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2251 .

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2248 Chemical Proteomics and Structural Biology Define EPHA2 Inhibition by Clinical Kinase Drugs.

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2242 Discovering the Microbial Enzymes Driving Drug Toxicity with Activity-Based Protein Profiling.

2241 Biochemical and Proteomic Studies of Human Pyridoxal 5-Phosphate-Binding Protein (PLPBP).

2240 Cyclopostins and Cyclophostin Analogues as Multitarget Inhibitors That Impair Growth of *Mycobacterium abscessus*.

2239 Development of Selective Histone Deacetylase 6 (HDAC6) Degraders Recruiting Von Hippel-Lindau (VHL) E3 Ubiquitin Ligase.

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2237 Identification of SLIRP as a G Quadruplex-Binding Protein.

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2233 Spatial Cross-Talk between Oxidative Stress and DNA Replication in Human Fibroblasts.

2232 Comprehensive Proteomic Investigation of Ebf1 Heterozygosity in ProB Lymphocytes Utilizing Data Independent Acquisition.

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2227 Chemoproteomic Selectivity Profiling of PIKK and PI3K Kinase Inhibitors.

2226 Development of a Photo-Cross-Linkable Diaminoquinazoline Inhibitor for Target Identification in *Plasmodium falciparum*.

2225 Design of KDM4 Inhibitors with Antiproliferative Effects in Cancer Models.

2224 Discovery of a First-in-Class Gut-Restricted RET Kinase Inhibitor as a Clinical Candidate for the Treatment of IBS.

2223 Biosynthesis of an Anti-Addiction Agent from the Iboga Plant.

2222 .

2221 A High-Throughput Targeted Proteomic Approach for Comprehensive Profiling of Methylglyoxal-Induced Perturbations of the Human Kinome.

2220 Quirks of Error Estimation in Cross-Linking/Mass Spectrometry.

2219 Accurate, Sensitive, and Precise Multiplexed Proteomics Using the Complement Reporter Ion Cluster.

2218 Analytical Pipeline for Discovery and Verification of Glycoproteins from Plasma-Derived Extracellular Vesicles as Breast Cancer Biomarkers.

2217 Targeted Quantitative Profiling of GTP-Binding Proteins in Cancer Cells Using Isotope-Coded GTP Probes.

2216 Simple Tip-Based Sample Processing Method for Urinary Proteomic Analysis.

2215 Microsampling Capillary Electrophoresis Mass Spectrometry Enables Single-Cell Proteomics in Complex Tissues: Developing Cell Clones in Live *Xenopus laevis* and Zebrafish Embryos.

2214 Surface Glycoproteomic Analysis Reveals That Both Unique and Differential Expression of Surface Glycoproteins Determine the Cell Type.

2213 Low-Background Acyl-Biotinyl Exchange Largely Eliminates the Coisolation of NonSAcylated Proteins and Enables Deep SAcyLproteomic Analysis.

2212 Targeted Diazotransfer Reagents Enable Selective Modification of Proteins with Azides.

2211 The Political Economy of Consumer Protection: an Examination of State Legislation. **1987**, 40, 343-359

5

2210 Evidence that SpoIVFB is a novel type of membrane metalloprotease governing intercompartmental communication during *Bacillus subtilis* sporulation. **2000**, 182, 3305-9

61

2209 Nasal saline for acute sinusitis. **2002**, 109, 165

34

2208 A SILAC-based DNA protein interaction screen that identifies candidate binding proteins to functional DNA elements. **2009**, 19, 284-93

125

2207 [Quantitative proteomics by SILAC: practicalities and perspectives for an evolving approach]. **2009**, 25, 835-42

6

2206 A proteomic view of an important human pathogen--towards the quantification of the entire *Staphylococcus aureus* proteome. **2009**, 4, e8176

126

2205 Actin remodeling by ADF/cofilin is required for cargo sorting at the trans-Golgi network. **2009**, 187, 1055-69

87

2204 Quantitative strategies to fuel the merger of discovery and hypothesis-driven shotgun proteomics. **2009**, 8, 114-25

14

2203 Normalization and statistical analysis of quantitative proteomics data generated by metabolic labeling. **2009**, 8, 2227-42

99

2202 Unbiased RNA-protein interaction screen by quantitative proteomics. **2009**, 106, 10626-31

109

2201 Advances in bioanalytical LC-MS using the Orbitrap mass analyzer. **2009**, 1, 741-54

42

2200 Inhibition of the soluble epoxide hydrolase by tyrosine nitration. **2009**, 284, 28156-28163

24

2199 Proteomics analysis of nucleolar SUMO-1 target proteins upon proteasome inhibition. **2009**, 8, 2243-55

78

2198	Quantitative proteomic analysis of single pancreatic islets. <b>2009</b> , 106, 18902-7	172
2197	Qupe--a Rich Internet Application to take a step forward in the analysis of mass spectrometry-based quantitative proteomics experiments. <b>2009</b> , 25, 3128-34	24
2196	Systems-wide analysis of a phosphatase knock-down by quantitative proteomics and phosphoproteomics. <b>2009</b> , 8, 1908-20	88
2195	Global effects of kinase inhibitors on signaling networks revealed by quantitative phosphoproteomics. <b>2009</b> , 8, 2796-808	165
2194	Approaches to biomarkers in human colorectal cancer: looking back, to go forward. <b>2009</b> , 3, 385-396	13
2193	Data handling and processing in proteomics. <b>2009</b> , 6, 217-9	10
2192	Mitochondria do not contain lipid rafts, and lipid rafts do not contain mitochondrial proteins. <b>2009</b> , 50, 988-98	57
2191	Comparative proteomic phenotyping of cell lines and primary cells to assess preservation of cell type-specific functions. <b>2009</b> , 8, 443-50	351
2190	A dual pressure linear ion trap Orbitrap instrument with very high sequencing speed. <b>2009</b> , 8, 2759-69	379
2189	Highly accelerated feature detection in proteomics data sets using modern graphics processing units. <b>2009</b> , 25, 1937-43	34
2188	MaXIC-Q Web: a fully automated web service using statistical and computational methods for protein quantitation based on stable isotope labeling and LC-MS. <b>2009</b> , 37, W661-9	9
2187	A genome-wide screen for genes affecting eisosomes reveals Nce102 function in sphingolipid signaling. <b>2009</b> , 185, 1227-42	99
2186	Bioinformatics analysis of mass spectrometry-based proteomics data sets. <b>2009</b> , 583, 1703-12	123
2185	Current literature in mass spectrometry. <b>2009</b> , 44, 848-859	1
2184	High-accuracy identification and bioinformatic analysis of in vivo protein phosphorylation sites in yeast. <b>2009</b> , 9, 4642-52	103
2183	A novel S3S-TAP-tag for the isolation of T-cell interaction partners of adhesion and degranulation promoting adaptor protein. <b>2009</b> , 9, 5288-95	15
2182	Quantitative proteomics in biological research. <b>2009</b> , 9, 4590-605	69
2181	When less can yield more - Computational preprocessing of MS/MS spectra for peptide identification. <b>2009</b> , 9, 4978-84	62

2180	Universal sample preparation method for proteome analysis. <b>2009</b> , 6, 359-62	4739
2179	Proteomics strategy for quantitative protein interaction profiling in cell extracts. <b>2009</b> , 6, 741-4	121
2178	News in brief. <b>2009</b> , 6, 115-115	
2177	Comparative analysis to guide quality improvements in proteomics. <b>2009</b> , 6, 717-19	56
2176	A practical guide to the MaxQuant computational platform for SILAC-based quantitative proteomics. <b>2009</b> , 4, 698-705	637
2175	The B-lymphoid Grb2 interaction code. <b>2009</b> , 232, 135-49	30
2174	Computational principles of determining and improving mass precision and accuracy for proteome measurements in an Orbitrap. <b>2009</b> , 20, 1477-85	55
2173	Lysine acetylation targets protein complexes and co-regulates major cellular functions. <b>2009</b> , 325, 834-40	3316
2172	System-wide changes to SUMO modifications in response to heat shock. <b>2009</b> , 2, ra24	367
2171	Proteomics: from technology developments to biological applications. <b>2009</b> , 81, 4585-99	40
2170	Directed sample interrogation utilizing an accurate mass exclusion-based data-dependent acquisition strategy (AMEx). <b>2009</b> , 8, 3154-60	33
2169	Large-scale identification and quantification of covalent modifications in therapeutic proteins. <b>2009</b> , 81, 8354-64	78
2168	Effect of peptide-to-TiO <sub>2</sub> beads ratio on phosphopeptide enrichment selectivity. <b>2009</b> , 8, 5375-81	108
2167	Quantitative analysis of the human spindle phosphoproteome at distinct mitotic stages. <b>2009</b> , 8, 4553-63	97
2166	Caenorhabditis elegans has a phosphoproteome atypical for metazoans that is enriched in developmental and sex determination proteins. <b>2009</b> , 8, 4039-49	59
2165	Proteome differences between brown and white fat mitochondria reveal specialized metabolic functions. <b>2009</b> , 10, 324-35	158
2164	Global analysis of the yeast osmotic stress response by quantitative proteomics. <b>2009</b> , 5, 1337-46	108
2163	A global view of protein expression in human cells, tissues, and organs. <b>2009</b> , 5, 337	142

2162	Receptor tyrosine kinase signaling: a view from quantitative proteomics. <b>2009</b> , 5, 1112-21	54
2161	Elective affinities--bioinformatic analysis of proteomic mass spectrometry data. <b>2009</b> , 115, 311-9	8
2160	Comparing cellular proteomes by mass spectrometry. <b>2009</b> , 10, 240	1
2159	Combination of FASP and StageTip-based fractionation allows in-depth analysis of the hippocampal membrane proteome. <b>2009</b> , 8, 5674-8	426
2158	Comparative proteomic profiling of membrane proteins in rat cerebellum, spinal cord, and sciatic nerve. <b>2009</b> , 8, 2418-25	37
2157	14-3-3 binding to LRRK2 is disrupted by multiple Parkinson's disease-associated mutations and regulates cytoplasmic localization. <b>2010</b> , 430, 393-404	289
2156	RRP1B targets PP1 to mammalian cell nucleoli and is associated with Pre-60S ribosomal subunits. <b>2010</b> , 21, 4212-26	28
2155	The phosphoproteome of toll-like receptor-activated macrophages. <b>2010</b> , 6, 371	113
2154	Establishment of a protein frequency library and its application in the reliable identification of specific protein interaction partners. <b>2010</b> , 9, 861-79	52
2153	Quantitation in mass-spectrometry-based proteomics. <b>2010</b> , 61, 491-516	257
2152	Proteomic analysis of sea urchin ( <i>Strongylocentrotus purpuratus</i> ) spicule matrix. <b>2010</b> , 8, 33	98
2151	Novel In Situ Collection of Tumor Interstitial Fluid from a Head and Neck Squamous Carcinoma Reveals a Unique Proteome with Diagnostic Potential. <b>2010</b> , 6, 75-82	16
2150	Antioxidant dysfunction: potential risk for neurotoxicity in ethylmalonic aciduria. <b>2010</b> , 33, 211-22	29
2149	WaveletQuant, an improved quantification software based on wavelet signal threshold de-noising for labeled quantitative proteomic analysis. <b>2010</b> , 11, 219	16
2148	Identifying differentially regulated subnetworks from phosphoproteomic data. <b>2010</b> , 11, 351	26
2147	The utility of mass spectrometry-based proteomic data for validation of novel alternative splice forms reconstructed from RNA-Seq data: a preliminary assessment. <b>2010</b> , 11 Suppl 11, S14	49
2146	Phosphoproteomes of <i>Strongylocentrotus purpuratus</i> shell and tooth matrix: identification of a major acidic sea urchin tooth phosphoprotein, phosphodontin. <b>2010</b> , 8, 6	27
2145	Methods for investigation of targeted kinase inhibitor therapy using chemical proteomics and phosphorylation profiling. <b>2010</b> , 80, 739-47	15



