachiatum LC and its cellulase hyper-producing mutants generated by heavy ion mutagenesis reveal the key genes involved in cellulolytic enzymes regulation. 2022 , 15,	1
642	Quantitative proteomics analysis reveals core and variable tick salivary proteins at the tick-vertebrate host interface.	Ο
641	Dataset for suppressors of amyloid-Itoxicity and their functions in recombinant protein production in yeast. 2022 , 42, 108322	
640	Use of MALDI-TOF mass spectrometry for virus identification: a review.	2
639	Identifying Specific Protein Interactors of Nucleosomes Carrying Methylated Histones Using Quantitative Mass Spectrometry. 2022 , 327-403	
638	LncRNA RUS shapes the gene expression program towards neurogenesis. 2022 , 5, e202201504	O
637	Analysis of the Arabidopsis coilin mutant reveals a positive role of AtCOILIN in plant immunity.	О
636	Tuning the protein corona of PLGA nanoparticles: Characterization of trastuzumab adsorption behavior and its cellular interaction with breast cancer cell lines. 2022 , 103543	

635	Dysbiosis of Gut Microbiota and Intestinal Barrier Dysfunction in Pigs with Pulmonary Inflammation Induced by Mycoplasma hyorhinis Infection.	0
634	Spatial centrosome proteome of human neural cells uncovers disease-relevant heterogeneity. 2022 , 376,	O
633	Proteomic and functional analyses of the periodic membrane skeleton in neurons. 2022, 13,	1
632	Pancreatic cancer cells spectral library by DIA-MS and the phenotype analysis of gemcitabine sensitivity. 2022 , 9,	O
631	Based on Network Pharmacology and Molecular Dynamics Simulations, Baicalein, an Active Ingredient of Yiqi Qingre Ziyin Method, Potentially Protects Patients With Atrophic Rhinitis From Cognitive Impairment. 14,	2
630	Serum Proteomic Analysis Identifies SAA1, FGA, SAP, and CETP as New Biomarkers for Eosinophilic Granulomatosis With Polyangiitis. 13,	0
629	Integrated multi-omics reveal polycomb repressive complex 2 restricts human trophoblast induction. 2022 , 24, 858-871	1
628	Mass spectrometry methods for analysis of extracellular matrix components in neurological diseases.	0
627	Comparative Study on the Characterization of Myofibrillar Proteins from Tilapia, Golden Pompano and Skipjack Tuna. 2022 , 11, 1705	1
626	iTRAQ -based quantitative proteomics reveals biomarkers/pathways in psoriasis that can predict the efficacy of methotrexate.	1
625	A database of accurate electrophoretic migration patterns for human proteins in cell lines	
624	Proteomic and Metabolomic Profiles of T Cell-Derived Exosomes Isolated from Human Plasma. 2022 , 11, 1965	1
623	Comparison of SWEET gene family between maize and foxtail millet through genomic, transcriptomic, and proteomic analyses.	1
622	Ubiquitylation of RIPK3 beyond-the-RHIM can limit RIPK3 activity and cell death. 2022, 104632	
621	Mass spectrometry-based retina proteomics.	
620	Proteomic Profiling Identifies Co-Regulated Expression of Splicing Factors as a Characteristic Feature of Intravenous Leiomyomatosis. 2022 , 14, 2907	
619	Proteomic Analysis Unravels Response and Antioxidation Defense Mechanism of Rice Plants to Copper Oxide Nanoparticles: Comparison with Bulk Particles and Dissolved Cu Ions. 2022 , 2, 671-683	1
618	In Vitro Toxicity Evaluation of Cyanotoxins Cylindrospermopsin and Microcystin-LR on Human Kidney HEK293 Cells. 2022 , 14, 429	O

617	Drought induces epitranscriptome and proteome changes in stem-differentiating xylem of Populus trichocarpa.	O
616	A new bacterial tRNA enhances antibiotic production in Streptomyces by circumventing inefficient wobble base-pairing.	1
615	NLRP3 inflammasome-mediated choroid plexus hypersecretion contributes to hydrocephalus after intraventricular hemorrhage via phosphorylated NKCC1 channels. 2022 , 19,	1
614	Proteomic profiling of the carbon-starved Escherichia coli reveals upregulation of stress-inducible pathways implicated in biological adhesion and methylglyoxal metabolism. 2022 , 103968	
613	Transcriptomic and proteomic profiling of peptidase expression in Fasciola hepatica eggs developing at host⊠ body temperature. 2022 , 12,	1
612	Comparative proteome and cis-regulatory element analysis reveals specific molecular pathways conserved in dog and human brains. 2022 , 100261	О
611	Comparison of urine proteomes from tumor-bearing mice with those from tumor-resected mice.	
610	Loss of core-fucosylation of SPARC impairs collagen binding and contributes to COPD. 2022 , 79,	
609	The Potential Tumor-Suppressor DHRS7 Inversely Correlates with EGFR Expression in Prostate Cancer Cells and Tumor Samples. 2022 , 14, 3074	
608	Glycoproteomics. 2022 , 2,	4
608 607	Glycoproteomics. 2022, 2, Human RIPK3 C-lobe phosphorylation is essential for necroptotic signaling. 2022, 13,	0
		0
607	Human RIPK3 C-lobe phosphorylation is essential for necroptotic signaling. 2022 , 13, Huaier Inhibits Gastric Cancer Growth and Hepatic Metastasis by Reducing Syntenin Expression and	
607 606	Human RIPK3 C-lobe phosphorylation is essential for necroptotic signaling. 2022, 13, Huaier Inhibits Gastric Cancer Growth and Hepatic Metastasis by Reducing Syntenin Expression and STAT3 Phosphorylation. 2022, 2022, 1-14 Toll-like receptor 3 (TLR3) overexpression induces invasion of prostate cancer cells, whereas its	1
607 606 605	Human RIPK3 C-lobe phosphorylation is essential for necroptotic signaling. 2022, 13, Huaier Inhibits Gastric Cancer Growth and Hepatic Metastasis by Reducing Syntenin Expression and STAT3 Phosphorylation. 2022, 2022, 1-14 Toll-like receptor 3 (TLR3) overexpression induces invasion of prostate cancer cells, whereas its activation triggers apoptosis. 2022,	1
607 606 605	Human RIPK3 C-lobe phosphorylation is essential for necroptotic signaling. 2022, 13, Huaier Inhibits Gastric Cancer Growth and Hepatic Metastasis by Reducing Syntenin Expression and STAT3 Phosphorylation. 2022, 2022, 1-14 Toll-like receptor 3 (TLR3) overexpression induces invasion of prostate cancer cells, whereas its activation triggers apoptosis. 2022, Proteome analysis of urinary biomarkers in a cigarette smoke-induced COPD rat model. 2022, 23, Responses of the Mushroom Pleurotus ostreatus under Different CO2 Concentration by	1
607 606 605 604	Human RIPK3 C-lobe phosphorylation is essential for necroptotic signaling. 2022, 13, Huaier Inhibits Gastric Cancer Growth and Hepatic Metastasis by Reducing Syntenin Expression and STAT3 Phosphorylation. 2022, 2022, 1-14 Toll-like receptor 3 (TLR3) overexpression induces invasion of prostate cancer cells, whereas its activation triggers apoptosis. 2022, Proteome analysis of urinary biomarkers in a cigarette smoke-induced COPD rat model. 2022, 23, Responses of the Mushroom Pleurotus ostreatus under Different CO2 Concentration by Comparative Proteomic Analyses. 2022, 8, 652	1

599	The role of peptidoglycan hydrolases in the formation and toxicity of Pseudomonas aeruginosa membrane vesicles. 2022 , 3,	1
598	Hanging drop sample preparation improves sensitivity of spatial proteomics.	2
597	Antioxidant Mechanism of Lactiplantibacillus plantarum KM1 Under H2O2 Stress by Proteomics Analysis. 13,	O
596	On the Compatibility of Fish Meal Replacements in Aquafeeds for Rainbow Trout. A Combined Metabolomic, Proteomic and Histological Study. 13,	
595	TCF4 trinucleotide repeat expansions and UV irradiation are associated with ferroptosis susceptibility in Fuchs endothelial corneal dystrophy.	
594	Transforming Chemical Proteomics Enrichment into a High-Throughput Method Using an SP2E Workflow.	O
593	Comparison of antibacterial activities and resistance mechanisms of omadacycline and tigecycline against Enterococcus faecium. 2022 , 75, 463-471	1
592	Quantitative Proteomics Analysis Reveals Proteins Associated with High Melatonin Content in Barley Seeds under NaCl-Induced Salt Stress. 2022 , 70, 8492-8510	O
591	Investigation of the location and secretion features of Candida albicans enolase with monoclonal antibodies. 2022 , 72,	0
590	High sensitivity limited material proteomics empowered by data-independent acquisition on linear ion traps.	O
589	Wiskott-Aldrich syndrome protein forms nuclear condensates and regulates alternative splicing. 2022 , 13,	1
588	Comparative Whey Proteome Profiling of Donkey Milk With Human and Cow Milk. 9,	O
587	Lack of TRPV1 Channel Modulates Mouse Gene Expression and Liver Proteome with Glucose Metabolism Changes. 2022 , 23, 7014	О
586	Osthole Induces Apoptosis and Caspase-3/GSDME-Dependent Pyroptosis via NQO1-Mediated ROS Generation in HeLa Cells. 2022 , 2022, 1-22	O
585	METTL18-mediated histidine methylation of RPL3 modulates translation elongation for proteostasis maintenance. 11,	1
584	Brain Somatic Variant in Ras-Like Small GTPase RALA Causes Focal Cortical Dysplasia Type II. 16,	
583	A Rapid and Universal Workflow for Label-Free-Quantitation-Based Proteomic and Phosphoproteomic Studies in Cereals. 2022 , 2,	
582	Solvent Precipitation SP3 (SP4) Enhances Recovery for Proteomics Sample Preparation without Magnetic Beads.	1

581	Proteomic Analysis of Arylamine N-Acetyltransferase 1 Knockout Breast Cancer Cells: Implications in Immune Evasion and Mitochondrial Biogenesis. 2022 ,	1
580	RELAB-Oxoguanine DNA Glycosylase1 Is an Epigenetic Regulatory Complex Coordinating the Hexosamine Biosynthetic Pathway in RSV Infection. 2022 , 11, 2210	
579	MicroRNA-22-3p ameliorates Alzheimer disease by targeting SOX9 through the NF-B signaling pathway in the hippocampus. 2022 , 19,	0
578	Multiple Myeloma-Derived Extracellular Vesicles Modulate the Bone Marrow Immune Microenvironment. 13,	1
577	Differential Protein Expression among Two Different Ovine ARDS Phenotypes Preclinical Randomized Study. 2022 , 12, 655	О
576	Proteome-Based Serotyping of the Food-Borne Pathogens Salmonella Enterica by Label-Free Mass Spectrometry. 2022 , 27, 4334	
575	Bioremediation of quinclorac injury on tobacco by a rhizosphere bacterium. 2022, 38,	
574	Characterization of Purified Mulberry Leaf Glycoprotein and Its Immunoregulatory Effect on Cyclophosphamide-Treated Mice. 2022 , 11, 2034	
573	Swapped genetic code blocks viral infections and gene transfer.	
572	Study of differential proteomics in granulosa cells of premature ovarian insufficiency (POI) and the roles and mechanism of RAC1 in granulosa cells. 2022 , 111719	
571	The SPARC complex defines RNAPII promoters in Trypanosoma brucei.	
570	Paleoproteomics.	5
569	A review of suspension trapping digestion method in bottom-up proteomics.	3
568	Decoupling Growth and Production by Removing the Origin of Replication from a Bacterial Chromosome.	O
567	2B and 3C Proteins of Senecavirus A Antagonize the Antiviral Activity of DDX21 via the Caspase-Dependent Degradation of DDX21. 13,	О
566	SimPLIT: Simplified Sample Preparation for Large-Scale Isobaric Tagging Proteomics.	1
565	Uncovering Hidden Members and Functions of the Soil Microbiome Using De Novo Metaproteomics.	О
564	Comparative iTRAQ-based quantitative proteomic analysis of spotted seal (Phoca largha) pups inhabiting different environments. 2022 , 15, 794-807	