2144	Evidence for a dynamic role of the linker histone variant H1x during retinoic acid-induced differentiation of NT2 cells. <b>2010</b> , 584, 4661-4	13
2143	Proteomic analysis of Chilo iridescent virus. <b>2010</b> , 405, 253-8	32
2142	Mass spectrometry analysis of complexes formed by myotonic dystrophy protein kinase (DMPK). <b>2010</b> , 1804, 1334-41	6
2141	Proteomic basics I: quantification and post-translational modifications of proteins: The 3rd European Summer School in Kloster Neustift. <b>2010</b> , 73, 697-700	
2140	Proteome analysis of mouse model systems: A tool to model human disease and for the investigation of tissue-specific biology. <b>2010</b> , 73, 2205-18	10
2139	Chemical proteomic and bioinformatic strategies for the identification and quantification of vascular antigens in cancer. <b>2010</b> , 73, 1954-73	17
2138	A survey of computational methods and error rate estimation procedures for peptide and protein identification in shotgun proteomics. <b>2010</b> , 73, 2092-123	387
2137	Coupling liquid chromatography to Orbitrap mass spectrometry. <b>2010</b> , 1217, 3938-45	158
2136	Quantitative proteomics reveals subset-specific viral recognition in dendritic cells. <b>2010</b> , 32, 279-89	435
2135	Quantitative phosphoproteomic analysis of prion-infected neuronal cells. <b>2010</b> , 8, 28	7
2134	A guided tour of the Trans-Proteomic Pipeline. <b>2010</b> , 10, 1150-9	590
2133	Rover: a tool to visualize and validate quantitative proteomics data from different sources. <b>2010</b> , 10, 1226-9	39
2132	ms_lims, a simple yet powerful open source laboratory information management system for MS-driven proteomics. <b>2010</b> , 10, 1261-4	65
2131	Shotgun proteomics data from multiple organisms reveals remarkable quantitative conservation of the eukaryotic core proteome. <b>2010</b> , 10, 1297-306	51
2130	Peptide and protein quantification: a map of the minefield. <b>2010</b> , 10, 650-70	89
2129	Quantitative analysis of SILAC data sets using spectral counting. <b>2010</b> , 10, 1408-15	11
2128	The minotaur proteome: avoiding cross-species identifications deriving from bovine serum in cell culture models. <b>2010</b> , 10, 3040-4	36
2127	Elucidation of the avian nucleolar proteome by quantitative proteomics using SILAC and changes in cells infected with the coronavirus infectious bronchitis virus. <b>2010</b> , 10, 3558-62	28

2126	Efficient extraction of nucleolar proteins for interactome analyses. <b>2010</b> , 10, 3045-50	22
2125	p53-Dependent subcellular proteome localization following DNA damage. <b>2010</b> , 10, 4087-97	44
2124	Quantitative proteomic analysis of A549 cells infected with human respiratory syncytial virus subgroup B using SILAC coupled to LC-MS/MS. <b>2010</b> , 10, 4320-34	42
2123	Phosphoproteomics. <b>2010</b> , 2, 255-276	35
2122	A targeted siRNA screen to identify SNAREs required for constitutive secretion in mammalian cells. <b>2010</b> , 11, 1191-204	90
2121	A plasma-membrane E-MAP reveals links of the eisosome with sphingolipid metabolism and endosomal trafficking. <b>2010</b> , 17, 901-8	79
2120	Architecture of the RNA polymerase II-TFIIF complex revealed by cross-linking and mass spectrometry. <b>2010</b> , 29, 717-26	322
2119	The human core exosome interacts with differentially localized processive RNases: hDIS3 and hDIS3L. <b>2010</b> , 29, 2342-57	189
2118	Native GABA(B) receptors are heteromultimers with a family of auxiliary subunits. <b>2010</b> , 465, 231-5	242
2117	Proteomics: a pragmatic perspective. <i>Nature Biotechnology</i> , <b>2010</b> , 28, 695-709	44.5 325
2116	SUMOylation of the GTPase Rac1 is required for optimal cell migration. <b>2010</b> , 12, 1078-85	131
2115	Super-SILAC mix for quantitative proteomics of human tumor tissue. <b>2010</b> , 7, 383-5	431
2114	Trans-SILAC: sorting out the non-cell-autonomous proteome. <b>2010</b> , 7, 923-7	27
2113	Decoding signalling networks by mass spectrometry-based proteomics. <b>2010</b> , 11, 427-39	484
2112	Generating and navigating proteome maps using mass spectrometry. <b>2010</b> , 11, 789-801	139
2111	Silencing mediated by the <i>Schizosaccharomyces pombe</i> HIRA complex is dependent upon the Hpc2-like protein, Hip4. <b>2010</b> , 5, e13488	25
2110	Global phosphoproteomics identifies a major role for AKT and 14-3-3 in regulating EDC3. <b>2010</b> , 9, 682-94	34
2109	Proteomic analysis of <i>Glossina pallidipes</i> salivary gland hypertrophy virus virions for immune intervention in tsetse fly colonies. <b>2010</b> , 91, 3065-74	24

2108	A robust error model for iTRAQ quantification reveals divergent signaling between oncogenic FLT3 mutants in acute myeloid leukemia. <b>2010</b> , 9, 780-90	67
2107	Protein export marks the early phase of gametocytogenesis of the human malaria parasite <i>Plasmodium falciparum</i> . <b>2010</b> , 9, 1437-48	191
2106	Synthetic peptide arrays for pathway-level protein monitoring by liquid chromatography-tandem mass spectrometry. <b>2010</b> , 9, 2460-73	12
2105	MSMSpdbb: providing protein databases of closely related organisms to improve proteomic characterization of prokaryotic microbes. <b>2010</b> , 26, 698-9	27
2104	An integrated phosphoproteomics work flow reveals extensive network regulation in early lysophosphatidic acid signaling. <b>2010</b> , 9, 1047-62	25
2103	Quantitative phosphoproteomics dissection of seven-transmembrane receptor signaling using full and biased agonists. <b>2010</b> , 9, 1540-53	115
2102	The rapamycin-sensitive phosphoproteome reveals that TOR controls protein kinase A toward some but not all substrates. <b>2010</b> , 21, 3475-86	179
2101	Plk1 negatively regulates Cep55 recruitment to the midbody to ensure orderly abscission. <b>2010</b> , 191, 751-60	110
2100	Family-wide characterization of the DENN domain Rab GDP-GTP exchange factors. <b>2010</b> , 191, 367-81	218
2099	Structure of hibernating ribosomes studied by cryoelectron tomography in vitro and in situ. <b>2010</b> , 190, 613-21	73
2098	Glycoprotein capture and quantitative phosphoproteomics indicate coordinated regulation of cell migration upon lysophosphatidic acid stimulation. <b>2010</b> , 9, 2337-53	13
2097	An alternatively spliced CXCL16 isoform expressed by dendritic cells is a secreted chemoattractant for CXCR6+ cells. <b>2010</b> , 87, 1029-39	29
2096	Defining the transcriptome and proteome in three functionally different human cell lines. <b>2010</b> , 6, 450	269
2095	Unbiased identification of protein-bait interactions using biochemical enrichment and quantitative proteomics. <b>2010</b> , 2010, pdb.prot5400	5
2094	The SILAC fly allows for accurate protein quantification in vivo. <b>2010</b> , 9, 2173-83	138
2093	Proteomics on an Orbitrap benchtop mass spectrometer using all-ion fragmentation. <b>2010</b> , 9, 2252-61	189
2092	Increased power for the analysis of label-free LC-MS/MS proteomics data by combining spectral counts and peptide peak attributes. <b>2010</b> , 9, 2704-18	35
2091	Quantitative site-specific phosphorylation dynamics of human protein kinases during mitotic progression. <b>2010</b> , 9, 1167-81	41

2090	Protein phosphatase 6 regulates mitotic spindle formation by controlling the T-loop phosphorylation state of Aurora A bound to its activator TPX2. <b>2010</b> , 191, 1315-32	137
2089	Stable-Isotope Labeling for Protein Quantitation by Mass Spectrometry. <b>2010</b> , 7, 144-155	8
2088	The cargo-selective retromer complex is a recruiting hub for protein complexes that regulate endosomal tubule dynamics. <b>2010</b> , 123, 3703-17	178
2087	Quantitative proteomic analysis of A549 cells infected with human respiratory syncytial virus. <b>2010</b> , 9, 2438-59	79
2086	Quantitative proteomics using stable isotope labeling with amino acids in cell culture reveals changes in the cytoplasmic, nuclear, and nucleolar proteomes in Vero cells infected with the coronavirus infectious bronchitis virus. <b>2010</b> , 9, 1920-36	70
2085	Quantitative proteomics combined with BAC TransgeneOmics reveals in vivo protein interactions. <b>2010</b> , 189, 739-54	341
2084	Site-specific phosphorylation dynamics of the nuclear proteome during the DNA damage response. <b>2010</b> , 9, 1314-23	195
2083	Mass spectrometry-based proteomics in biomedical research: emerging technologies and future strategies. <b>2010</b> , 12, e30	24
2082	EGFR promotes lung tumorigenesis by activating miR-7 through a Ras/ERK/Myc pathway that targets the Ets2 transcriptional repressor ERF. <b>2010</b> , 70, 8822-31	217
2081	Canonical and alternate functions of the microRNA biogenesis machinery. <b>2010</b> , 24, 1951-60	178
2080	A highly unusual thioester bond in a pilus adhesin is required for efficient host cell interaction. <b>2010</b> , 285, 33858-66	64
2079	Quantitative proteomics of the Cav2 channel nano-environments in the mammalian brain. <b>2010</b> , 107, 14950-7	219
2078	The generating function of CID, ETD, and CID/ETD pairs of tandem mass spectra: applications to database search. <b>2010</b> , 9, 2840-52	193
2077	A dynamic wavelet-based algorithm for pre-processing tandem mass spectrometry data. <b>2010</b> , 26, 2242-9	11
2076	Evolutionary constraints of phosphorylation in eukaryotes, prokaryotes, and mitochondria. <b>2010</b> , 9, 2642-53	70
2075	A genetic engineering solution to the "arginine conversion problem" in stable isotope labeling by amino acids in cell culture (SILAC). <b>2010</b> , 9, 1567-77	59
2074	Proteogenomics of <i>Pristionchus pacificus</i> reveals distinct proteome structure of nematode models. <b>2010</b> , 20, 837-46	128
2073	Quantitative proteomics for the analysis of spatio-temporal protein dynamics during autophagy. <b>2010</b> , 6, 1009-16	28

2072	Toward quantitative proteomics of organ substructures: implications for renal physiology. <b>2010</b> , 30, 487-99	7
2071	Synaptonemal complex protein SYCP3 exists in two isoforms showing different conservation in mammalian evolution. <b>2010</b> , 128, 162-8	13
2070	Brain phosphoproteome obtained by a FASP-based method reveals plasma membrane protein topology. <b>2010</b> , 9, 3280-9	221
2069	Overview of peptide and protein analysis by mass spectrometry. <b>2010</b> , Chapter 16, Unit16.1	25
2068	Strategies for quantitation of phosphoproteomic data. <b>2010</b> , 7, 439-56	19
2067	A rapid, reproducible, on-the-fly orthogonal array optimization method for targeted protein quantification by LC/MS and its application for accurate and sensitive quantification of carbonyl reductases in human liver. <b>2010</b> , 82, 2680-9	39
2066	MSQuant, an open source platform for mass spectrometry-based quantitative proteomics. <b>2010</b> , 9, 393-403	225
2065	Quantitative phosphoproteomics reveals widespread full phosphorylation site occupancy during mitosis. <b>2010</b> , 3, ra3	1106
2064	Stable-isotope dilution LC/MS for quantitative biomarker analysis. <b>2010</b> , 2, 311-41	175
2063	Analysis of detergent-insoluble and whole cell lysate fractions of resting neutrophils using high-resolution mass spectrometry. <b>2010</b> , 9, 2030-6	18
2062	Proteome, phosphoproteome, and N-glycoproteome are quantitatively preserved in formalin-fixed paraffin-embedded tissue and analyzable by high-resolution mass spectrometry. <b>2010</b> , 9, 3688-700	193
2061	Proteomics analysis of cellular imatinib targets and their candidate downstream effectors. <b>2010</b> , 9, 6033-43	25
2060	Proteome-wide quantitation by SILAC. <b>2010</b> , 658, 187-204	20
2059	Systems Biology in Drug Discovery and Development. <b>2010</b> ,	2
2058	A quantitative proteomics analysis of subcellular proteome localization and changes induced by DNA damage. <b>2010</b> , 9, 457-70	144
2057	Quantitative analysis of HGF and EGF-dependent phosphotyrosine signaling networks. <b>2010</b> , 9, 2734-42	46
2056	Differential phosphoproteomics of fibroblast growth factor signaling: identification of Src family kinase-mediated phosphorylation events. <b>2010</b> , 9, 2317-28	44
2055	Optimal decharging and clustering of charge ladders generated in ESI-MS. <b>2010</b> , 9, 2688-95	4

2054	Integrated post-experiment monoisotopic mass refinement: an integrated approach to accurately assign monoisotopic precursor masses to tandem mass spectrometric data. <b>2010</b> , 82, 8510-8	16
2053	Quantitative proteomics reveals a "poised quiescence" cellular state after triggering the DNA replication origin activation checkpoint. <b>2010</b> , 9, 5445-60	6
2052	Quantitative analysis of kinase-proximal signaling in lipopolysaccharide-induced innate immune response. <b>2010</b> , 9, 2539-49	26
2051	Peptide labeling with isobaric tags yields higher identification rates using iTRAQ 4-plex compared to TMT 6-plex and iTRAQ 8-plex on LTQ Orbitrap. <b>2010</b> , 82, 6549-58	146
2050	Feasibility of large-scale phosphoproteomics with higher energy collisional dissociation fragmentation. <b>2010</b> , 9, 6786-94	139
2049	Quantitative proteomics using SILAC coupled to LC-MS/MS reveals changes in the nucleolar proteome in influenza A virus-infected cells. <b>2010</b> , 9, 5335-45	69
2048	Yeast expression proteomics by high-resolution mass spectrometry. <b>2010</b> , 470, 259-80	8
2047	Advanced identification of proteins in uncharacterized proteomes by pulsed in vivo stable isotope labeling-based mass spectrometry. <b>2010</b> , 9, 1157-66	37
2046	Improved quantitative analysis of mass spectrometry using quadratic equations. <b>2010</b> , 9, 2775-85	11
2045	A proteomic screen for nucleolar SUMO targets shows SUMOylation modulates the function of Nop5/Nop58. <b>2010</b> , 39, 618-31	60
2044	Site-specific identification of SUMO-2 targets in cells reveals an inverted SUMOylation motif and a hydrophobic cluster SUMOylation motif. <b>2010</b> , 39, 641-52	215
2043	A cytoplasmic ATM-TRAF6-cIAP1 module links nuclear DNA damage signaling to ubiquitin-mediated NF- $\kappa$ B activation. <b>2010</b> , 40, 63-74	213
2042	Precision mapping of an in vivo N-glycoproteome reveals rigid topological and sequence constraints. <b>2010</b> , 141, 897-907	700
2041	Chromatin-Remodeling Components of the BAF Complex Facilitate Reprogramming. <b>2010</b> , 141, 943-55	299
2040	The protein composition of mitotic chromosomes determined using multiclassifier combinatorial proteomics. <b>2010</b> , 142, 810-21	217
2039	Quantitative interaction proteomics and genome-wide profiling of epigenetic histone marks and their readers. <b>2010</b> , 142, 967-80	579
2038	Nucleosome-interacting proteins regulated by DNA and histone methylation. <b>2010</b> , 143, 470-84	448
2037	SIRT3 deacetylates mitochondrial 3-hydroxy-3-methylglutaryl CoA synthase 2 and regulates ketone body production. <b>2010</b> , 12, 654-61	357

2036	The insulin secretory granule as a signaling hub. <b>2010</b> , 21, 599-609	125
2035	Protein quantitation using mass spectrometry. <b>2010</b> , 673, 211-22	40
2034	Mass spectrometry-based proteomics in cell biology. <b>2010</b> , 190, 491-500	310
2033	Red blood cell proteomics. <b>2010</b> , 17, 151-64	14
2032	The mucilage proteome of maize ( <i>Zea mays</i> L.) primary roots. <b>2010</b> , 9, 2968-76	42
2031	SILACAnalyzer - A Tool for Differential Quantitation of Stable Isotope Derived Data. <b>2010</b> , 45-55	6
2030	Computational Intelligence Methods for Bioinformatics and Biostatistics. <b>2010</b> ,	1
2029	Bioinformatics for LC-MS/MS-based proteomics. <b>2010</b> , 658, 61-91	20
2028	Quantitative proteome and transcriptome analysis of the archaeon <i>Thermoplasma acidophilum</i> cultured under aerobic and anaerobic conditions. <b>2010</b> , 9, 4839-50	35
2027	Antimicrobial activity of lipophilic avian eggshell surface extracts. <b>2010</b> , 58, 10156-61	19
2026	LC-MS/MS in Proteomics. <b>2010</b> ,	3
2025	CDK2AP1/DOC-1 is a bona fide subunit of the Mi-2/NuRD complex. <b>2010</b> , 6, 1700-6	43
2024	Identification of phosphorylation-dependent interaction partners of the adapter protein ADAP using quantitative mass spectrometry: SILAC vs (18)O-labeling. <b>2010</b> , 9, 4113-22	56
2023	Site-specific proteomics approach for study protein S-nitrosylation. <b>2010</b> , 82, 7160-8	52
2022	Stable isotope labeling by amino acids in cell culture (SILAC) applied to quantitative proteomics of <i>Bacillus subtilis</i> . <b>2010</b> , 9, 3638-46	91
2021	Pinpointing phosphorylation sites: Quantitative filtering and a novel site-specific x-ion fragment. <b>2011</b> , 10, 2937-48	24
2020	Quantitative proteomics by amino acid labeling in <i>C. elegans</i> . <b>2011</b> , 8, 845-7	45
2019	IsobariQ: software for isobaric quantitative proteomics using IPTL, iTRAQ, and TMT. <b>2011</b> , 10, 913-20	73

2018	Proteomics and pluripotency. <b>2011</b> , 46, 493-506	12
2017	MAPA distinguishes genotype-specific variability of highly similar regulatory protein isoforms in potato tuber. <b>2011</b> , 10, 2979-91	26
2016	Comparison of three quantitative phosphoproteomic strategies to study receptor tyrosine kinase signaling. <b>2011</b> , 10, 5454-62	25
2015	Enhancing the identification of phosphopeptides from putative basophilic kinase substrates using Ti (IV) based IMAC enrichment. <b>2011</b> , 10, M110.006452	77
2014	Unraveling pancreatic islet biology by quantitative proteomics. <b>2011</b> , 8, 495-504	10
2013	Fourier transform mass spectrometry. <b>2011</b> , 10, M111.009431	140
2012	The problem with peptide presumption and low Mascot scoring. <b>2011</b> , 10, 1432-5	28
2011	Mass spectrometry-based proteomics using Q Exactive, a high-performance benchtop quadrupole Orbitrap mass spectrometer. <b>2011</b> , 10, M111.011015	614
2010	Andromeda: a peptide search engine integrated into the MaxQuant environment. <b>2011</b> , 10, 1794-805	3402
2009	Threshold-avoiding proteomics pipeline. <b>2011</b> , 83, 7786-94	14
2008	Quantitative proteomic analysis of the adipocyte plasma membrane. <b>2011</b> , 10, 4970-82	25
2007	RockerBox: analysis and filtering of massive proteomics search results. <b>2011</b> , 10, 1420-4	28
2006	IsoformResolver: A peptide-centric algorithm for protein inference. <b>2011</b> , 10, 3060-75	30
2005	T cell receptor (TCR)-induced tyrosine phosphorylation dynamics identifies THEMIS as a new TCR signalosome component. <b>2011</b> , 286, 7535-47	64
2004	Absolute SILAC-compatible expression strain allows Sumo-2 copy number determination in clinical samples. <b>2011</b> , 10, 4869-75	33
2003	Pulsed stable isotope labeling of amino acids in cell culture uncovers the dynamic interactions between HIV-1 and the monocyte-derived macrophage. <b>2011</b> , 10, 2852-62	18
2002	Improved precision of iTRAQ and TMT quantification by an axial extraction field in an Orbitrap HCD cell. <b>2011</b> , 83, 1469-74	45
2001	Thermo-msf-parser: an open source Java library to parse and visualize Thermo Proteome Discoverer msf files. <b>2011</b> , 10, 3840-3	36