563	Characterization of human tear proteome reveals differentially abundance proteins in thyroid-associated ophthalmopathy. 10, e13701	
562	Complete proteomic profiling of regenerative bio-scaffolds with a two-step trypsinization method.	О
561	A Protocol for the Acquisition of Comprehensive Proteomics Data from Single Cases Using Formalin-Fixed Paraffin Embedded Sections. 2022 , 5, 57	1
560	Human Basal and Suprabasal Keratinocytes Are Both Able to Generate and Maintain Dermo E pidermal Skin Substitutes in Long-Term In Vivo Experiments. 2022 , 11, 2156	
559	Comparison of oxidation extent, structural characteristics, and oxidation sites of myofibrillar protein affected by hydroxyl radicals and lipid-oxidizing system. 2022 , 133710	1
558	Simplifying MS1 and MS2 spectra to achieve lower mass error, more dynamic range, and higher peptide identification confidence on the Bruker timsTOF Pro. 2022 , 17, e0271025	
557	Resolution of R-loops by topoisomerase III-[I] (TOP3B) in coordination with the DEAD-box helicase DDX5. 2022 , 40, 111067	1
556	Mass Spectrometry-Based Quantification of the Antigens in Aluminum Hydroxide-Adjuvanted Diphtheria-Tetanus-Acellular-Pertussis Combination Vaccines. 2022 , 10, 1078	
555	Metabolomic and proteomic responses of Phaeodactylum tricornutum to hypoxia.	
554	Proteomic Analysis Reveals the Vital Role of Synaptic Plasticity in the Pathogenesis of Temporal Lobe Epilepsy. 2022 , 2022, 1-12	1
553	Emerging Computational Approaches for Antimicrobial Peptide Discovery. 2022 , 11, 936	1
552	Evolution of ipsilateral breast cancer decoded by proteogenomics[]	
551	Seamlessly Integrated Miniaturized Filter-Aided Sample Preparation Method to Fractionation Techniques for Fast, Loss-Less, and In-Depth Proteomics Analysis of 1 g of Cell Lysates at Low Cost. 2022 , 94, 10135-10141	1
550	Phosphoproteome profiling of hippocampal synaptic plasticity. 2022 ,	О
549	Transcriptomic and proteomic analyses reveal the common and unique pathway(s) underlying different skin colors of leopard coral grouper (Plectropomus leopardus). 2022 , 266, 104671	О
548	Quantitative label-free proteomic analysis of human follicle fluid to identify novel candidate protein biomarker for endometriosis-associated infertility. 2022 , 266, 104680	1
547	Overexpression of heat shock protein 70 induces apoptosis of intestinal epithelial cells in heat-stressed pigs: A proteomics approach. 2022 , 108, 103289	О
546	Controlled atmosphere storage alleviates internal browning in flat peach fruit by regulating energy and sugar metabolisms. 2022 , 186, 107-120	

545	The quantitative proteomic analysis reveals schisantherin a prevents liver fibrosis through regulating extracellular matrix organization. 2022 , 480, 116898	
544	Tandem Mass Tag-based proteomics analysis reveals the vital role of inflammation in traumatic brain injury in a mouse model. 2023 , 18, 155	O
543	Dissecting the Chloroplast Proteome of the Potato (Solanum Tuberosum L.) and Its Comparison with the Tuber Amyloplast Proteome. 2022 , 11, 1915	0
542	Solid-phase alkylation: a low-loss and anti-interference sample preparation strategy for low-input proteome profiling. 2022 ,	
541	mTORC1 activation induced proximal tubular damage via the pentose phosphate pathway in lupus nephritis. 2022 ,	
540	Irradiated Triple-Negative Breast Cancer Co-Culture Produces a Less Oncogenic Extracellular Matrix. 2022 , 23, 8265	O
539	Protein Abundance of Drug Transporters in Human Hepatitis C Livers. 2022, 23, 7947	2
538	Glutathione S-transferase interactions enhance wheat resistance to powdery mildew but not wheat stripe rust.	1
537	High-Resolution Secretome Analysis of Chemical Hypoxia Treated Cells Identifies Putative Biomarkers of Chondrosarcoma. 2022 , 10, 25	
536	Comparative analysis of differentially abundant proteins between high and low intramuscular fat content groups in donkeys. 9,	1
535	FAM69C, a kinase critical for synaptic function and memory, is defective in neurodegenerative dementia. 2022 , 40, 111101	0
534	Knockout of UBE2S inhibits the proliferation of gastric cancer cells and induces apoptosis by FAS-mediated death receptor pathway. 2022 , 113293	1
533	Locality-sensitive hashing enables efficient and scalable signal classification in high-throughput mass spectrometry raw data. 2022 , 23,	
532	Evaluation of protein extraction methods for metaproteomic analyses of root-associated microbes.	O
531	Amnion Cells in Tailored Hydrogels Deposit Human Amnion Native Extracellular Matrix. 2204543	1
530	Recent Progress in Biomarker Bioanalysis and Target Engagement Assessment. 2022 , 87-140	
529	A Proteomic Approach to Study the Biological Role of Hepatitis C Virus Protein Core+1/ARFP. 2022 , 14, 1694	0
528	Reduced miR-184-3p expression protects pancreatic I-cells from lipotoxic and proinflammatory apoptosis in type 2 diabetes via CRTC1 upregulation. 2022 , 8,	1

5 2 7	Changes in the liver proteome in apoE knockout mice exposed to inhalation of silica nanoparticles indicate mitochondrial damage and impairment of ER stress responses associated with microvesicular steatosis.	
526	Proteomic analysis of hepatic effects of phenobarbital in mice with humanized liver. 2022 , 96, 2739-2754	1
525	Physiological mechanisms underlying reduced photosynthesis in wheat leaves grown in the field under conditions of nitrogen and water deficiency. 2022 ,	0
524	Validated Growth Rate-Dependent Regulation of Lipid Metabolism in Yarrowia lipolytica. 2022 , 23, 8517	O
523	ADOLESCENT EXPOSURE TO LOW-DOSE THC DISRUPTS ENERGY BALANCE AND ADIPOSE ORGAN HOMEOSTASIS IN ADULTHOOD.	
522	The molecular diversity of transcriptional factor TfoX is a determinant in natural transformation in Glaesserella parasuis. 13,	
521	In Search of a Universal Method: A Comparative Survey of Bottom-Up Proteomics Sample Preparation Methods.	4
520	SAMHD1 as a prognostic and predictive biomarker in stage II colorectal cancer: A multicenter cohort study. 12,	O
519	Targeting FAPEexpressing hepatic stellate cells overcomes resistance to anti-angiogenics in colorectal cancer liver metastasis models.	1
518	Serum exosomal coronin 1A and dynamin 2 as neural tube defect biomarkers. 2022 , 100, 1307-1319	
517	Proteomics-based evaluation of the mechanism underlying vascular injury via DNA interstrand crosslinks, glutathione perturbation, mitogen-activated protein kinase, and Wnt and ErbB signaling pathways induced by crotonaldehyde. 2022 , 19,	
516	Analysis of Human and Microbial Salivary Proteomes in Children Offers Insights on the Molecular Pathogenesis of Molar-Incisor Hypomineralization. 2022 , 10, 2061	O
515	Novel Online Three-Dimensional Separation Expands the Detectable Functional Landscape of Cellular Phosphoproteome.	
514	Parental salt priming improves the low temperature tolerance in wheat offspring via modulating the seed proteome. 2022 , 111428	1
513	High-throughput proteomic sample preparation using pressure cycling technology.	3
512	The molecular mechanism of Ang II induced-AAA models based on proteomics analysis in ApoE加and CD57BL/6J mice. 2022 , 104702	1
511	Spruce versus Arabidopsis: different strategies of photosynthetic acclimation to light intensity change.	
510	Metabolomic and Proteomic Profile of Dried Hop Inflorescences (Humulus lupulus L. cv. Chinook and cv. Cascade) by SPME-GC-MS and UPLC-MS-MS. 2022 , 9, 204	1

509	AtPRMT5-mediated AtLCD methylation improves Cd2+ tolerance via increased H2S production in Arabidopsis.	O
508	Poor maternal diet during gestation alters offspring muscle proteome in sheep. 2022 , 100,	O
507	Proteogenomics reveals sex biased aging genes and coordinated splicing in cardiac aging.	1
506	High-Temperature-and-Humidity Reduces Plasma Insulin and Gut Hormones through FXR Activation Accompanied by a Metabolic Compensatory Gut Microbiota.	
505	Transposon-activated POU5F1B promotes colorectal cancer growth and metastasis. 2022 , 13,	О
504	Different Diets Change Milk Extracellular Vesicle-Protein Profile in Lactating Cows. 2022 , 12, 1234	
503	Exploring the overall effects of two traditional Chinese medicines on the body by urinary proteome. 2022 , 52, 1269-1280	
502	Adaptation and Resistance: How Bacteroides thetaiotaomicron Copes with the Bisphenol A Substitute Bisphenol F. 2022 , 10, 1610	
501	LINE-1 RNA causes heterochromatin erosion and is a target for amelioration of senescent phenotypes in progeroid syndromes. 2022 , 14,	2
500	Low expression of RBP4 in the vitreous humour of patients with proliferative diabetic retinopathy who underwent Conbercept intravitreal injection. 2022 , 109197	
499	Urinary proteome changes during pregnancy in rats.	
498	Urinary Proteome Analysis of Global Cerebral Ischemia R eperfusion Injury Rat Model via Data-Independent Acquisition and Parallel Reaction Monitoring Proteomics. 2022 , 72, 2020-2029	O
497	Proteomics reveals multiple effects of titanium dioxide and silver nanoparticles in the metabolism of turbot, Scophthalmus maximus. 2022 , 136110	О
496	mTORC1 controls Golgi architecture and vesicle secretion by phosphorylation of SCYL1. 2022 , 13,	
495	Antifungal mechanism of isothiocyanates against Cochliobolus heterostrophus.	
494	Increased expression and accumulation of GDF15 in IPF extracellular matrix contribute to fibrosis. 2022 , 7,	O
493	Scaling-up and proteomic analysis reveals photosynthetic and metabolic insights toward prolonged H2 photoproduction in Chlamydomonas hpm91 mutant lacking proton gradient regulation 5 (PGR5).	
492	Mechanism by which PF-3758309, a Pan Isoform Inhibitor of p21-Activated Kinases, Blocks Reactivation of HIV-1 Latency.	