2000	Comparison of ERLIC-TiO <sub>2</sub> , HILIC-TiO <sub>2</sub> , and SCX-TiO <sub>2</sub> for global phosphoproteomics approaches. <b>2011</b> , 10, 3474-83	75
1999	Deep and highly sensitive proteome coverage by LC-MS/MS without prefractionation. <b>2011</b> , 10, M110.003699	264
1998	The fasted/fed mouse metabolic acetylome: N6-acetylation differences suggest acetylation coordinates organ-specific fuel switching. <b>2011</b> , 10, 4134-49	58
1997	GeLCMS for in-depth protein characterization and advanced analysis of proteomes. <b>2011</b> , 753, 143-55	31
1996	Proteome-wide mapping of the Drosophila acetylome demonstrates a high degree of conservation of lysine acetylation. <b>2011</b> , 4, ra48	204
1995	A case study on the comparison of different software tools for automated quantification of peptides. <b>2011</b> , 753, 373-98	14
1994	Proteome analysis of erythrocytes lacking AMP-activated protein kinase reveals a role of PAK2 kinase in eryptosis. <b>2011</b> , 10, 1690-7	77
1993	Lgr5 homologues associate with Wnt receptors and mediate R-spondin signalling. <b>2011</b> , 476, 293-7	903
1992	Quantitative proteomic analysis revealed lovastatin-induced perturbation of cellular pathways in HL-60 cells. <b>2011</b> , 10, 5463-71	11
1991	Relative quantification of the proteomic changes associated with the mycotoxin zearalenone in the H295R steroidogenesis model. <b>2011</b> , 58, 533-42	13
1990	System-wide temporal characterization of the proteome and phosphoproteome of human embryonic stem cell differentiation. <b>2011</b> , 4, rs3	347
1989	Bioinformatics and Database Searching. <b>2011</b> , 231-252	
1988	Uncovering ubiquitin and ubiquitin-like signaling networks. <b>2011</b> , 111, 7923-40	60
1987	Quantitative Mass Spectrometry-Based Proteomics. <b>2011</b> , 419-438	
1986	Bioinformatics for qualitative and quantitative proteomics. <b>2011</b> , 719, 331-49	3
1985	Deep proteome and transcriptome mapping of a human cancer cell line. <b>2011</b> , 7, 548	723
1984	SCFIA: a statistical corresponding feature identification algorithm for LC/MS. <b>2011</b> , 12, 439	6
1983	Disclosure of erlotinib as a multikinase inhibitor in pancreatic ductal adenocarcinoma. <b>2011</b> , 13, 1026-34	37

1982	Titanium dioxide enrichment of sialic acid-containing glycopeptides. <b>2011</b> , 753, 309-22	28
1981	SILACtor: software to enable dynamic SILAC studies. <b>2011</b> , 83, 8403-10	10
1980	Software for quantitative proteomic analysis using stable isotope labeling and data independent acquisition. <b>2011</b> , 83, 6971-9	12
1979	UNiquant, a program for quantitative proteomics analysis using stable isotope labeling. <b>2011</b> , 10, 1228-37	18
1978	Quantitative phosphoproteomics strategies for understanding protein kinase-mediated signal transduction pathways. <b>2011</b> , 8, 81-94	62
1977	Quantitative analysis of the intra- and inter-individual variability of the normal urinary proteome. <b>2011</b> , 10, 637-45	175
1976	Analysis of the resolution limitations of peptide identification algorithms. <b>2011</b> , 10, 5555-61	48
1975	Multidimensional strategy for sensitive phosphoproteomics incorporating protein prefractionation combined with SIMAC, HILIC, and TiO(2) chromatography applied to proximal EGF signaling. <b>2011</b> , 10, 5383-97	61
1974	Mass spectrometry-driven proteomics: an introduction. <b>2011</b> , 753, 1-27	4
1973	Universal and confident phosphorylation site localization using phosphoRS. <b>2011</b> , 10, 5354-62	564
1972	Quantitative proteome and phosphoproteome analysis of human pluripotent stem cells. <b>2011</b> , 767, 297-312	12
1971	Examining the mechanism of action of a kinesin inhibitor using stable isotope labeled inhibitors for cross-linking (SILIC). <b>2011</b> , 133, 12386-9	10
1970	Accurate proteome-wide protein quantification from high-resolution 15N mass spectra. <b>2011</b> , 12, R122	15
1969	Human Pluripotent Stem Cells. <b>2011</b> ,	3
1968	Mass spectrometry at the interface of proteomics and genomics. <b>2011</b> , 7, 284-91	33
1967	Amyloid-like aggregates sequester numerous metastable proteins with essential cellular functions. <b>2011</b> , 144, 67-78	520
1966	Regulation of mitochondrial protein import by cytosolic kinases. <b>2011</b> , 144, 227-39	186
1965	Systematic discovery of TLR signaling components delineates viral-sensing circuits. <b>2011</b> , 147, 853-67	148

1964	The catalytic activity of Ubp6 enhances maturation of the proteasomal regulatory particle. <b>2011</b> , 42, 637-49	60
1963	Quantitative proteomics reveals the basis for the biochemical specificity of the cell-cycle machinery. <b>2011</b> , 43, 406-17	101
1962	The oxidized thiol proteome in fission yeast--optimization of an ICAT-based method to identify H2O2-oxidized proteins. <b>2011</b> , 74, 2476-86	43
1961	Composition and topology of the endoplasmic reticulum-mitochondria encounter structure. <b>2011</b> , 413, 743-50	124
1960	Protein composition of the occlusion derived virus of Chrysodeixis chalcites nucleopolyhedrovirus. <b>2011</b> , 158, 1-7	12
1959	Extracting gene function from protein-protein interactions using Quantitative BAC InteraCtomics (QUBIC). <b>2011</b> , 53, 453-9	85
1958	Analyzing protein-protein interactions by quantitative mass spectrometry. <b>2011</b> , 54, 387-95	51
1957	Ion channels and their molecular environments--glimpses and insights from functional proteomics. <b>2011</b> , 22, 132-44	26
1956	MSSimulator: Simulation of mass spectrometry data. <b>2011</b> , 10, 2922-9	36
1955	Unraveling the dynamics of protein interactions with quantitative mass spectrometry. <b>2011</b> , 46, 216-28	18
1954	Evaluation of the deuterium isotope effect in zwitterionic hydrophilic interaction liquid chromatography separations for implementation in a quantitative proteomic approach. <b>2011</b> , 83, 8352-6	25
1953	A phospho-proteomic screen identifies substrates of the checkpoint kinase Chk1. <b>2011</b> , 12, R78	102
1952	Comparative proteomic analysis identifies a role for SUMO in protein quality control. <b>2011</b> , 4, rs4	136
1951	Spermidine and resveratrol induce autophagy by distinct pathways converging on the acetylproteome. <b>2011</b> , 192, 615-29	362
1950	High recovery FASP applied to the proteomic analysis of microdissected formalin fixed paraffin embedded cancer tissues retrieves known colon cancer markers. <b>2011</b> , 10, 3040-9	228
1949	Proteomics moves from expression to turnover: update and future perspective. <b>2011</b> , 8, 325-34	16
1948	Systems-wide proteomic analysis in mammalian cells reveals conserved, functional protein turnover. <b>2011</b> , 10, 5275-84	179
1947	Proteomic analysis of mouse oocytes reveals 28 candidate factors of the "reprogrammome". <b>2011</b> , 10, 2140-53	70

1946	Ultra-high-pressure RPLC hyphenated to an LTQ-Orbitrap Velos reveals a linear relation between peak capacity and number of identified peptides. <b>2011</b> , 83, 2699-704	114
1945	. <b>2011</b> ,	3
1944	Network-guided analysis of genes with altered somatic copy number and gene expression reveals pathways commonly perturbed in metastatic melanoma. <b>2011</b> , 6, e18369	40
1943	The host defense proteome of human and bovine milk. <b>2011</b> , 6, e19433	167
1942	Quantitative proteomic and interaction network analysis of cisplatin resistance in HeLa cells. <b>2011</b> , 6, e19892	30
1941	Quantitative proteomics identify novel miR-155 target proteins. <b>2011</b> , 6, e22146	26
1940	Quantitative phosphoproteomics of CXCL12 (SDF-1) signaling. <b>2011</b> , 6, e24918	34
1939	Quantitative proteomics reveals cellular targets of celastrol. <b>2011</b> , 6, e26634	42
1938	Proteogenomic analysis of polymorphisms and gene annotation divergences in prokaryotes using a clustered mass spectrometry-friendly database. <b>2011</b> , 10, M110.002527	46
1937	The kinesin KIF9 and reggie/flotillin proteins regulate matrix degradation by macrophage podosomes. <b>2011</b> , 22, 202-15	47
1936	Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC) An Introduction for Biologists. <b>2011</b> , 8, 2-16	3
1935	Proteomic analysis of palmitoylated platelet proteins. <b>2011</b> , 118, e62-73	90
1934	Proteomic snapshot of the EGF-induced ubiquitin network. <b>2011</b> , 7, 462	53
1933	Comparative proteomics and activity of a green sulfur bacterium through the water column of Lake Cadagno, Switzerland. <b>2011</b> , 13, 203-215	32
1932	Proteomics of extremophiles. <b>2011</b> , 13, 1934-55	16
1931	The genome and surface proteome of <i>Carnobacterium dalmaticum</i> reveal a key role of glycan foraging systems in host glycoproteins deglycosylation. <b>2011</b> , 81, 1050-60	38
1930	Phosphoproteomic analysis reveals an intrinsic pathway for the regulation of histone deacetylase 7 that controls the function of cytotoxic T lymphocytes. <b>2011</b> , 12, 352-61	83
1929	Combining quantitative proteomics data processing workflows for greater sensitivity. <b>2011</b> , 8, 481-3	16

1928	Use of stable isotope labeling by amino acids in cell culture as a spike-in standard in quantitative proteomics. <b>2011</b> , 6, 147-57	232
1927	Novel asymmetrically localizing components of human centrosomes identified by complementary proteomics methods. <b>2011</b> , 30, 1520-35	235
1926	SHARPIN forms a linear ubiquitin ligase complex regulating NF- $\kappa$ B activity and apoptosis. <b>2011</b> , 471, 637-41	526
1925	Acetylation-dependent regulation of endothelial Notch signalling by the SIRT1 deacetylase. <b>2011</b> , 473, 234-8	298
1924	Global quantification of mammalian gene expression control. <b>2011</b> , 473, 337-42	4063
1923	The dynamic state of protein turnover: It's about time. <b>2011</b> , 21, 293-303	102
1922	Driving biochemical discovery with quantitative proteomics. <b>2011</b> , 36, 170-7	10
1921	Filter-aided sample preparation with dimethyl labeling to identify and quantify milk fat globule membrane proteins. <b>2011</b> , 75, 34-43	91
1920	Building mitotic chromosomes. <b>2011</b> , 23, 114-21	31
1919	Proteomic biosignatures for monocyte-macrophage differentiation. <b>2011</b> , 271, 239-55	17
1918	Quantitative, high-resolution proteomics for data-driven systems biology. <b>2011</b> , 80, 273-99	550
1917	A proteome-wide, quantitative survey of in vivo ubiquitylation sites reveals widespread regulatory roles. <b>2011</b> , 10, M111.013284	644
1916	In vivo quantitative proteomics: the SILAC mouse. <b>2012</b> , 757, 435-50	69
1915	Stable-isotope labeling with amino acids in nematodes. <b>2011</b> , 8, 849-51	95
1914	[Proteomics and peptidomics in fundamental and applied medical studies]. <b>2011</b> , 37, 199-215	9
1913	Gel-Free Proteomics. <b>2011</b> ,	7
1912	Bioinformatics for Omics Data. <b>2011</b> ,	14
1911	In vivo and transcriptome-wide identification of RNA binding protein target sites. <b>2011</b> , 44, 828-40	124

1910	Large-scale phosphosite quantification in tissues by a spike-in SILAC method. <b>2011</b> , 8, 655-8	126
1909	Analysis of phosphoproteomics data. <b>2011</b> , 696, 41-57	11
1908	SILAC-based proteomic analysis to dissect the "histone modification signature" of human breast cancer cells. <b>2011</b> , 41, 387-99	64
1907	Functional analysis of proteins and protein species using shotgun proteomics and linear mathematics. <b>2011</b> , 41, 329-41	8
1906	Altered Mascot search results by changing the m/z range of MS/MS spectra: analysis and potential applications. <b>2011</b> , 400, 2339-47	2
1905	A novel two-stage tandem mass spectrometry approach and scoring scheme for the identification of O-GlcNAc modified peptides. <b>2011</b> , 22, 931-42	22
1904	Software lock mass by two-dimensional minimization of peptide mass errors. <b>2011</b> , 22, 1373-80	103
1903	In-depth analysis of the chicken egg white proteome using an LTQ Orbitrap Velos. <b>2011</b> , 9, 7	107
1902	Evaluating the potential of a novel oral lesion exudate collection method coupled with mass spectrometry-based proteomics for oral cancer biomarker discovery. <b>2011</b> , 8, 13	11
1901	Identification of a functional docking site in the Rpn1 LRR domain for the UBA-UBL domain protein Ddi1. <b>2011</b> , 9, 33	55
1900	Dynamic proteomic profiling of a unicellular cyanobacterium <i>Cyanothece</i> ATCC51142 across light-dark diurnal cycles. <b>2011</b> , 5, 194	34
1899	MRCQuant- an accurate LC-MS relative isotopic quantification algorithm on TOF instruments. <b>2011</b> , 12, 74	8
1898	High-throughput peptide quantification using mTRAQ reagent triplex. <b>2011</b> , 12 Suppl 1, S46	14
1897	Updated genome assembly and annotation of <i>Paenibacillus</i> larvae, the agent of American foulbrood disease of honey bees. <b>2011</b> , 12, 450	31
1896	Comparison of membrane proteins of <i>Mycobacterium tuberculosis</i> H37Rv and H37Ra strains. <b>2011</b> , 11, 18	58
1895	Catch me if you can: mass spectrometry-based phosphoproteomics and quantification strategies. <b>2011</b> , 11, 554-70	84
1894	Statistical issues in quality control of proteomic analyses: good experimental design and planning. <b>2011</b> , 11, 1037-48	42
1893	A posteriori quality control for the curation and reuse of public proteomics data. <b>2011</b> , 11, 2182-94	25

1892	Quantification of proteins using data-independent analysis (MSE) in simple and complex samples: a systematic evaluation. <b>2011</b> , 11, 3273-87	69
1891	ErbB2-associated changes in the lysosomal proteome. <b>2011</b> , 11, 2830-8	21
1890	Comparative evaluation of label-free SING normalized spectral index quantitation in the central proteomics facilities pipeline. <b>2011</b> , 11, 2790-7	100
1889	Current methodologies for proteomics of bacterial surface-exposed and cell envelope proteins. <b>2011</b> , 11, 3169-89	64
1888	Site-specific analysis of bacterial phosphoproteomes. <b>2011</b> , 11, 3002-11	39
1887	A proteomic view of mycobacteria. <b>2011</b> , 11, 3118-27	17
1886	AAK1 identified as an inhibitor of neuregulin-1/ErbB4-dependent neurotrophic factor signaling using integrative chemical genomics and proteomics. <b>2011</b> , 18, 891-906	26
1885	Comparison of ultrafiltration units for proteomic and N-glycoproteomic analysis by the filter-aided sample preparation method. <b>2011</b> , 410, 307-9	138
1884	Preventing arginine-to-proline conversion in a cell-line-independent manner during cell cultivation under stable isotope labeling by amino acids in cell culture (SILAC) conditions. <b>2011</b> , 412, 123-5	39
1883	Proteomics of human cerebrospinal fluid: discovery and verification of biomarker candidates in neurodegenerative diseases using quantitative proteomics. <b>2011</b> , 74, 371-88	107
1882	A quantitative view on Mycobacterium leprae antigens by proteomics. <b>2011</b> , 74, 1711-9	8
1881	A perturbed ubiquitin landscape distinguishes between ubiquitin in trafficking and in proteolysis. <b>2011</b> , 10, M111.009753	98
1880	Research resource: New and diverse substrates for the insulin receptor isoform A revealed by quantitative proteomics after stimulation with IGF-II or insulin. <b>2011</b> , 25, 1456-68	40
1879	Liquid chromatography-mass spectrometry-based proteomics of Nitrosomonas. <b>2011</b> , 486, 465-82	17
1878	Quantification of proteins and their modifications using QconCAT technology. <b>2011</b> , 500, 113-31	7
1877	Quantitative mass spectrometry of DENV-2 RNA-interacting proteins reveals that the DEAD-box RNA helicase DDX6 binds the DB1 and DB2 3' UTR structures. <b>2011</b> , 8, 1173-86	144
1876	Accurate quantification of more than 4000 mouse tissue proteins reveals minimal proteome changes during aging. <b>2011</b> , 10, M110.004523	101
1875	Improved Quantification of Labeled LC-MS. <b>2011</b> ,	1

1874	Quantitative shotgun proteomics using a uniform <sup>15</sup> N-labeled standard to monitor proteome dynamics in time course experiments reveals new insights into the heat stress response of <i>Chlamydomonas reinhardtii</i> . <b>2011</b> , 10, M110.004739	68
1873	Bioinformatics for Comparative Proteomics. <b>2011</b> ,	2
1872	aPKC phosphorylates NuMA-related LIN-5 to position the mitotic spindle during asymmetric division. <b>2011</b> , 13, 1132-8	55
1871	DeltAMT: a statistical algorithm for fast detection of protein modifications from LC-MS/MS data. <b>2011</b> , 10, M110.000455	30
1870	Phosphoproteomic profiling of the myocyte. <b>2011</b> , 4, 575	11
1869	Improved recovery and identification of membrane proteins from rat hepatic cells using a centrifugal proteomic reactor. <b>2011</b> , 10, O111.008425	29
1868	Proteomic profiling of a layered tissue reveals unique glycolytic specializations of photoreceptor cells. <b>2011</b> , 10, M110.002469	66
1867	Misfolded proteins impose a dosage-dependent fitness cost and trigger a cytosolic unfolded protein response in yeast. <b>2011</b> , 108, 680-5	202
1866	Broad activation of the ubiquitin-proteasome system by Parkin is critical for mitophagy. <b>2011</b> , 20, 1726-37	737
1865	The Plk1-dependent phosphoproteome of the early mitotic spindle. <b>2011</b> , 10, M110.004457	179
1864	Discovering mercury protein modifications in whole proteomes using natural isotope distributions observed in liquid chromatography-tandem mass spectrometry. <b>2011</b> , 10, M110.004853	14
1863	The cellular protein tyrosine kinase interacts with HIV-1 Gag. <b>2011</b> , 85, 13322-32	19
1862	Mass spectrometric analysis of lysine ubiquitylation reveals promiscuity at site level. <b>2011</b> , 10, M110.003590	241
1861	GProX, a user-friendly platform for bioinformatics analysis and visualization of quantitative proteomics data. <b>2011</b> , 10, O110.007450	121
1860	Quantitative proteomics and dynamic imaging of the nucleolus reveal distinct responses to UV and ionizing radiation. <b>2011</b> , 10, M111.009241	90
1859	A QUICK screen for Lrrk2 interaction partners--leucine-rich repeat kinase 2 is involved in actin cytoskeleton dynamics. <b>2011</b> , 10, M110.001172	94
1858	A screen for novel phosphoinositide 3-kinase effector proteins. <b>2011</b> , 10, M110.003178	25
1857	Wobble base-pairing slows in vivo translation elongation in metazoans. <b>2011</b> , 17, 2063-73	138



1856	libfbi: a C++ implementation for fast box intersection and application to sparse mass spectrometry data. <b>2011</b> , 27, 1166-7	4
1855	Microproteomics: quantitative proteomic profiling of small numbers of laser-captured cells. <b>2011</b> , 2011, pdb.prot5573	24
1854	Proteomic characterization of plasma membrane-proximal T cell activation responses. <b>2011</b> , 286, 4072-80	19
1853	Multivalent binding of formin-binding protein 21 (FBP21)-tandem-WW domains fosters protein recognition in the pre-spliceosome. <b>2011</b> , 286, 38478-38487	18
1852	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. <b>2011</b> , 10, M110.000679	50
1851	Confident phosphorylation site localization using the Mascot Delta Score. <b>2011</b> , 10, M110.003830	225
1850	Quantitative proteomic analysis of cellular protein modulation upon inhibition of the NEDD8-activating enzyme by MLN4924. <b>2011</b> , 10, M111.009183	54
1849	Enhanced information output from shotgun proteomics data by protein quantification and peptide quality control (PQPQ). <b>2011</b> , 10, M111.010264	24
1848	Large-scale de novo prediction of physical protein-protein association. <b>2011</b> , 10, M111.010629	42
1847	Global phosphoproteome profiling reveals unanticipated networks responsive to cisplatin treatment of embryonic stem cells. <b>2011</b> , 31, 4964-77	49
1846	A role for SUMOylation in snoRNP biogenesis revealed by quantitative proteomics. <b>2011</b> , 2, 30-37	20
1845	Mitotic substrates of the kinase aurora with roles in chromatin regulation identified through quantitative phosphoproteomics of fission yeast. <b>2011</b> , 4, rs6	90
1844	Large scale phosphoproteome profiles comprehensive features of mouse embryonic stem cells. <b>2011</b> , 10, M110.001750	25
1843	Chromatin affinity purification and quantitative mass spectrometry defining the interactome of histone modification patterns. <b>2011</b> , 10, M110.005371	66
1842	Quantitative proteomic analysis of chromatin reveals that Ctf18 acts in the DNA replication checkpoint. <b>2011</b> , 10, M110.005561	53
1841	The steady-state repertoire of human SCF ubiquitin ligase complexes does not require ongoing Nedd8 conjugation. <b>2011</b> , 10, M110.006460	50
1840	Extending SILAC to proteomics of plant cell lines. <b>2011</b> , 23, 1701-5	40
1839	Methods for Biomarker Verification and Assay Development. <b>2011</b> , 8, 138-152	3