491	Emergent Role of IFITM1/3 towards Splicing Factor (SRSF1) and Antigen-Presenting Molecule (HLA-B) in Cervical Cancer. 2022 , 12, 1090	
490	Comparative Proteomics Study on the Postharvest Senescence of Volvariella volvacea. 2022 , 8, 819	O
489	Changes in life-history traits, antioxidant defense, energy metabolism and molecular outcomes in the cladoceran Daphnia pulex after exposure to polystyrene microplastics. 2022 , 136066	
488	Decellularization of xenografted tumors provides cell-specific in vitro 3D environment. 12,	
487	Discovery of Small-Molecule Degraders of the CDK9-Cyclin T1 Complex for Targeting Transcriptional Addiction in Prostate Cancer. 2022 , 65, 11034-11057	5
486	The Improved Biocontrol Agent, F1-35, Protects Watermelon against Fusarium Wilt by Triggering Jasmonic Acid and Ethylene Pathways. 2022 , 10, 1710	O
485	Comparative proteomics of adult Paragonimus kellicotti excretion/secretion products released in vitro or present in the lung cyst nodule. 2022 , 16, e0010679	O
484	Asymmetric depth-filtration: A versatile and scalable method for high-yield isolation of extracellular vesicles with low contamination. 2022 , 11,	O
483	Effects of Natural Rheum tanguticum on the Cell Wall Integrity of Resistant Phytopathogenic Pectobacterium carotovorum subsp. Carotovorum. 2022 , 27, 5291	O
482	Predictive value of proteomic markers for advanced rectal cancer with neoadjuvant chemoradiotherapy. 2022 , 22,	O
481	A highly selective JAK3 inhibitor is developed for treating rheumatoid arthritis by suppressing Elective JAK-STAT signal. 2022 , 8,	1
480	Associated bacterial microbiome responds opportunistic once algal host Scenedesmus vacuolatus is attacked by endoparasite Amoeboaphelidium protococcarum. 2022 , 12,	O
479	The MDM2 inhibitor Navtemadlin arrests mouse melanoma growth in vivo and potentiates radiotherapy.	О
478	Chronic Fluoxetine Treatment of Socially Isolated Rats Modulates Prefrontal Cortex Proteome. 2022 ,	O
477	TMT-based quantitative membrane proteomics identified PRRs potentially involved in the perception of MSP1 in rice leaves. 2022 , 267, 104687	2
476	Uncovering the functions of plasma proteins in ulcerative colitis and identifying biomarkers for BPA-induced severe ulcerative colitis: A plasma proteome analysis. 2022 , 242, 113897	O
475	Evaluation and minimization of over-alkylation in proteomic sample preparation. 2022, 481, 116919	
474	Biological mass spectrometry analysis for traceability of production method and harvesting seasons of sea cucumber (Apostichopus japonicus). 2023 , 143, 109297	

473	Proteomics of serum exosomes identified fibulin-1 as a novel biomarker for mild cognitive impairment. 2023 , 18, 587	О
472	IgG+ Extracellular Vesicles Measure Therapeutic Response in Advanced Pancreatic Cancer. 2022 , 11, 2800	O
471	Comparative Proteomic Analysis of Proteins in Breast Milk during Different Lactation Periods. 2022 , 14, 3648	1
470	MultiOMICs landscape of SARS-CoV-2-induced host responses in human lung epithelial cells.	О
469	Photoprotective carbon redistribution in mixotrophic Haematococcus pluvialis under high light stress. 2022 , 362, 127761	О
468	Comparison of protein extraction protocols and allergen mapping from black soldier fly Hermetia illucens. 2022 , 269, 104724	1
467	Lysine acetylome profiling in mouse hippocampus and its alterations upon FMRP deficiency linked to abnormal energy metabolism. 2022 , 269, 104720	О
466	Effect of dietary Spirulina (Arthrospira platensis) on the intestinal function of post-weaned piglet: An approach combining proteomics, metabolomics and histological studies. 2022 , 269, 104726	O
465	Up-regulated 60S ribosomal protein L18 in PEDV N protein-induced S-phase arrested host cells promotes viral replication. 2022 , 321, 198916	О
464	Phosphodiesterase 10A deactivation induces long-term neurological recovery, Peri-infarct remodeling and pyramidal tract plasticity after transient focal cerebral ischemia in mice. 2022 , 358, 114221	O
463	Integrated transcriptome and proteome unveiled distinct toxicological effects of long-term cadmium pollution on the silk glands of Pardosa pseudoannulata. 2023 , 854, 158841	О
462	Chameleon-like microbes promote microecological differentiation of Daqu. 2023, 109, 104144	1
461	Mechanism of improving solubility and emulsifying properties of wheat gluten protein by pH cycling treatment and its application in powder oils. 2023 , 135, 108132	О
460	Comparative maternal protein profiling of mouse biparental and uniparental embryos. 2022, 11,	1
459	Analysis of the Human Pineal Proteome by Mass Spectrometry. 2022 , 123-132	О
458	Pyrroloquinoline quinone regulates glycolipid metabolism in the jejunum via inhibiting AMPK phosphorylation of weaned pigs. 2022 , 13, 9610-9621	O
457	Protein Extraction and Sample Preparation Methods for Shotgun Proteomics with Central Nervous System Cells and Brain Tissue. 2022 , 1-15	О
456	Non-targeted proteomics reveals altered immune response in geographically distinct populations of green sea turtles (Chelonia mydas). 2023 , 216, 114352	1

455	HnRNPK maintains single strand RNA through controlling double-strand RNA in mammalian cells. 2022 , 13,	О
454	SPOP promotes cervical cancer progression by inducing the movement of PD-1 away from PD-L1 in spatial localization. 2022 , 20,	O
453	Comprehensive acetyl-proteomic analysis of Cytospora mali provides insight into its response to the biocontrol agent Bacillus velezensis L-1. 6,	О
452	Release of VAMP5-positive extracellular vesicles by retinal Mller glia in vivo. 2022, 11,	O
451	Kinetic proofreading through the multi-step activation of the ZAP70 kinase underlies early T cell ligand discrimination. 2022 , 23, 1355-1364	0
450	Proteomic evaluation of human osteoblast responses to titanium implants over time.	O
449	A comprehensive mouse brain acetylome-the cellular-specific distribution of acetylated brain proteins. 16,	О
448	CDK7/GRP78 signaling axis contributes to tumor growth and metastasis in osteosarcoma. 2022 , 41, 452	4-45360
447	SMNDC1 links chromatin remodeling and splicing to regulate pancreatic hormone expression. 2022 , 40, 111288	О
446	Disulfiram Oxy-Derivatives Suppress Protein Retrotranslocation across the ER Membrane to the Cytosol and Initiate Paraptosis-like Cell Death. 2022 , 12, 845	O
445	Changes of urinary proteome in high-fat diet ApoE-/- mice.	О
444	Comprehensive comparison between azacytidine and decitabine treatment in an acute myeloid leukemia cell line. 2022 , 14,	O
443	Unraveling axonal mechanisms of traumatic brain injury. 2022, 10,	2
442	In vivo Safety and Immunoactivity of Oncolytic Jurona Virus in Hepatocellular Carcinoma: A Comprehensive Proteogenomic Analysis.	O
441	Comparative Surfaceome Analysis of Clonal Histomonas meleagridis Strains with Different Pathogenicity Reveals Strain-Dependent Profiles. 2022 , 10, 1884	0
440	The SPARC complex defines RNAPII promoters in Trypanosoma brucei. 11,	O
439	Proteomic and immunoproteomic insights into the exoproteome of Actinobacillus pleuropneumoniae, the causative agent of porcine pleuropneumonia. 2022 , 105759	0
438	TrpR-like protein PXO_00831, regulated by the sigma factor RpoD, is involved in motility, oxidative stress tolerance, and virulence in Xanthomonas oryzae pv. oryzae.	O

437	Cottonseed Meal Protein Isolate as a New Source of Alternative Proteins: A Proteomics Perspective. 2022 , 23, 10105	1
436	A Highly Accumulated Secretory Protein from Cotton Bollworm Interacts with bHLHs to dampen Plant Defense.	O
435	Proteomic Analysis Identifies Molecular Players and Biological Processes Specific to SARS-CoV-2 Exposure in Endothelial Cells. 2022 , 23, 10452	1
434	Proteomic changes associated with maternal dietary low B :B ratio in piglets supplemented with seaweed part I: Serum proteomes. 2022 , 104740	O
433	Pursuing Diabetic Nephropathy through Aqueous Humor Proteomics Analysis. 2022 , 2022, 1-10	0
432	ABP1IIMK auxin perception for global phosphorylation and auxin canalization. 2022, 609, 575-581	3
431	Integrated Transcriptome and Proteome Analysis Reveals that the Antimicrobial Griseofulvin Targets Didymella segeticola beta-Tubulin to Control Tea Leaf Spot.	0
430	Proteome Analysis of Swine Macrophages after Infection with Two Genotype II African Swine Fever Isolates of Different Pathogenicity. 2022 , 14, 2140	O
429	Perilipin-2 promotes lipid droplet-plasma membrane interactions that facilitate apocrine lipid secretion in secretory epithelial cells of the mouse mammary gland. 10,	1
428	The Proteomics and Metabolomics Studies of GZU001 on Promoting the Merisis of Maize (Zea mays L.) Roots.	O
427	Proteomic Analysis of Human Breast Cancer MCF-7 Cells to Identify Cellular Targets of the Anticancer Pigment OR3 from Streptomyces coelicolor JUACT03.	0
426	Establishment and characterization of a tumoroid biobank derived from dog patients[mammary tumors for translational research.	0
425	Extracellular vesicles derived from PPRV-infected cells enhance signaling lymphocyte activation molecular (SLAM) receptor expression and facilitate virus infection. 2022 , 18, e1010759	0
424	Mitochondrial protein import clogging as a mechanism of disease.	O
423	Label-free quantitative proteomic analysis of ethanamizuril-resistant versus -sensitive strains of Eimeria tenella. 2022 , 15,	0
422	Differential Protein Content between Fresh and Freeze-Dried Plasma Rich in Growth Factors Eye Drops. 2022 , 12, 1215	O
421	Temporal Proteomic and Phosphoproteomic Analysis of EV-A71-Infected Human Cells. 2022 , 21, 2367-2384	0
420	Size-Based Proteome Fractionation through Polyacrylamide Gel Electrophoresis Combined with LCEAIMSMS for In-Depth Top-Down Proteomics. 2022 , 94, 12815-12821	2

419	Diethyl ether anesthesia induces transient cytosolic [Ca2+] increase, heat shock proteins, and heat stress tolerance of photosystem II in Arabidopsis. 13,	0
418	A filarial parasite-encoded human IL-10 receptor antagonist reveals a novel strategy to modulate host responses.	Ο
417	Genome-wide association, RNA-seq and iTRAQ analyses identify candidate genes controlling radicle length of wheat. 13,	1
416	Proteomic characterization of gastric cancer response to chemotherapy and targeted therapy reveals new therapeutic strategies. 2022 , 13,	2
415	Changes in and asymmetry of the proteome in the human fetal frontal lobe during early development. 2022 , 5,	0
414	Tuning heterologous glucan biosynthesis in yeast to understand and exploit plant starch diversity. 2022 , 20,	O
413	Extracellular vesicles from Listeria monocytogenes-infected dendritic cells alert the innate immune response. 13,	0
412	Proteomics Characteristics Reveal the Risk of T1 Colorectal Cancer Metastasis to Lymph Nodes.	Ο
411	Tear proteome profile in eyes with keratoconus after intracorneal ring segment implantation or corneal crosslinking. 9,	0
410	Carnitine palmitoyltransferase 1A promotes mitochondrial fission and regulates autophagy by enhancing MFF succinylation in ovarian cancer.	Ο
409	Novel biochemical, structural, and systems insights into inflammatory signaling revealed by contextual interaction proteomics. 2022 , 119,	1
408	The inhibition of putrescine synthesis affects the in vitro shoot development of Cedrela fissilis Vell. (Meliaceae) by altering endogenous polyamine metabolism and the proteomic profile.	Ο
407	Lifetime development changes in rats tracked by urinary proteome.	0
406	Mirror image serum lipid carrier protein profiles in pup and lactating mother Atlantic grey seals reflect contrasting resource mobilisation challenges. 9,	O
405	Proteomic analysis reveals the mechanism of green regulation in garlic puree induced by purple light stress.	0
404	SARS-CoV-2 Nsp6 damages Drosophila heart and mouse cardiomyocytes through MGA/MAX complex-mediated increased glycolysis. 2022 , 5,	1
403	Physiological and proteomic dissection of the rice roots in response to iron deficiency and excess. 2022 , 267, 104689	0
402	Multi-omics insights into potential mechanism of SGLT2 inhibitors cardiovascular benefit in diabetic cardiomyopathy. 9,	Ο