1838	Multiple molecular architectures of the eye lens chaperone <b>B</b> -crystallin elucidated by a triple hybrid approach. <b>2011</b> , 108, 20491-6	118
1837	Beta1 integrin cytoplasmic tyrosines promote skin tumorigenesis independent of their phosphorylation. <b>2011</b> , 108, 15213-8	28
1836	Protein interactions of phosphatase and tensin homologue (PTEN) and its cancer-associated G20E mutant compared by using stable isotope labeling by amino acids in cell culture-based parallel affinity purification. <b>2011</b> , 286, 18093-103	22
1835	Complement receptor Mac-1 is an adaptor for NB1 (CD177)-mediated PR3-ANCA neutrophil activation. <b>2011</b> , 286, 7070-81	61
1834	The astrin-kinastrin/SKAP complex localizes to microtubule plus ends and facilitates chromosome alignment. <b>2011</b> , 192, 959-68	82
1833	iTRAQ protein profile analysis of Arabidopsis roots reveals new aspects critical for iron homeostasis. <b>2011</b> , 155, 821-34	177
1832	De novo assembly and validation of planaria transcriptome by massive parallel sequencing and shotgun proteomics. <b>2011</b> , 21, 1193-200	90
1831	Proteomics unravels the exportability of mitochondrial respiratory chains. <b>2011</b> , 8, 231-9	47
1830	Digitoxin-induced cytotoxicity in cancer cells is mediated through distinct kinase and interferon signaling networks. <b>2011</b> , 10, 2083-93	69
1829	General overview: biomarkers in neuroscience research. <b>2011</b> , 101, 1-17	26
1828	Genome-wide characterization of miR-34a induced changes in protein and mRNA expression by a combined pulsed SILAC and microarray analysis. <b>2011</b> , 10, M111.010462	158
1827	Assigning spectrum-specific P-values to protein identifications by mass spectrometry. <b>2011</b> , 27, 1128-34	27
1826	Computational mass spectrometry-based proteomics. <b>2011</b> , 7, e1002277	47
1825	Protein kinase C and NF- $\kappa$ B-dependent CD4 downregulation in macrophages induced by T cell-derived soluble factors: consequences for HIV-1 infection. <b>2011</b> , 187, 748-59	10
1824	The mitochondrial contact site complex, a determinant of mitochondrial architecture. <b>2011</b> , 30, 4356-70	315
1823	Mass spectrometric-based quantitative proteomics using SILAC. <b>2011</b> , 500, 133-50	20
1822	SIMA: simultaneous multiple alignment of LC/MS peak lists. <b>2011</b> , 27, 987-93	24
1821	Quantitative in vivo analyses reveal calcium-dependent phosphorylation sites and identifies a novel component of the Toxoplasma invasion motor complex. <b>2011</b> , 7, e1002222	74

1820	The salivary secretome of the tsetse fly <i>Glossina pallidipes</i> (Diptera: Glossinidae) infected by salivary gland hypertrophy virus. <b>2011</b> , 5, e1371	21
1819	Elevated proteasome capacity extends replicative lifespan in <i>Saccharomyces cerevisiae</i> . <b>2011</b> , 7, e1002253	167
1818	Identification of increased amounts of eppin protein complex components in sperm cells of diabetic and obese individuals by difference gel electrophoresis. <b>2011</b> , 10, M110.007187	32
1817	Phosphosignature predicts dasatinib response in non-small cell lung cancer. <b>2012</b> , 11, 651-68	80
1816	Dicer-dependent and -independent Argonaute2 protein interaction networks in mammalian cells. <b>2012</b> , 11, 1442-56	43
1815	Proteome-wide analysis of disease-associated SNPs that show allele-specific transcription factor binding. <b>2012</b> , 8, e1002982	74
1814	BPDA2d--a 2D global optimization-based Bayesian peptide detection algorithm for liquid chromatograph-mass spectrometry. <b>2012</b> , 28, 564-72	7
1813	CYK4 inhibits Rac1-dependent PAK1 and ARHGEF7 effector pathways during cytokinesis. <b>2012</b> , 198, 865-80	83
1812	Protein interaction profiling of the p97 adaptor UBXD1 points to a role for the complex in modulating ERGIC-53 trafficking. <b>2012</b> , 11, M111.016444	21
1811	Platform-independent and label-free quantitation of proteomic data using MS1 extracted ion chromatograms in skyline: application to protein acetylation and phosphorylation. <b>2012</b> , 11, 202-14	328
1810	Hyperplexing: a method for higher-order multiplexed quantitative proteomics provides a map of the dynamic response to rapamycin in yeast. <b>2012</b> , 5, rs2	116
1809	Labeling and identification of direct kinase substrates. <b>2012</b> , 5, pl3	10
1808	Quantitative proteomics reveals that Hsp90 inhibition preferentially targets kinases and the DNA damage response. <b>2012</b> , 11, M111.014654	77
1807	Proteomic cornerstones of hematopoietic stem cell differentiation: distinct signatures of multipotent progenitors and myeloid committed cells. <b>2012</b> , 11, 286-302	52
1806	$\alpha$ 1 integrin NPXY motifs regulate kidney collecting-duct development and maintenance by induced-fit interactions with cytosolic proteins. <b>2012</b> , 32, 4080-91	8
1805	Novel NEDD1 phosphorylation sites regulate $\beta$ -tubulin binding and mitotic spindle assembly. <b>2012</b> , 125, 3745-51	29
1804	A crucial role for Mim2 in the biogenesis of mitochondrial outer membrane proteins. <b>2012</b> , 125, 3464-73	60
1803	Quantitative proteomics profiling of murine mammary gland cells unravels impact of annexin-1 on DNA damage response, cell adhesion, and migration. <b>2012</b> , 11, 381-93	35

1802	Analysis of high accuracy, quantitative proteomics data in the MaxQB database. <b>2012</b> , 11, M111.014068	116
1801	Nucleolar protein trafficking in response to HIV-1 Tat: rewiring the nucleolus. <b>2012</b> , 7, e48702	43
1800	Systematic identification of the HSP90 candidate regulated proteome. <b>2012</b> , 11, M111.016675	72
1799	File formats commonly used in mass spectrometry proteomics. <b>2012</b> , 11, 1612-21	66
1798	Novel roles of <i>Caenorhabditis elegans</i> heterochromatin protein HP1 and linker histone in the regulation of innate immune gene expression. <b>2012</b> , 32, 251-65	28
1797	Proteomic portrait of human breast cancer progression identifies novel prognostic markers. <b>2012</b> , 72, 2428-39	107
1796	An essential novel component of the noncanonical mitochondrial outer membrane protein import system of trypanosomatids. <b>2012</b> , 23, 3420-8	22
1795	A quantitative spatial proteomics analysis of proteome turnover in human cells. <b>2012</b> , 11, M111.011429	270
1794	On marathons and Sprints: an integrated quantitative proteomics and transcriptomics analysis of differences between slow and fast muscle fibers. <b>2012</b> , 11, M111.010801	65
1793	RNA ligase RtcB splices 3'-phosphate and 5'-OH ends via covalent RtcB-(histidiny)-GMP and polynucleotide-(3')pp(5')G intermediates. <b>2012</b> , 109, 6072-7	66
1792	Quantitative acetylome analysis reveals the roles of SIRT1 in regulating diverse substrates and cellular pathways. <b>2012</b> , 11, 1048-62	151
1791	Quantitative proteomics reveals regulation of karyopherin subunit alpha-2 (KPNA2) and its potential novel cargo proteins in nonsmall cell lung cancer. <b>2012</b> , 11, 1105-22	60
1790	RUNX3 interactome reveals novel centrosomal targeting of RUNX family of transcription factors. <b>2012</b> , 11, 1938-47	16
1789	The mitosis and neurodevelopment proteins NDE1 and NDEL1 form dimers, tetramers, and polymers with a folded back structure in solution. <b>2012</b> , 287, 32381-93	26
1788	MINOS1 is a conserved component of mitofilin complexes and required for mitochondrial function and cristae organization. <b>2012</b> , 23, 247-57	141
1787	Extending the dynamic range of label-free mass spectrometric quantification of affinity purifications. <b>2012</b> , 11, M111.007955	39
1786	PDK1 regulation of mTOR and hypoxia-inducible factor 1 integrate metabolism and migration of CD8+ T cells. <b>2012</b> , 209, 2441-53	389
1785	Mgr2 promotes coupling of the mitochondrial presequence translocase to partner complexes. <b>2012</b> , 197, 595-604	67