401	Characterization of serum protein expression profiles in the early sarcopenia older adults with low grip strength: a cross-sectional study. 2022 , 23,	1
400	Changes in the urinary proteome before and after quadrivalent influenza vaccine and COVID-19 vaccination. 13,	O
399	RNAlater facilitates remote sampling of aquaculture Atlantic salmon liver for proteomic analysis.	О
398	Proteomics and bioinformatics analysis of cardiovascular related proteins in offspring exposed to gestational diabetes mellitus. 9,	O
397	CBTRUS Statistical Report: Primary Brain and Other Central Nervous System Tumors Diagnosed in the United States in 2015 2019. 2022, 24, v1-v95	14
396	Panomics reveals patient-individuality as the major driver for colorectal cancer progression.	O
395	Optimized protocol for obtaining and characterizing primary neuron-enriched cultures from embryonic chicken brains. 2022 , 3, 101753	О
394	Dataset for proteomic analysis of arylamine N-acetyltransferase 1 knockout MDA-MB-231 breast cancer cells. 2022 , 45, 108634	O
393	Influence of different sample preparation strategies on hypothesis-driven shotgun proteomic analysis of human saliva. 2022 , 20, 1000-1018	1
392	Using one-to-many urine proteome comparisons to provide clues for fever of unknown origin. 2022 , 4, 32-42	O
391	Proteomics-based molecular and functional characteristic profiling of muscle tissue in Triploid crucian carp.	О
390	Physiological and Biochemical Characteristics of Rainbow Trout with Severe, Moderate and Asymptomatic Course of Vibrio anguillarum Infection. 2022 , 12, 2642	O
389	Identification of Arginine Phosphorylation in Mycolicibacterium smegmatis. 2022, 10,	1
388	Changes to Urinary Proteome in High-Fat-Diet ApoE/IMice. 2022 , 12, 1569	O
387	Effect of high-fat diet and empagliflozin on cardiac proteins in mice. 2022, 19,	O
386	Tandem mass tag-based proteomics analysis reveals the multitarget mechanisms of Phyllanthus emblica against liver fibrosis. 13,	O
385	Comprehensive Interactome Analysis for the Sole Adenylyl Cyclase Cyr1 of Candida albicans.	О
384	Study on saltiness sensing during oral processing of dry-cured pork base on salivary proteomics. 2022 , 1, 100127	O

383	Identification of Novel Genes and Proteoforms in Angiostrongylus costaricensis through a Proteogenomic Approach. 2022 , 11, 1273	0
382	In vitro transdifferentiated signatures of goat preadipocytes into mammary epithelial cells revealed by DNA methylation and transcriptome profiling. 2022 , 102604	Ο
381	Targeting Myd88 using peptide-loaded mesenchymal stem cell membrane-derived synthetic vesicles to treat systemic inflammation. 2022 , 20,	О
380	Nuclear Proteomics of Induced Leukemia Cell Differentiation. 2022 , 11, 3221	Ο
379	Study on Tissue Homogenization Buffer Composition for Brain Mass Spectrometry-Based Proteomics. 2022 , 10, 2466	1
378	High Sensitivity Limited Material Proteomics Empowered by Data-Independent Acquisition on Linear Ion Traps.	1
377	Proteomic Identification of Markers of Membrane Repair, Regeneration and Fibrosis in the Aged and Dystrophic Diaphragm. 2022 , 12, 1679	1
376	A naturally occurring lytic bioprocess improves sustainability of phycocyanin production from cyanobacteria.	O
375	E3-specific degrader discovery by dynamic tracing of substrate receptor abundance.	Ο
374	Algal photosystem I dimer and high-resolution model of PSI-plastocyanin complex. 2022 , 8, 1191-1201	2
373	Coelenterazine sulfotransferase from Renilla muelleri. 2022 , 17, e0276315	Ο
372	Multi-omics reveals diet-induced metabolic disorders and liver inflammation via microbiota-gut-liver axis. 2022 , 109183	О
371	Proteomic Profiling of Extracellular Vesicles Released by Leptin-Treated Breast Cancer Cells: A Potential Role in Cancer Metabolism. 2022 , 23, 12941	Ο
370	Glycoproteomics Landscape of Asymptomatic and Symptomatic Human Alzheimer Disease Brain. 2022 , 100433	Ο
369	Subtyping of cardiac amyloidosis by mass spectrometry-based proteomics of endomyocardial biopsies. 1-13	О
368	Interactome analysis identifies MSMEI_3879 as a substrate ofMycolicibacterium smegmatisClpC1.	Ο
367	Red blood cell-based vaccines for ameliorating cancer chemoimmunotherapy. 2022,	Ο
366	CKL2 mediates the crosstalk between abscisic acid and brassinosteroid signaling to promote swift growth recovery after stress in Arabidopsis.	Ο

365	Single-gene knockout-coupled omics analysis identifies C9orf85 and CXorf38 as two uncharacterized human proteins associated with ZIP8 malfunction. 9,	О
364	Phosphorylation-mediated PI3K-Art signalling pathway as a therapeutic mechanism in the hydrogen-induced alleviation of brain injury in septic mice.	O
363	ROS induction as a strategy to target persister cancer cells with low metabolic activity in NRAS mutated melanoma.	0
362	Responses of carbapenemase-producing and non-producing carbapenem-resistantPseudomonas aeruginosastrains to meropenem revealed by quantitative tandem mass spectrometry proteomics.	O
361	Integrated proteogenomic characterization across major histological types of pituitary neuroendocrine tumors.	0
360	In-depth characterization of the Clostridioides difficile phosphoproteome to identify Ser/Thr kinase substrates. 2022 , 100428	1
359	Chemoproteomic Approach for the Quantitative Identification of Arsenic-Binding Proteins.	0
358	GLYCOSYLATION NETWORK MAPPING AND SITE-SPECIFIC GLYCAN MATURATION IN VIVO. 2022 , 105417	O
357	Proteomic Analysis of a Hypervirulent Mutant of the Insect-Pathogenic Fungus Metarhizium anisopliae Reveals Changes in Pathogenicity and Terpenoid Pathways.	1
356	OTUB2 exerts tumor-suppressive roles via STAT1-mediated CALML3 activation and increased phosphatidylserine synthesis. 2022 , 41, 111561	O
355	Hydrodynamic conditions affect the proteomic profile of marine biofilms formed by filamentous cyanobacterium. 2022 , 8,	O
354	TLCD1 and TLCD2 regulate cellular phosphatidylethanolamine composition and promote the progression of non-alcoholic steatohepatitis. 2022 , 13,	O
353	Quantitative Proteomic Analysis Reveals the Key Molecular Events Driving Phaeocystis globosa Bloom and Dissipation. 2022 , 23, 12668	0
352	Proteome integral solubility alteration assay combined with multi-criteria decision-making analysis for developing adverse outcome pathways.	O
351	Integrative transcriptomic and TMT-based proteomic analysis reveals the mechanism by which AtENO2 affects seed germination under salt stress. 13,	О
350	In-Depth Metaproteomics Analysis of Oral Microbiome for Lung Cancer. 2022 , 2022, 1-18	O
349	Intramembrane client recognition potentiates the chaperone functions of calnexin.	О
348	Physiological and protein profiling analysis provides insight into the underlying molecular mechanism of potato tuber development regulated by jasmonic acid in vitro. 2022 , 22,	2

347	Highly efficient TiO2-based one-step strategy for micro volume plasma-derived extracellular vesicles isolation and multiomics sample preparation. 2022 , 116971	0
346	The mechanisms underlying montelukast's neuropsychiatric effects - new insights from a combined metabolic and multiomics approach. 2022 , 310, 121056	1
345	Correlation between biological responses in vitro and in vivo to Ca-doped sol-gel coatings assessed using proteomic analysis. 2022 , 220, 112962	0
344	Investigating the loss of major yolk proteins during the processing of sea cucumber (Apostichopus japonicus) using an MRM-based targeted proteomics strategy. 2023 , 404, 134670	O
343	Miniprep assisted proteomics (MAP) for rapid proteomics sample preparation.	0
342	Proteome analysis of Campylobacter jejuni poultry strain 2704 survival during 45 min exposure to peracetic acid. 2023 , 385, 110000	O
341	A subtractive proteomics approach for the identification of immunodominant Acinetobacter baumannii vaccine candidate proteins. 13,	0
340	An equine Endothelin 3 cis-regulatory variant links blood pressure modulation to elite racing performance.	O
339	Yangyinqingfei decoction attenuates PM2.5-induced lung injury by enhancing arachidonic acid metabolism. 13,	0
338	Storage Drives Alterations of Proteomic and Protein Structural Properties in Rice (Oryza sativa L.). 2022 , 11, 3541	O
337	Molecular docking and proteomics reveals the synergistic antibacterial mechanism of theaflavin with 🛮 lactam antibiotics against MRSA. 13,	0
336	Dynamic SILAC to Determine Protein Turnover in Neurons and Glia. 2023, 1-17	O
335	Detergent-Assisted Protein Digestion In the Way to Avoid the Key Bottleneck of Shotgun Bottom-Up Proteomics. 2022 , 23, 13903	2
334	Ubiquitin-based pathway acts inside chloroplasts to regulate photosynthesis. 2022, 8,	1
333	Spatial regulation of the glycocalyx component Podocalyxin is a switch for pro-metastatic function.	0
332	Effect of anemoside B4 on milk whey in clinical mastitis-affected cows elucidated using tandem mass tag (TMT)-based quantitative proteomics. 2022 , 12,	O
331	Fluid flow structures gut microbiota biofilm communities by distributing public goods.	0
330	Repurposing live attenuated trivalent MMR vaccine as cost-effective cancer immunotherapy. 12,	O

329	Retinal regions shape human and murine MIler cell proteome profile and functionality.	O
328	Identification of novel interferon responsive protein partners of human leukocyte antigen A (HLA-A) using cross-linking mass spectrometry (CLMS) approach. 2022 , 12,	O
327	Ydj1 interaction at nucleotide-binding-domain of yeast Ssa1 impacts Hsp90 collaboration and client maturation. 2022 , 18, e1010442	0
326	Vaping Additives Cannabinoid Oil and Vitamin E Acetate Adhere to and Damage the Human Airway Epithelium.	2
325	Chemoproteomic Profiling of Geranyl Pyrophosphate-Binding Proteins. 2023, 127-138	0
324	Pivotal biological processes and proteins for selenite reduction and methylation in Ganoderma lucidum. 2022 , 130409	O
323	Type IV Pili Are a Critical Virulence Factor in Clinical Isolates of Paenibacillus thiaminolyticus.	О
322	Proteomic mapping reveals dysregulated angiogenesis in the cerebral arteries of rats with early-onset hypertension.	O
321	Proteomic characterization and comparison of milk fat globule membrane proteins collected from two ethnic groups of women in China using DIA technique. 2022 , 50, 102192	O
320	Integrative analysis of differentially expressed mRNAs and proteins induced by PGC-1 in breast cancer cells. 2022 , 637, 73-82	O
319	A stable reference human transcriptome and proteome as a standard for reproducible omics experiments.	0
318	Multifunctional properties of the transmembrane LPxTG-motif protein derived from Limosilactobacillus reuteri SH-23.	O
317	Pancreatic cancer cells crave glutamine for glycosylation and CA19-9 biosynthesis through hexosamine biosynthetic pathway.	О
316	Understanding of Networks In Vitro and/or In Vivo. 2016 , 344-355	O
315	Simultaneous extraction of calcium phosphates and proteins from fish bones. Innovative valorisation of food by-products. 2023 , 385, 135656	1
314	Proteins in Tumor-Derived Plasma Extracellular Vesicles Indicate Tumor Origin. 2023 , 22, 100476	O
313	Direct Proteomic Detection and Prioritization of 19 Onchocerciasis Biomarker Candidates in Humans. 2023 , 22, 100454	О
312	Dipyridamole interacts with the N-terminal domain of HSP90 and antagonizes the function of the chaperone in multiple cancer cell lines. 2023 , 207, 115376	O

311	Fully integrated on-line strategy for highly sensitive proteome profiling of 10B00 mammalian cells. 2022 , 148, 120-127	1
310	Serum proteomics analysis of biomarkers for evaluating clinical response to MTX/IGU therapy in early rheumatoid arthritis. 2023 , 153, 119-125	О
309	Alternative transcribed 3' isoform of long non-coding RNA Malat1 inhibits mouse retinal oxidative stress. 2023 , 26, 105740	O
308	iTRAQ-based quantitative proteome analysis in liver of large yellow croaker Larimichthys crocea under high temperature stress. 2023 , 28, 101444	О
307	TMT-based quantitative proteome data of MSP1 overexpressed rice. 2023, 46, 108791	0
306	Triploidization of rainbow trout affects proteins related to ovary development and reproductive activity. 2023 , 565, 739145	О
305	Predicting the efficacy of escitalopram in the treatment of depression through urinary proteome. 2023 , 484, 116980	O
304	Proteomic alterations in the cerebellum and hippocampus in an Alzheimer disease mouse model: Alleviating effect of palmatine. 2023 , 158, 114111	1
303	Comprehensive proteomic analysis of the main liver and attached liver of <i>Glyptosternum maculatum</i> on the basis of data-independent mass spectrometry acquisition. 2022,	О
302	Does filter-aided sample preparation provide sufficient method linearity for quantitative plant shotgun proteomics?. 13,	О
301	Calredoxin regulates the chloroplast NADPH-dependent thioredoxin reductase inChlamydomonas reinhardtii.	О
300	Integrated proteomic and transcriptomic landscape of macrophages in mouse tissues. 2022, 13,	O
299	The mechanical regulation of RNA binding protein hnRNPC in the failing heart. 2022, 14,	О
298	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
297	Proteomic overview of hepatocellular carcinoma cell lines and generation of the spectral library. 2022 , 9,	О
296	Multi-omics analyses reveal new insights into nutritional quality changes of alfalfa leaves during the flowering period. 13,	О
295	The Role of Extracellular Vesicles in Optic Nerve Injury: Neuroprotection and Mitochondrial Homeostasis. 2022 , 11, 3720	2
294	Multi-Omics of Corynebacterium Pseudotuberculosis 12CS0282 and an In Silico Reverse Vaccinology Approach Reveal Novel Vaccine and Drug Targets. 2022 , 10, 39	O

293	Label-free quantitative proteomics and stress responses in pigsThe case of short or long road transportation. 2022 , 17, e0277950	O
292	A Bottom-up Proteomics Workflow for a System Containing Multiple Organisms.	О
291	Proteomics reveals unique identities of human TGF-I-induced and thymus-derived CD4+ regulatory T cells. 2022 , 12,	0
2 90	Study of SarA by DNA Affinity Capture Assay (DACA) Employing Three Promoters of Key Virulence and Resistance Genes in Methicillin-Resistant Staphylococcus aureus. 2022 , 11, 1714	O
289	A Label-Free Quantitative Analysis for the Search of Proteomic Differences between Goat Breeds. 2022 , 12, 3336	О
288	Carbon nanoparticles induce DNA repair and PARP inhibitor resistance associated with nanozyme activity in cancer cells. 2022 , 13,	1
287	Genetic and Pharmacological Inhibition of Astrocytic Mysm1 Alleviates Depressive-Like Disorders by Promoting ATP Production. 2204463	О
286	Pitfalls in Proteomics: Avoiding Problems That Can Occur Before Data Acquisition Begins. 2022 , 524-528	O
285	Discovering new peripheral plasma biomarkers to identify cognitive decline in type 2 diabetes. 10,	О
284	Sphingosine 1-phosphate mediates adiponectin receptor signaling essential for lipid homeostasis and embryogenesis. 2022 , 13,	1
283	Peptide-based LDH5 inhibitors enter cancer cells and impair proliferation. 2022, 79,	О
282	Multiomics of Colorectal Cancer Organoids Reveals Putative Mediators of Cancer Progression Resulting from SMAD4 Inactivation.	О
281	Effects of pre-partum dietary crude protein level on colostrum fat globule membrane proteins and the performance of Hu ewes and their offspring. 9,	0
280	Proteogenomic insights into the biology and treatment of pancreatic ductal adenocarcinoma. 2022 , 15,	O
279	Photosynthetic mechanism of maize yield under fluctuating light environments in the field.	O
278	Proteogenomic characterization of MiT family translocation renal cell carcinoma. 2022, 13,	O
277	Liver Proteome Alterations in Red Deer (Cervus elaphus) Infected by the Giant Liver Fluke Fascioloides magna. 2022 , 11, 1503	0
276	A database of accurate electrophoretic migration patterns for human proteins. 2022 , 167933	O

275	TMT-based quantitative proteomics analysis of the effects of Jiawei Danshen decoction myocardial ischemia-reperfusion injury. 2022 , 20,	0
274	Quantitative proteomic analysis uncovers protein-expression profiles during gonadotropin-dependent folliculogenesis in mice.	Ο
273	Complementary hepatic metabolomics and proteomics reveal the adaptive mechanisms of dairy cows to the transition period. 2022 ,	0
272	The hibernation-derived compound SUL-138 shifts the mitochondrial proteome towards fatty acid metabolism and prevents cognitive decline and amyloid plaque formation in an Alzheimer disease mouse model. 2022, 14,	1
271	Integrated proteomics and metabolomics analysis of lumbar in a rat model of osteoporosis treated with Gushukang capsules. 2022 , 22,	О
270	Label-free relative quantitative proteomics reveals extracellular vesicles as a vehicle for Salmonella effector protein delivery. 13,	Ο
269	Comparative proteomic analysis and antioxidant enzyme activity provide new insights into the embryogenic competence of Guadua chacoensis (Bambusoideae, Poaceae). 2022 , 104790	1
268	Label-free proteomics analysis on the envelope of budded viruses of Bombyx mori nucleopolyhedrovirus harboring differential localized GP64.	1
267	Efficient TurboID-based proximity labelling method for identifying terminal sialic acid glycosylation in living cells. 2022 ,	0
266	A novel fusion transcription factor drives high cellulase and xylanase production on glucose in Trichoderma reesei. 2022 , 128520	Ο
265	The proteomic landscape shows oncologic relevance in cystitis glandularis.	О
264	3D ECM-rich environment sustains the identity of naive human iPSCs. 2022 , 29, 1703-1717.e7	O
263	A novel lncRNA MDHDH suppresses glioblastoma multiforme by acting as a scaffold for MDH2 and PSMA1 to regulate NAD+ metabolism and autophagy. 2022 , 41,	1
262	RRBP1 depletion of bone metastatic cancer cells contributes to enhanced expression of the osteoblastic phenotype. 12,	Ο
261	Clinical application of serum-based proteomics technology in human tumor research. 2022 , 115031	Ο
2 60	In situ digestion of alcohol-fixed cells for quantitative proteomics.	Ο
259	Drug synergy discovery of tavaborole and aminoglycosides against Escherichia coli using high throughput screening. 2022 , 12,	0
258	Identification of Molecular Network of Gut-Brain Axis Associated with Neuroprotective Effects of PPARELigand Erucic Acid in Rotenone-Induced Parkinson's Disease Model in Zebrafish.	Ο

257	Multi-omics analyses reveal the difference of stone cell distribution in pear fruit.	О
256	Remodeling of algal photosystem I through phosphorylation.	O
255	Observation of the dynamic changes in the urinary proteome in rats during immunization.	O
254	Targeting myeloid cell coagulation signaling blocks MAP kinase/TGF-🛮 driven fibrotic remodeling in ischemic heart failure.	O
253	Metabolomics and Proteomics Characterizing Hepatic Reactions to Dietary Linseed Oil in Duck. 2022 , 23, 15690	O
252	Proteome analysis of Ehrlichia chaffeensis containing phagosome membranes revealed the presence of numerous bacterial and host proteins. 12,	1
251	Identification of noninvasive and disease-specific biomarkers in hereditary angioedema using urinary proteomics.	0
250	Pathway-guided monitoring of the disease course in bladder cancer with longitudinal urine proteomics. 2023 , 3,	O
249	Mass Spectrometry Proteomic Analysis of Four p53 Patterns in Differentiated Vulvar Intraepithelial Neoplasia. Publish Ahead of Print,	O
248	Antitumor Effects of Poplar Propolis on DLBCL SU-DHL-2 Cells. 2023 , 12, 283	O
248 247	Antitumor Effects of Poplar Propolis on DLBCL SU-DHL-2 Cells. 2023, 12, 283 Plasmepsin X activates function of the PCRCR complex in P. falciparum by processing PfRh5 for binding to basigin and invasion of human erythrocytes.	0
	Plasmepsin X activates function of the PCRCR complex in P. falciparum by processing PfRh5 for	
247	Plasmepsin X activates function of the PCRCR complex in P. falciparum by processing PfRh5 for binding to basigin and invasion of human erythrocytes. The involvement of the primo vascular system in local enteritis and its modification by	0
247 246	Plasmepsin X activates function of the PCRCR complex in P. falciparum by processing PfRh5 for binding to basigin and invasion of human erythrocytes. The involvement of the primo vascular system in local enteritis and its modification by electroacupuncture. 13, Quantitative proteomics of differentiated primary bronchial epithelial cells from chronic obstructive pulmonary disease and control identifies potential novel host factors post-influenza A	0
247 246 245	Plasmepsin X activates function of the PCRCR complex in P. falciparum by processing PfRh5 for binding to basigin and invasion of human erythrocytes. The involvement of the primo vascular system in local enteritis and its modification by electroacupuncture. 13, Quantitative proteomics of differentiated primary bronchial epithelial cells from chronic obstructive pulmonary disease and control identifies potential novel host factors post-influenza A virus infection. 13,	0 0
247246245244	Plasmepsin X activates function of the PCRCR complex in P. falciparum by processing PfRh5 for binding to basigin and invasion of human erythrocytes. The involvement of the primo vascular system in local enteritis and its modification by electroacupuncture. 13, Quantitative proteomics of differentiated primary bronchial epithelial cells from chronic obstructive pulmonary disease and control identifies potential novel host factors post-influenza A virus infection. 13, Nonspecific Amyloid Aggregation of Chicken Smooth-Muscle Titin: In Vitro Investigations. 2023, 24, 1056	0 0
247246245244243	Plasmepsin X activates function of the PCRCR complex in P. falciparum by processing PfRh5 for binding to basigin and invasion of human erythrocytes. The involvement of the primo vascular system in local enteritis and its modification by electroacupuncture. 13, Quantitative proteomics of differentiated primary bronchial epithelial cells from chronic obstructive pulmonary disease and control identifies potential novel host factors post-influenza A virus infection. 13, Nonspecific Amyloid Aggregation of Chicken Smooth-Muscle Titin: In Vitro Investigations. 2023, 24, 1056 Pitfalls and Solutions in Mass Spectrometry-Based Identification of Protein Glycation. Uptake-independent killing of macrophages by extracellular aggregates of Mycobacterium	0 0 0