1784	H2A.Z.2.2 is an alternatively spliced histone H2A.Z variant that causes severe nucleosome destabilization. <b>2012</b> , 40, 5951-64	71
1783	Multivariate proteomic profiling identifies novel accessory proteins of coated vesicles. <b>2012</b> , 197, 141-60	123
1782	The CHR promoter element controls cell cycle-dependent gene transcription and binds the DREAM and MMB complexes. <b>2012</b> , 40, 1561-78	72
1781	Characterization of MRFAP1 turnover and interactions downstream of the NEDD8 pathway. <b>2012</b> , 11, M111.014407	18
1780	Coupled activation and degradation of eEF2K regulates protein synthesis in response to genotoxic stress. <b>2012</b> , 5, ra40	68
1779	Systematic analysis of protein pools, isoforms, and modifications affecting turnover and subcellular localization. <b>2012</b> , 11, M111.013680	45
1778	High performance phosphorylation site assignment algorithm for mass spectrometry data using multicore systems. <b>2012</b> ,	2
1777	Proteomic analyses reveal divergent ubiquitylation site patterns in murine tissues. <b>2012</b> , 11, 1578-85	214
1776	Mitochondrial nucleoid interacting proteins support mitochondrial protein synthesis. <b>2012</b> , 40, 6109-21	139
1775	An Efficient Dynamic Programming Algorithm for Phosphorylation Site Assignment of Large-Scale Mass Spectrometry Data. <b>2012</b> , 618-625	13
1774	Complementary proteome and transcriptome profiling in phosphate-deficient Arabidopsis roots reveals multiple levels of gene regulation. <b>2012</b> , 11, 1156-66	180
1773	Localization of the proteasomal ubiquitin receptors Rpn10 and Rpn13 by electron cryomicroscopy. <b>2012</b> , 109, 1479-84	93
1772	RNA binding proteins accumulate at the postsynaptic density with synaptic activity. <b>2012</b> , 32, 599-609	44
1771	Dynein light chain 1 and a spindle-associated adaptor promote dynein asymmetry and spindle orientation. <b>2012</b> , 198, 1039-54	65
1770	The Ph1 locus suppresses Cdk2-type activity during premeiosis and meiosis in wheat. <b>2012</b> , 24, 152-62	82
1769	System response of metabolic networks in Chlamydomonas reinhardtii to total available ammonium. <b>2012</b> , 11, 973-88	78
1768	Distinct energy metabolism of auditory and vestibular sensory epithelia revealed by quantitative mass spectrometry using MS2 intensity. <b>2012</b> , 109, E268-77	24
1767	Global quantitative phosphoproteome analysis of human tumor xenografts treated with a CD44 antagonist. <b>2012</b> , 72, 4329-39	29

1766	Cross-talk between phosphorylation and lysine acetylation in a genome-reduced bacterium. <b>2012</b> , 8, 571	144
1765	Quantitative proteomics targeting classes of motif-containing peptides using immunoaffinity-based mass spectrometry. <b>2012</b> , 11, 342-54	20
1764	Novel murine dendritic cell lines: a powerful auxiliary tool for dendritic cell research. <b>2012</b> , 3, 331	72
1763	Global detection of protein kinase D-dependent phosphorylation events in nocodazole-treated human cells. <b>2012</b> , 11, 160-70	60
1762	Quantitative mass spectrometry and PAR-CLIP to identify RNA-protein interactions. <b>2012</b> , 40, 9897-902	36
1761	Misacylation of tRNA with methionine in <i>Saccharomyces cerevisiae</i> . <b>2012</b> , 40, 10494-506	61
1760	AIRE-PHD fingers are structural hubs to maintain the integrity of chromatin-associated interactome. <b>2012</b> , 40, 11756-68	30
1759	Phosphoproteome of <i>Pristionchus pacificus</i> provides insights into architecture of signaling networks in nematode models. <b>2012</b> , 11, 1631-9	11
1758	Novel proteomic tools reveal essential roles of SRP and importance of proper membrane protein biogenesis. <b>2012</b> , 11, M111.011585	12
1757	System-wide perturbation analysis with nearly complete coverage of the yeast proteome by single-shot ultra HPLC runs on a bench top Orbitrap. <b>2012</b> , 11, M111.013722	313
1756	5-Aza-2'-deoxycytidine induced growth inhibition of leukemia cells through modulating endogenous cholesterol biosynthesis. <b>2012</b> , 11, M111.016915	21
1755	Precision, proteome coverage, and dynamic range of <i>Arabidopsis</i> proteome profiling using (15)N metabolic labeling and label-free approaches. <b>2012</b> , 11, 619-28	15
1754	Combination of chemical genetics and phosphoproteomics for kinase signaling analysis enables confident identification of cellular downstream targets. <b>2012</b> , 11, O111.012351	47
1753	Sam50 functions in mitochondrial intermembrane space bridging and biogenesis of respiratory complexes. <b>2012</b> , 32, 1173-88	131
1752	PEAKS DB: de novo sequencing assisted database search for sensitive and accurate peptide identification. <b>2012</b> , 11, M111.010587	612
1751	A framework for intelligent data acquisition and real-time database searching for shotgun proteomics. <b>2012</b> , 11, M111.013185	40
1750	Identification of autophagosome-associated proteins and regulators by quantitative proteomic analysis and genetic screens. <b>2012</b> , 11, M111.014035	99
1749	Proteome-wide analysis of lysine acetylation suggests its broad regulatory scope in <i>Saccharomyces cerevisiae</i> . <b>2012</b> , 11, 1510-22	200

1748	A Protein Epitope Signature Tag (PrEST) library allows SILAC-based absolute quantification and multiplexed determination of protein copy numbers in cell lines. <b>2012</b> , 11, O111.009613	116
1747	Liquid Chromatography and Mass Spectrometry (LC-MS) Based Strategies for Quantitative Phosphoproteomics. <b>2012</b> , 8, 3-21	5
1746	Mitotic chromosomes are compacted laterally by KIF4 and condensin and axially by topoisomerase IIβ <b>2012</b> , 199, 755-70	118
1745	An insight into iTRAQ: where do we stand now?. <b>2012</b> , 404, 1011-27	247
1744	TBC1D13 is a RAB35 specific GAP that plays an important role in GLUT4 trafficking in adipocytes. <b>2012</b> , 13, 1429-41	32
1743	Detection and quantitation of SUMO chains by mass spectrometry. <b>2012</b> , 832, 239-47	8
1742	Proteomic evaluation of inflammatory proteins in rat spleen interstitial fluid and lymph during LPS-induced systemic inflammation reveals increased levels of ADAMST1. <b>2012</b> , 11, 5338-49	27
1741	Multimodel pathway enrichment methods for functional evaluation of expression regulation. <b>2012</b> , 11, 2955-67	2
1740	A high-throughput approach for measuring temporal changes in the interactome. <b>2012</b> , 9, 907-9	236
1739	Quantitative proteomic analysis of mouse embryonic fibroblasts and induced pluripotent stem cells using 16O/18O labeling. <b>2012</b> , 11, 2091-102	9
1738	Consecutive proteolytic digestion in an enzyme reactor increases depth of proteomic and phosphoproteomic analysis. <b>2012</b> , 84, 2631-7	229
1737	Mediator phosphorylation prevents stress response transcription during non-stress conditions. <b>2012</b> , 287, 44017-26	26
1736	Loss of perivascular adipose tissue on peroxisome proliferator-activated receptor-γ deletion in smooth muscle cells impairs intravascular thermoregulation and enhances atherosclerosis. <b>2012</b> , 126, 1067-78	227
1735	Extensive quantitative remodeling of the proteome between normal colon tissue and adenocarcinoma. <b>2012</b> , 8, 611	174
1734	Expert system for computer-assisted annotation of MS/MS spectra. <b>2012</b> , 11, 1500-9	53
1733	MITRAC links mitochondrial protein translocation to respiratory-chain assembly and translational regulation. <b>2012</b> , 151, 1528-41	141
1732	Proteomic analysis of stem cell differentiation and early development. <b>2012</b> , 4,	19
1731	Proteome turnover in the green alga <i>Ostreococcus tauri</i> by time course 15N metabolic labeling mass spectrometry. <b>2012</b> , 11, 476-86	49

1730	A universally conserved ATPase regulates the oxidative stress response in Escherichia coli. <b>2012</b> , 287, 43585-98	23
1729	Current methods for global proteome identification. <b>2012</b> , 9, 519-32	41
1728	Characterization of novel components of the baculovirus per os infectivity factor complex. <b>2012</b> , 86, 4981-8	58
1727	Urinary secretion and extracellular aggregation of mutant uromodulin isoforms. <b>2012</b> , 81, 769-78	14
1726	Complementary workflow for global phosphoproteome analysis. <b>2012</b> , 33, 3291-8	10
1725	SILAC-based proteomic analysis to investigate the impact of amyloid precursor protein expression in neuronal-like B103 cells. <b>2012</b> , 33, 3728-37	14
1724	LFQuant: a label-free fast quantitative analysis tool for high-resolution LC-MS/MS proteomics data. <b>2012</b> , 12, 3475-84	23
1723	Proteome-wide analysis of temporal phosphorylation dynamics in lysophosphatidic acid-induced signaling. <b>2012</b> , 12, 3485-98	8
1722	Enhanced N-glycosylation site exploitation of sialoglycopeptides by peptide IPG-IEF assisted TiO2 chromatography. <b>2012</b> , 29, 433-43	11
1721	Proteomics pipeline for biomarker discovery of laser capture microdissected breast cancer tissue. <b>2012</b> , 17, 155-64	68
1720	Protein group modification and synergy in the SUMO pathway as exemplified in DNA repair. <b>2012</b> , 151, 807-820	331
1719	Analysis of protein palmitoylation reveals a pervasive role in Plasmodium development and pathogenesis. <b>2012</b> , 12, 246-58	148
1718	Data extraction from proteomics raw data: an evaluation of nine tandem MS tools using a large Orbitrap data set. <b>2012</b> , 75, 5293-303	16
1717	Comparison and applications of label-free absolute proteome quantification methods on Escherichia coli. <b>2012</b> , 75, 5437-48	126
1716	Quantitative proteomic analysis reveals protein expression changes in the murine neuronal secretome during apoptosis. <b>2012</b> , 77, 394-405	14
1715	Quantitative proteomics reveals novel functions of osteoclast-associated receptor in STAT signaling and cell adhesion in human endothelial cells. <b>2012</b> , 53, 829-37	15
1714	Quantitative proteomic analysis of yeast DNA replication proteins. <b>2012</b> , 57, 196-202	16
1713	De novo correction of mass measurement error in low resolution tandem MS spectra for shotgun proteomics. <b>2012</b> , 23, 2075-82	9