239	Ultrasensitive Proteomics Depicted an In-depth Landscape for Mouse Embryo.	O
238	Proteome Mapping of Cervical Mucus and Its Potential as a Source of Biomarkers in Female Tract Disorders. 2023 , 24, 1038	O
237	TMT proteomics analysis of cerebrospinal fluid from patients with cerebral venous sinus thrombosis. 2023 , 104820	0
236	Insights into peptide profiling of sturgeon myofibrillar proteins with low temperature vacuum heating (LTVH).	O
235	Multi-OMICs landscape of SARS-CoV-2-induced host responses in human lung epithelial cells. 2023 , 26, 105895	O
234	Depletion of the RNA-binding protein PURA triggers changes in posttranscriptional gene regulation and loss of P-bodies.	O
233	Serine-threonine phosphoregulation by PknB and Stp contributes to quiescence and antibiotic tolerance in Staphylococcus aureus. 2023 , 16,	0
232	Expression of virulence and antimicrobial related proteins in Burkholderia mallei and Burkholderia pseudomallei. 2023 , 17, e0011006	O
231	Toward Systems-Informed Models for Biologics Disposition: Covariates of the Abundance of the Neonatal Fc Receptor (FcRn) in Human Tissues and Implications for Pharmacokinetic Modelling. 2023 , 106375	0
230	NeuroLINCS Proteomics: Defining human-derived iPSC proteomes and protein signatures of pluripotency. 2023 , 10,	0
229	Degradation Kinetics of Lignocellulolytic Enzymes in a Biogas Reactor Using Quantitative Mass Spectrometry. 2023 , 9, 67	0
228	Mass Spectrometry-Based Proteomics Workflows in Cancer Research: The Relevance of Choosing the Right Steps. 2023 , 15, 555	Ο
227	Knockout of Targeted Plasmid-Borne 🖟 Lactamase Genes in an Extended-Spectrum- 🖟 Lactamase-Producing Escherichia coli Strain: Impact on Resistance and Proteomic Profile.	0
226	Integrated transcriptome and proteome analyses reveal candidate genes for ginsenoside biosynthesis in Panax japonicus C. A. Meyer. 13,	O
225	Proteome adaptations of the organohalide-respiring Desulfitobacterium hafniense strain DCB-2 to various energy metabolisms. 14,	0
224	Biological mass spectrometry enables spatiotemporal Bmics: From tissues to cells to organelles.	Ο
223	Label-free quantitative proteomics of arbuscular mycorrhizal Elaeagnus angustifolia seedlings provides insights into salt-stress tolerance mechanisms. 13,	0
222	Mechanism by Which PF-3758309, a Pan Isoform Inhibitor of p21-Activated Kinases, Blocks Reactivation of HIV-1 Latency. 2023 , 13, 100	O

221	Auxenochlorella pyrenoidosa extract supplementation replacing fetal bovine serum for Carassius auratus muscle cell culture under low-serum conditions. 2023 , 164, 112438	О
220	TMT-based quantitative proteomic analysis reveals the underlying mechanisms of glycidyl methacrylate-induced 16HBE cell malignant transformation. 2023 , 485, 153427	O
219	PAX8 modulates the tumor microenvironment of high grade serous ovarian cancer through changes in the secretome. 2023 , 36, 100866	0
218	Proteome profiling of the prefrontal cortex of Fmr1 knockout mouse reveals enhancement of complement and coagulation cascades. 2023 , 274, 104822	O
217	Comparative proteomics analyses of whey proteins from breastmilk collected from two ethnic groups in northeast China. 2023 , 17, 100568	0
216	Analysis of texture properties and water-soluble fraction proteome of sea cucumber body wall with different boiling heating treatment. 2023 , 409, 135333	О
215	Proteomic Analysis in Nifedipine Induced Gingival Overgrowth: A Pilot Study.	О
214	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	О
213	Human TRMT2A methylates different components of the translation machinery and contributes to translation fidelity.	0
212	Plant age-dependent dynamics of annatto pigment (bixin) biosynthesis inBixa orellanaL	O
211	TBK1 phosphorylation activates LIR-dependent degradation of the inflammation repressor TNIP1. 2023 , 222,	2
210	Urinary Proteome Changes during Pregnancy in Rats. 2023 , 13, 34	O
209	DonEllet go Ito-fractionation mass spectrometry for untargeted mapping of protein-metabolite interactomes.	0
208	Fiber-Type Shifting in Sarcopenia of Old Age: Proteomic Profiling of the Contractile Apparatus of Skeletal Muscles. 2023 , 24, 2415	1
207	The Influence of the FFAR4 Agonist TUG-891 on Liver Steatosis in ApoE-Knockout Mice.	0
206	Quantitative proteomics combined with network pharmacology analysis unveils the biological basis of Schisandrin B in treating diabetic nephropathy.	O
205	Panomics reveals patient individuality as the major driver of colorectal cancer progression. 2023 , 21,	0

203	Integrating Transcriptomics and Metabolomics to Explore the Novel Pathway of Fusobacterium nucleatum Invading Colon Cancer Cells. 2023 , 12, 201	О
202	Neoplastic signatures: Comparative proteomics of canine hepatobiliary neuroendocrine tumors to normal niche tissue. 2023 , 18, e0280928	О
201	Proteo-metabolomic technologies in context of fishery/aquacultural research and applications. 2023 , 259-274	О
200	Salt-induced phosphoproteomic changes in the subfornical organ in rats with chronic kidney disease. 2023 , 45,	O
199	Cardiac Plin5 interacts with SERCA2 and promotes calcium handling and cardiomyocyte contractility. 2023 , 6, e202201690	O
198	ChipFilter: Microfluidic Based Comprehensive Sample Preparation Methodology for Metaproteomics.	O
197	Comparison of urine proteomes from tumor-bearing mice with those from tumor-resected mice. 11, e14737	0
196	Comparative proteomics of human milk casein fraction collected from women of Korean and Han ethnic groups in China. 10,	O
195	Neuronal glutathione loss leads to neurodegeneration involving gasdermin activation. 2023, 13,	О
194	Integrated Network Pharmacology and Proteomic Analyses of Targets and Mechanisms of Jianpi Tianjing Decoction in Treating Vascular Dementia. 2023 , 2023, 1-18	Ο
193	The heme-responsive PrrH sRNA regulatesPseudomonas aeruginosapyochelin gene expression.	О
192	An efficient in-gel digestion method on small amounts of protein sample from large intact gel pieces. 2200121	O
191	Platelets derived citrullinated proteins and microparticles are potential autoantibodies ACPA targets in RA patients. 14,	0
190	Antifatigue and microbiome reshaping effects of yak bone collagen peptides on Balb/c mice. 2023, 102447	O
189	Proteomics of Animal Viruses. 2023 , 89-199	О
188	DNA and protein analyses of hair in forensic genetics.	О
187	Metabolic and proteomic indications of diabetes progression in human aqueous humor. 2023 , 18, e0280491	O
186	Proteogenomics decodes the evolution of human ipsilateral breast cancer. 2023 , 6,	1

185	Establishment and characterization of canine mammary tumoroids for translational research. 2023 , 21,	O
184	Effects of plasma-derived exosomes from the normal and thin Bactrian camels on hepatocellular carcinoma and their differences at transcriptome and proteomics levels. 13,	O
183	An angled-shape tip-based strategy for highly sensitive proteomic profiling of a low number of cells. 2023 , 15, 1215-1222	O
182	Potential role of the mTOR-C1-PGC1中PAR	O
181	Diagnosis of T-cell-mediated kidney rejection by biopsy-based proteomic biomarkers and machine learning. 14,	0
180	FHF2 phosphorylation and regulation of native myocardial NaV1.5 channels.	O
179	Large-Scale Quantitative Proteomic Analysis during Different Stages of Somatic Embryogenesis in Larix olgensis. 2023 , 45, 2021-2034	0
178	Widespread readthrough events in plants reveal unprecedented plasticity of stop codons.	O
177	Detection of early proteomic alterations in 5xFAD Alzheimer's disease neonatal mouse model via MALDI-MSI.	0
176	The effect of G0S2 on insulin sensitivity: A proteomic analysis in a G0S2-overexpressed high-fat diet mouse model. 14,	O
175	Proteomic analysis reveals semaglutide impacts lipogenic protein expression in epididymal adipose tissue of obese mice. 14,	0
174	PI3KAkt pathway-independent PIK3AP1 identified as a replication inhibitor of the African swine fever virus based on iTRAQ proteomic analysis. 2023 , 327, 199052	O
173	Lysine Acetylome of Breast Cancer-Derived Small Extracellular Vesicles Reveals Specific Acetylation Patterns for Metabolic Enzymes. 2023 , 11, 1076	0
172	SM22Deletion Contributes to Neurocognitive Impairment in Mice through Modulating Vascular Smooth Muscle Cell Phenotypes. 2023 , 24, 7117	O
171	A bidirectional phosphate transporter relieves phosphate limitations of photosynthesis to improve grain yield in rice.	0
170	Current Methods for Identifying Plasma Membrane Proteins as Cancer Biomarkers. 2023 , 13, 409	O
169	Unique proteomic signature of JCPyV-infected human astrocytes: from cells to extracellular vesicles.	O
168	Impact of tropospheric ozone on root proteomes of two soybean genotypes with contrasting sensitivity to ozone. 2023 , 208, 105269	O

167	Targeting FABP4 in elderly mice rejuvenates liver metabolism and ameliorates aging-associated metabolic disorders. 2023 , 142, 155528	О
166	Time-lapse proteomics unveil constant high exposure of non-antibiotic drug induces synthetic susceptibility towards regular antibiotics. 2023 , 269, 127320	O
165	Ferric chloride induces ferroptosis in Pseudomonas aeruginosa and heals wound infection in a mouse model. 2023 , 61, 106794	О
164	S100-A8/A9 activated TLR4 in renal tubular cells to promote ischemiafleperfusion injury and fibrosis. 2023 , 118, 110110	О
163	Saliva proteome of partially- and fully-engorged adult female Haemaphysalis flava ticks. 2023 , 318, 109933	О
162	Melanopsin (OPN4) is a novel player in skin homeostasis and attenuates UVA-induced effects. 2023 , 242, 112702	О
161	An in vitro model that mimics the foreign body response in the peritoneum: Study of the bioadhesive properties of HA-based materials. 2023 , 310, 120701	О
160	New insight into the composition of extracellular traps released by macrophages exposed to different types of inducers. 2023 , 202, 97-109	O
159	Post-prandial response in hepatopancreas and haemolymph of Penaeus monodon fed different diets. Omics insights into glycoconjugate metabolism, energy utilisation, chitin biosynthesis, immune function, and autophagy. 2023 , 46, 101073	О
158	Metabolism of hydrogen peroxide by Lactobacillus plantarum NJAU-01: A proteomics study. 2023 , 112, 104246	О
157	Egg protein profile and dynamics during embryogenesis in Haemaphysalis flava ticks. 2023 , 14, 102180	О
156	Exploiting bioactive natural products of marine origin: Evaluation of the meroterpenoid metachromin V as a novel potential therapeutic drug for colorectal cancer. 2023 , 162, 114679	Ο
155	Bioengineering of air-filled protein nanoparticles by genetic and chemical functionalization. 2023 , 21,	О
154	ADAD2 interacts with RNF17 in P-bodies to repress the Ping-pong cycle in pachytene piRNA biogenesis. 2023 , 222,	О
153	Incongruence between transcriptional and vascular pathophysiological cell states.	О
152	Understanding the response in Pugionium cornutum (L.) Gaertn. seedling leaves under drought stress using transcriptome and proteome integrated analysis. 11, e15165	О
151	The alteration of proteins and metabolites in leaf apoplast and the related gene expression associated with the adaptation of Ammopiptanthus mongolicus to winter freezing stress. 2023 , 240, 124479	O
150	Differential protein response to different light quality conditions of industrial hemp cultivation based on DIA technology. 2023 , 197, 116650	О

149	The growth, lipid accumulation and adaptation mechanism in response to variation of temperature and nitrogen supply in psychrotrophic filamentous microalga Xanthonema hormidioides (Xanthophyceae). 2023 , 16,	0
148	Physiological, proteomic and metabolomic analysis provide insights into Ca2+ tolerance in Drynaria roosii leaves. 2023 , 7, 100132	О
147	Impact of Coenzyme Q10 Supplementation on Skeletal Muscle Respiration, Antioxidants, and the Muscle Proteome in Thoroughbred Horses. 2023 , 12, 263	О
146	Single-copy locus proteomics of early- and late-firing DNA replication origins identifies a role of Ask1/DASH complex in replication timing control. 2023 , 42, 112045	О
145	Dysregulation of metalloproteins in ischemic heart disease patients with systolic dysfunction. 2023 , 232, 123435	О
144	Isolation and Characterization of NpCI, a New Metallocarboxypeptidase Inhibitor from the Marine Snail Nerita peloronta with Anti-Plasmodium falciparum Activity. 2023 , 21, 94	О
143	Proteome Analysis of Male Accessory Gland Secretions in the Diamondback Moth, Plutella xylostella (Lepidoptera: Plutellidae). 2023 , 14, 132	О
142	MST2 Acts via AKT Activity to Promote Neuronal Axon Regeneration and Functional Recovery after Spinal Cord Injury in Mice.	О
141	ASAP-Automated Sonication-Free Acid-Assisted Proteomes-from Cells and FFPE Tissues. 2023 , 95, 3291-3299	О
140	CP204L Is a Multifunctional Protein of African Swine Fever Virus That Interacts with the VPS39 Subunit of the Homotypic Fusion and Vacuole Protein Sorting Complex and Promotes Lysosome Clustering. 2023 , 97,	О
139	Proteomic and metabolomic approaches elucidate the molecular mechanism of emodin against neuropathic pain through modulating the gamma-aminobutyric acid (GABA)-ergic pathway and PI3K / AKT / NF-B pathway.	О
138	The role of pneumococcal extracellular vesicles on the pathophysiology of the kidney disease Hemolytic Uremic Syndrome.	О
137	Bioactive photocrosslinkable resin solely based on refined decellularized small intestine submucosa for vat photopolymerization of in vitro tissue mimics. 2023 , 64, 103439	О
136	Eukaryotic-like gephyrin and cognate membrane receptor coordinate corynebacterial cell division and polar elongation.	О
135	Getting Ready for Large-Scale Proteomics in Crop Plants. 2023 , 15, 783	O
134	Spatial regulation of the glycocalyx component podocalyxin is a switch for prometastatic function. 2023 , 9,	О
133	Chemo-sEVs release in cisplatin-resistance ovarian cancer cells are regulated by the lysosomal function.	O
132	Phenotypic effects of mutations observed in the neuraminidase of human origin H5N1 influenza A viruses. 2023 , 19, e1011135	О

131	Investigation of the Pathogenic Mechanism of Ciprofloxacin in Aortic Aneurysm and Dissection by an Integrated Proteomics and Network Pharmacology Strategy. 2023 , 12, 1270	О
130	Transcriptomics-proteomics Integration reveals alternative polyadenylation driving inflammation-related protein translation in patients with diabetic nephropathy. 2023 , 21,	О
129	Proteomic Analysis Comparison on the Ecological Adaptability of Quinclorac-Resistant Echinochloa crus-galli. 2023 , 12, 696	О
128	Muc2-dependent microbial colonization of the jejunal mucus layer is diet sensitive and confers local resistance to enteric pathogen infection. 2023 , 42, 112084	О
127	Piperlongumine conjugates induce targeted protein degradation. 2023, 30, 203-213.e17	1
126	Integrated transcriptome and proteome analysis provides insights into the mechanism of cytoplasmic male sterility (CMS) in tobacco (Nicotiana tabacum L.). 2023 , 275, 104825	O
125	Examining the Effect of Notocactus ottonis Cold Vacuum Isolated Plant Cell Extract on Hair Growth in C57BL/6 Mice Using a Combination of Physiological and OMICS Analyses. 2023 , 28, 1565	О
124	Data-Independent Acquisition Mass Spectrometry of EPS-Urine Coupled to Machine Learning: A Predictive Model for Prostate Cancer. 2023 , 8, 6244-6252	O
123	Ultra-sensitive isotope probing to quantify activity and substrate assimilation in microbiomes. 2023 , 11,	0
122	Millet Fermented by Different Combinations of Yeasts and Lactobacilli: Effects on Phenolic Composition, Starch, Mineral Content and Prebiotic Activity. 2023 , 12, 748	O
121	Comparative Proteomic Analyses within Three Developmental Stages of the Mushroom White Hypsizygus marmoreus. 2023 , 9, 225	О
120	Differences in aqueous humor protein profiles in patients with proliferative diabetic retinopathy before and after conbercept treatment. 2023 , 276, 104838	O
119	Responses of carbapenemase-producing and non-producing carbapenem-resistant Pseudomonas aeruginosa strains to meropenem revealed by quantitative tandem mass spectrometry proteomics. 13,	O
118	Splicing factor SRSF1 deficiency in the liver triggers NASH-like pathology and cell death. 2023 , 14,	Ο
117	Unique DUOX2+ACE2+ small cholangiocytes are pathogenic targets for primary biliary cholangitis. 2023 , 14,	0
116	Mass Spectrometry-Based Atlas of Extracellular Matrix Proteins across 25 Mouse Organs. 2023 , 22, 790-801	Ο
115	Effect of 3D Spheroid Culturing on NF-B Signaling Pathway and Neurogenic Potential in Human Amniotic Fluid Stem Cells. 2023 , 24, 3584	О
114	Metabolic handoffs between multiple symbionts may benefit the deep-sea bathymodioline mussels.	O

113	Transferrin Receptor Protein 1 Cooperates with mGluR2 To Mediate the Internalization of Rabies Virus and SARS-CoV-2. 2023 , 97,	О
112	Proteomic Analysis Reveals a Critical Role of the Glycosyl Hydrolase 17 Protein in Panax ginseng Leaves under Salt Stress. 2023 , 24, 3693	O
111	Early flora colonization affects intestinal immunoglobulin G uptake in piglets, which may be mediated by NF- B -FcRn pathway. 14,	0
110	The Ixodes ricinus salivary gland proteome during feeding and B. Afzelii infection: New avenues for an anti-tick vaccine. 2023 , 41, 1951-1960	O
109	Transcriptome and Proteome of Methicillin-Resistant Staphylococcus aureus Small-Colony Variants Reveal Changed Metabolism and Increased Immune Evasion. 2023 , 11,	О
108	Reperfusion after hypoxia-ischemia exacerbates brain injury with compensatory activation of the anti- ferroptosis system: based on a novel rat model. 2023 , 18, 2229	O
107	Mechanism of Saffron Extract against Cardiotoxicity Induced by Doxorubicin: 4D Label-Free Quantitative proteomics Analysis and Bioinformatic Study.	О
106	An intramolecular bivalent degrader glues an intrinsic BRD4-DCAF16 interaction.	O
105	Exosomes from M2c macrophages alleviate intervertebral disc degeneration by promoting synthesis of the extracellular matrix via MiR -124/ CILP / TGF - \square	О
104	Changes of RAS Pathway Phosphorylation in Lymphoblastoid Cell Lines from Noonan Syndrome Patients Carrying Hypomorphic Variants in Two NS Genes. 2023 , 24, 4035	O
103	STE20-Type Kinases MST3 and MST4 Act Non-Redundantly to Promote the Progression of Hepatocellular Carcinoma.	О
102	Glutamine is a substrate for glycosylation and CA19-9 biosynthesis through hexosamine biosynthetic pathway in pancreatic cancer. 2023 , 14,	O
101	Prophylactic and therapeutic vaccination protects sperm health fromChlamydia muridarum-induced abnormalities.	О
100	Multilevel proteomic analyses reveal molecular diversity between diffuse-type and intestinal-type gastric cancer. 2023 , 14,	О
99	OMICS Analyses Unraveling Related Gene and Protein-Driven Molecular Mechanisms Underlying PACAP 38-Induced Neurite Outgrowth in PC12 Cells. 2023 , 24, 4169	О
98	m6A methylation-induced NR1D1 ablation disrupts the HSC circadian clock and promotes hepatic fibrosis. 2023 , 189, 106704	O
97	Integrative Analysis of the Identified Transcriptome and Proteome Major Metabolism Pathways Involved in the Development of Grafted Apricot Hybrids. 2023 , 14, 417	О
96	Space Omics and Tissue Response in Astronaut Skeletal Muscle after Short and Long Duration Missions. 2023 , 24, 4095	O

95	SVEP1 is an endogenous ligand for the orphan receptor PEAR1. 2023, 14,	O
94	The proteomics and metabolomics studies of GZU001 on promoting the Merisis of maize (Zea mays L.) roots. 2023 , 23,	O
93	High-quality Cymbidium mannii genome and multifaceted regulation of crassulacean acid metabolism in epiphytes. 2023 , 100564	0
92	The Alzheimer disease-linked protease BACE1 modulates neuronal IL-6 signaling through shedding of the receptor gp130. 2023 , 18,	O
91	The structural components of the Azotobacter vinelandii iron-only nitrogenase, AnfDKG, form a protein complex within the plant mitochondrial matrix.	0
90	Investigation of changes in proteomes of beef exudate and meat quality attributes during wet-aging. 2023 , 17, 100608	O
89	Changes in the urine proteome in patients with advanced lung cancer after different drug treatments. 2023 , 5, 1-12	O
88	A Suspension Trapping ${f B}$ as ed Sample Preparation Workflow for Sensitive Plant Phosphoproteomics.	O
87	Protein Abundance of Drug Metabolizing Enzymes in Human Hepatitis C Livers. 2023, 24, 4543	O
86	Identification of Antioxidative Peptides Derived from Arthrospira maxima in the Biorefinery Process after Extraction of C-Phycocyanin and Lipids. 2023 , 21, 146	O
85	The alphavirus nonstructural protein 2 NTPase induces a host translational shut-off through phosphorylation of eEF2 via cAMP-PKA-eEF2K signaling. 2023 , 19, e1011179	0
84	Characteristics of behavioral reactions and the profile of brain isatin-binding proteins of rats with the rotenone-induced experimental parkinsonism. 2023 , 69, 46-54	O
83	Defining the filarial N-glycoproteome by glycosite mapping in the human parasitic nematode Brugia malayi.	O
82	Proteomic analysis reveals CAAP1 negatively correlates with platinum resistance in ovarian cancer. 2023 , 277, 104864	O
81	Heat inactivation of foetal bovine serum causes protein contamination of extracellular vesicles.	O
80	Quantitative proteomics identified a novel invasion biomarker associated with EMT in pituitary adenomas. 14,	O
79	Unique metabolism and protein expression signature in human decidual NK cells. 14,	0
78	Transcriptomics and Proteomics of Haemonchus contortus in Response to Ivermectin Treatment. 2023 , 13, 919	О

77	Changes in the urine proteome after massage in healthy people.	O
76	Proteome profiling of hippocampus reveals the neuroprotective effect of mild hypothermia on global cerebral ischemia-reperfusion injury in rats.	O
75	The double homeodomain protein DUX4c is associated with regenerating muscle fibers and RNA-binding proteins. 2023 , 13,	O
74	Comparison of Plasma Exosome Proteomes Between Obese and Non-Obese Patients with Type 2 Diabetes Mellitus. Volume 16, 629-642	O
73	Quality Control A Stepchild in Quantitative Proteomics: A Case Study for the Human CSF Proteome. 2023 , 13, 491	O
72	Uterine luminal-derived extracellular vesicles: potential nanomaterials to improve embryo implantation. 2023 , 21,	O
71	Acidotic and hypoxic tumor microenvironment induces changes to histone acetylation and methylation in oral squamous cell carcinoma.	О
70	Temperature-induced embryonic diapause in chickens is mediated by PKC-NF- B -IRF1 signaling. 2023 , 21,	O
69	The MYO1B and MYO5B motor proteins and the SNX27 sorting nexin regulate membrane mucin MUC17 trafficking in enterocytes.	О
68	Tizoxanide Antiviral Activity on Dengue Virus Replication. 2023 , 15, 696	O
67	Study of the long-finned pilot whale (Globicephala melas) bile content - An indicator of ocean health. 2023 , 189, 114795	O
66	Potential of Negative Ion Mode Proteomics: MS1-Only Approach.	O
65	Integrated transcriptomics-proteomics analysis reveals the regulatory network of ethanol vapor on softening of postharvest blueberry. 2023 , 180, 114649	О
64	Discovery of a Potent, Cooperative, and Selective SOS1 PROTAC ZZ151 with In Vivo Antitumor Efficacy in KRAS-Mutant Cancers. 2023 , 66, 4197-4214	O
63	Phosphorylation-linked complex profiling identifies assemblies required for Hippo signal integration. 2023 , 19,	O
62	Bottom-Up Proteomics: Advancements in Sample Preparation. 2023 , 24, 5350	O
61	Comparative Study on Growth and Proteomics of Oats Under Alkali Stress in Heading Stage.	O
60	Urine proteomic characterization of active and recovered COVID-19 patients.	O

59	Quantitative proteomics identifies and validates urinary biomarkers of rhabdomyosarcoma in children. 2023 , 20,	О
58	Investigating the dynamics of proteinprotein interactions in plants.	О
57	Uptake-independent killing of macrophages by extracellular Mycobacterium tuberculosis aggregates.	0
56	A swapped genetic code prevents viral infections and gene transfer. 2023 , 615, 720-727	O
55	Phosphoproteomics analysis of the effect of target of rapamycin kinase inhibition on Cucumis sativus in response to Podosphaera xanthii. 2023 , 197, 107641	0
54	Spatial Proteome Reorganization of a Photosynthetic Model Cyanobacterium in Response to Abiotic Stresses. 2023 , 22, 1255-1269	O
53	A proinsulin-dependent interaction between ENPL-1 and ASNA-1 in neurons is required to maintain insulin secretion in C. elegans. 2023 , 150,	0
52	Non-Oncogene Addiction of KRAS-Mutant Cancers to IL-1 via Versican and Mononuclear IKK 2023, 15, 1866	О
51	Arabidopsis ISRPKII family proteins regulate flowering via phosphorylation of SR proteins and effects on gene expression and alternative splicing.	О
50	Discovery Proteomics and Absolute Protein Quantification Can Be Performed Simultaneously on an Orbitrap-Based Mass Spectrometer. 2023 , 8, 12573-12583	O
49	Loss of respiratory complex I subunit NDUFB10 affects complex I assembly and supercomplex formation. 2023 , 404, 399-415	1
48	Identification of mitogen-activated protein kinase phosphatase-1 (MKP-1) protein partners using tandem affinity purification and mass spectrometry. 2023 , 75, 474-481	O
47	Metabolic Difference Analysis of Clostridium cellulovorans Grown on Glucose and Cellulose. 2023 , 9, 321	O
46	Reference proteomes of five wheat species as starting point for future design of cultivars with lower allergenic potential. 2023 , 7,	O
45	Functional and structural diversification of incomplete phosphotransferase system in cellulose-degrading clostridia.	0
44	Tissue and plasma proteomic profiling indicates AHSG as a potential biomarker for ascending thoracic aortic aneurysms. 2023 , 23,	O
43	Quantification of absolute transcription factor binding affinities in the native chromatin context using BANC-seq.	0
42	Kinome-wide synthetic lethal screen identifies PANK4 as modulator of resistance in glioblastoma	О

41	Proteomic Landscape of Human Sperm in Patients with Different Spermatogenic Impairments. 2023 , 12, 1017	0
40	Effects of GHR Deficiency and Juvenile Hypoglycemia on Immune Cells of a Porcine Model for Laron Syndrome. 2023 , 13, 597	O
39	NUSAP1 Binds ILF2 to Modulate R-Loop Accumulation and DNA Damage in Prostate Cancer. 2023 , 24, 6258	O
38	Proteomics analysis of a tobacco variety resistant to brown spot disease and functional characterization of NbMLP423 in Nicotiana benthamiana.	O
37	Proteomic Profiling of Fallopian Tube-Derived Extracellular Vesicles Using a Microfluidic Tissue-on-Chip System. 2023 , 10, 423	O
36	Comparison of SPEED, S-Trap, and In-Solution-Based Sample Preparation Methods for Mass Spectrometry in Kidney Tissue and Plasma. 2023 , 24, 6290	O
35	Proteins in pregnant swine serum promote the African swine fever virus replication: an iTRAQ-based quantitative proteomic analysis. 2023 , 20,	0
34	ULK4 and Fused/STK36 interact to mediate assembly of a motile flagellum.	O
33	Proteomic analysis of metronidazole resistance in the human facultative pathogen Bacteroides fragilis. 14,	O
32	Changes of development from childhood to late adulthood in rats tracked by urinary proteome. 2023 , 100539	O
31	Peptide CoA conjugates for in situ proteomics profiling of acetyltransferase activities. 2023,	O
30	Scutellarin Alleviates Ischemic Brain Injury in the Acute Phase by Affecting the Activity of Neurotransmitters in Neurons. 2023 , 28, 3181	O
29	Comparative physiological and proteomic response to phosphate deficiency between two wheat genotypes differing in phosphorus utilization efficiency. 2023 , 280, 104894	O
28	Characterization of methionine dependence in melanoma cells.	O
27	TGF-Induces matrisome pathological alterations and EMT in patient-derived prostate cancer tumoroids.	O
26	Label-Free Quantification Mass Spectrometry Identifies Protein Markers of Chemotherapy Response in High-Grade Serous Ovarian Cancer. 2023 , 15, 2172	O
25	Integrative proteomic and phosphoproteomic analysis in the female goat hypothalamus to study the onset of puberty.	О
24	DT-109 ameliorates nonalcoholic steatohepatitis in nonhuman primates. 2023 ,	O

23	Hydroxyanthracene derivates citotoxicity: A differential evaluation between single molecule and whole plant extract. 14,	0
22	Urinary complement proteins in IgA nephropathy progression from a relative quantitative proteomic analysis. 11, e15125	O
21	An ERK1/2-driven RNA-binding switch in nucleolin drives ribosome biogenesis and pancreatic tumorigenesis downstream of RAS oncogene.	О
20	Changes in the urine proteome after massage in healthy people.	O
19	Fusobacterium nucleatum aggravates rheumatoid arthritis through FadA-containing outer membrane vesicles. 2023 ,	0
18	Proteomic analysis of extracellular vesicles from tick hemolymph and uptake of extracellular vesicles by salivary glands and ovary cells. 2023 , 16,	o
17	Mining and Validation of Novel Hemp Seed-Derived DPP-IV-Inhibiting Peptides Using a Combination of Multi-omics and Molecular Docking.	0
16	Analysis of Nipah Virus Replication and Host Proteome Response Patterns in Differentiated Porcine Airway Epithelial Cells Cultured at the Airliquid Interface. 2023 , 15, 961	О
15	A proteomics study to explore differential proteins associated with the pathogenesis of ameloblastoma.	0
14	SMARCAD1 and TOPBP1 contribute to heterochromatin maintenance at the transition from the 2C-like to the pluripotent state.	O
13	A five-protein prognostic signature with GBP2 functioning in immune cell infiltration of clear cell renal cell carcinoma. 2023 , 21, 2621-2630	O
12	Plasmepsin X activates the PCRCR complex of Plasmodium falciparum by processing PfRh5 for erythrocyte invasion. 2023 , 14,	O
11	Amino acids downregulate SIRT4 to detoxify ammonia through the urea cycle.	O
10	Elevated Nuclear PHGDH Synergistically Functions with cMyc to Reshape the Immune Microenvironment of Liver Cancer.	O
9	The Antimicrobial Potential and Aquaculture Wastewater Treatment Ability of Penaeidins 3a Transgenic Duckweed. 2023 , 12, 1715	0
8	Physiological response and proteomic profiling of biochar-induced tomato resistance to bacterial wilt. 2023 , 317, 112055	0
7	Peridroplet mitochondria in fatty liver and their role in the prevention of NAFLD by diethyldithiocarbamate.	0
6	Suspension TRAPping Filter (sTRAP) Sample Preparation for Quantitative Proteomics in the Low µg Input Range Using a Plasmid DNA Micro-Spin Column: Analysis of the Hippocampus from the 5xFAD Alzheimer Disease Mouse Model. 2023 , 12, 1242	O

5	A multiomic approach to defining the essential genome of the globally important pathogen Corynebacterium diphtheriae. 2023 , 19, e1010737	О
4	Ferroptosis-Protective Membrane Domains in Quiescence.	O
3	Proteomic characteristics reveal the signatures and the risks of T1 colorectal cancer metastasis to lymph nodes. 12,	O
2	Defining the filarial N-glycoproteome by glycosite mapping in the human parasitic nematode Brugia malayi. 2023 , 13,	O
1	The Glomerulus Multiomics Analysis Provides Deeper Insights into Diabetic Nephropathy.	0