1712	Quantitative proteome profiling of normal human circulating microparticles. <b>2012</b> , 11, 2154-63	45
1711	From quantitative protein complex analysis to disease mechanism. <b>2012</b> , 75, 108-11	2
1710	A software toolkit and interface for performing stable isotope labeling and top3 quantification using Progenesis LC-MS. <b>2012</b> , 16, 489-95	35
1709	Find pairs: the module for protein quantification of the PeakQuant software suite. <b>2012</b> , 16, 457-67	1
1708	An SILAC quantification algorithm for LC-FTMS. <b>2012</b> ,	
1707	Self-hydroxylation of the splicing factor lysyl hydroxylase, JMJD6. <b>2012</b> , 3, 80-85	15
1706	DVC1 (C1orf124) is a DNA damage-targeting p97 adaptor that promotes ubiquitin-dependent responses to replication blocks. <b>2012</b> , 19, 1084-92	135
1705	Annotator: postprocessing software for generating function-based signatures from quantitative mass spectrometry. <b>2012</b> , 11, 1521-36	1
1704	Comparative and targeted proteomic analyses of urinary microparticles from bladder cancer and hernia patients. <b>2012</b> , 11, 5611-29	150
1703	Global mapping of protein phosphorylation events identifies Ste20, Sch9 and the cell-cycle regulatory kinases Cdc28/Pho85 as mediators of fatty acid starvation responses in <i>Saccharomyces cerevisiae</i> . <b>2012</b> , 8, 796-803	9
1702	The ubiquitin E1 enzyme Ube1 mediates NEDD8 activation under diverse stress conditions. <b>2012</b> , 11, 1142-50	88
1701	Effects of the miR-143/-145 microRNA cluster on the colon cancer proteome and transcriptome. <b>2012</b> , 11, 4744-54	38
1700	Cloud CFP: a shotgun proteomics data analysis pipeline using cloud and high performance computing. <b>2012</b> , 11, 6282-90	44
1699	Spiked-in pulsed in vivo labeling identifies a new member of the CCN family in regenerating newt hearts. <b>2012</b> , 11, 4693-704	27
1698	Re-fraction: a machine learning approach for deterministic identification of protein homologues and splice variants in large-scale MS-based proteomics. <b>2012</b> , 11, 3035-45	6
1697	Global snapshot of the influence of endocytosis upon EGF receptor signaling output. <b>2012</b> , 11, 5157-66	15
1696	Combinatorial use of electrostatic repulsion-hydrophilic interaction chromatography (ERLIC) and strong cation exchange (SCX) chromatography for in-depth phosphoproteome analysis. <b>2012</b> , 11, 4269-76	32
1695	Correction to Feasibility of Large-Scale Phosphoproteomics with Higher Energy Collisional Dissociation Fragmentation. <b>2012</b> , 11, 3506-3508	10

1694	Evaluation of database search programs for accurate detection of neuropeptides in tandem mass spectrometry experiments. <b>2012</b> , 11, 6044-55	12
1693	Identification of core components and transient interactors of the peroxisomal importomer by dual-track stable isotope labeling with amino acids in cell culture analysis. <b>2012</b> , 11, 2567-80	41
1692	Use of stable isotope dimethyl labeling coupled to selected reaction monitoring to enhance throughput by multiplexing relative quantitation of targeted proteins. <b>2012</b> , 84, 4999-5006	14
1691	C-terminal heat shock protein 90 inhibitor decreases hyperglycemia-induced oxidative stress and improves mitochondrial bioenergetics in sensory neurons. <b>2012</b> , 11, 2581-93	44
1690	Quantitative proteomic analysis revealed 4-(methylnitrosamino)-1-(3-pyridinyl)-1-butanone-induced up-regulation of 20S proteasome in cultured human fibroblast cells. <b>2012</b> , 11, 2347-54	3
1689	Global analysis of phosphoproteome regulation by the Ser/Thr phosphatase Ppt1 in <i>Saccharomyces cerevisiae</i> . <b>2012</b> , 11, 2397-408	21
1688	Cnn1 inhibits the interactions between the KMN complexes of the yeast kinetochore. <b>2012</b> , 14, 614-24	79
1687	Proteomic study of the mucin granulae in an intestinal goblet cell model. <b>2012</b> , 11, 1879-90	23
1686	SIMPATIQCO: a server-based software suite which facilitates monitoring the time course of LC-MS performance metrics on Orbitrap instruments. <b>2012</b> , 11, 5540-7	43
1685	Comparative proteomic analysis of eleven common cell lines reveals ubiquitous but varying expression of most proteins. <b>2012</b> , 11, M111.014050	566
1684	BuildSummary: using a group-based approach to improve the sensitivity of peptide/protein identification in shotgun proteomics. <b>2012</b> , 11, 1494-502	42
1683	Reduction in database search space by utilization of amino acid composition information from electron transfer dissociation and higher-energy collisional dissociation mass spectra. <b>2012</b> , 84, 6638-45	13
1682	The problem with peptide presumption and the downfall of target-decoy false discovery rates. <b>2012</b> , 84, 9663-7	10
1681	Triple SILAC to determine stimulus specific interactions in the Wnt pathway. <b>2012</b> , 11, 982-94	56
1680	A review of current proteomics technologies with a survey on their widespread use in reproductive biology investigations. <b>2012</b> , 77, 738-765.e52	59
1679	Reorganized PKA-AKAP associations in the failing human heart. <b>2012</b> , 52, 511-8	59
1678	Parasites, proteomes and systems: has Descartes' clock run out of time?. <b>2012</b> , 139, 1103-18	19
1677	iTRAQ labeling is superior to mTRAQ for quantitative global proteomics and phosphoproteomics. <b>2012</b> , 11, M111.014423	140

1676	Quantitative phosphoproteome profiling of iron-deficient Arabidopsis roots. <b>2012</b> , 159, 403-17	65
1675	Computational approaches for analyzing information flow in biological networks. <b>2012</b> , 5, re1	134
1674	Stable isotope labeling with amino acids in cell culture (SILAC)-based quantitative proteomics study of a thyroid hormone-regulated secretome in human hepatoma cells. <b>2012</b> , 11, M111.011270	27
1673	Identifying cellular targets of small-molecule probes and drugs with biochemical enrichment and SILAC. <b>2012</b> , 803, 129-40	24
1672	Proteomic analysis of mitotic RNA polymerase II reveals novel interactors and association with proteins dysfunctional in disease. <b>2012</b> , 11, M111.011767	9
1671	Analysis of seminal plasma from patients with non-obstructive azoospermia and identification of candidate biomarkers of male infertility. <b>2012</b> , 11, 1503-11	57
1670	Selective enrichment of newly synthesized proteins for quantitative secretome analysis. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 984-90	44.5 184
1669	Quantitative mass spectrometry-based proteomics: an overview. <b>2012</b> , 893, 85-100	59
1668	In vivo quantitative proteome profiling: planning and evaluation of SILAC experiments. <b>2012</b> , 893, 175-99	14
1667	A systematic investigation into the nature of tryptic HCD spectra. <b>2012</b> , 11, 5479-91	85
1666	Systems-wide analysis of ubiquitylation dynamics reveals a key role for PAF15 ubiquitylation in DNA-damage bypass. <b>2012</b> , 14, 1089-98	195
1665	Optimized fast and sensitive acquisition methods for shotgun proteomics on a quadrupole orbitrap mass spectrometer. <b>2012</b> , 11, 3487-97	221
1664	Research resource: identification of novel growth hormone-regulated phosphorylation sites by quantitative phosphoproteomics. <b>2012</b> , 26, 1056-73	8
1663	SAINT-MS1: protein-protein interaction scoring using label-free intensity data in affinity purification-mass spectrometry experiments. <b>2012</b> , 11, 2619-24	51
1662	Methods for quantification of in vivo changes in protein ubiquitination following proteasome and deubiquitinase inhibition. <b>2012</b> , 11, 148-59	127
1661	Temporal profiling and pulsed SILAC labeling identify novel secreted proteins during ex vivo osteoblast differentiation of human stromal stem cells. <b>2012</b> , 11, 989-1007	64
1660	Important issues in planning a proteomics experiment: statistical considerations of quantitative proteomic data. <b>2012</b> , 893, 3-21	9
1659	Proteomic investigations reveal a role for RNA processing factor THRAP3 in the DNA damage response. <b>2012</b> , 46, 212-25	239

1658	Mapping N-glycosylation sites across seven evolutionarily distant species reveals a divergent substrate proteome despite a common core machinery. <b>2012</b> , 46, 542-8	199
1657	The mRNA-bound proteome and its global occupancy profile on protein-coding transcripts. <b>2012</b> , 46, 674-90	833
1656	Mapping in vivo signal transduction defects by phosphoproteomics. <b>2012</b> , 18, 43-51	33
1655	Phosphotyrosine mediated protein interactions of the discoidin domain receptor 1. <b>2012</b> , 75, 3465-77	53
1654	Proteomic analysis of a multi-resistant clinical Escherichia coli isolate of unknown genomic background. <b>2012</b> , 75, 1830-7	12
1653	Proteomics in chromatin biology and epigenetics: Elucidation of post-translational modifications of histone proteins by mass spectrometry. <b>2012</b> , 75, 3419-33	105
1652	Detecting outlier peptides in quantitative high-throughput mass spectrometry data. <b>2012</b> , 75, 3230-9	5
1651	Quantitative proteomic analysis of human osteoblast-like MG-63 cells in response to bioinert implant material titanium and polyetheretherketone. <b>2012</b> , 75, 3560-73	38
1650	Mass spectrometry and animal science: protein identification strategies and particularities of farm animal species. <b>2012</b> , 75, 4190-206	55
1649	Effective correction of experimental errors in quantitative proteomics using stable isotope labeling by amino acids in cell culture (SILAC). <b>2012</b> , 75, 3720-32	47
1648	Targeted proteome investigation via selected reaction monitoring mass spectrometry. <b>2012</b> , 75, 3495-513	52
1647	Comprehensive profiling of proteome changes upon sequential deletion of deubiquitylating enzymes. <b>2012</b> , 75, 3886-97	17
1646	Functional repurposing revealed by comparing S. pombe and S. cerevisiae genetic interactions. <b>2012</b> , 149, 1339-52	122
1645	Label-free mass spectrometry-based proteomics for biomarker discovery and validation. <b>2012</b> , 12, 343-59	42
1644	Selectivity, cocrystal structures, and neuroprotective properties of leucettines, a family of protein kinase inhibitors derived from the marine sponge alkaloid leucettamine B. <b>2012</b> , 55, 9312-30	146
1643	Quantitative proteomics of Trypanosoma cruzi during metacyclogenesis. <b>2012</b> , 12, 2694-703	59
1642	The 15N isotope effect in Escherichia coli: a neutron can make the difference. <b>2012</b> , 12, 3121-8	23
1641	Proteome dynamics and early salt stress response of the photosynthetic organism Chlamydomonas reinhardtii. <b>2012</b> , 13, 215	66

1640	Proteome remodelling during development from blood to insect-form <i>Trypanosoma brucei</i> quantified by SILAC and mass spectrometry. <b>2012</b> , 13, 556	92
1639	In-depth proteomic analysis of a mollusc shell: acid-soluble and acid-insoluble matrix of the limpet <i>Lottia gigantea</i> . <b>2012</b> , 10, 28	64
1638	Proteomics wants cRacker: automated standardized data analysis of LC-MS derived proteomic data. <b>2012</b> , 11, 5548-55	28
1637	Highly coordinated proteome dynamics during reprogramming of somatic cells to pluripotency. <b>2012</b> , 2, 1579-92	183
1636	SPEECHLESS integrates brassinosteroid and stomata signalling pathways. <b>2012</b> , 14, 548-54	218
1635	Mutant p53 interactome identifies nardilysin as a p53R273H-specific binding partner that promotes invasion. <b>2012</b> , 13, 638-44	55
1634	Super-SILAC allows classification of diffuse large B-cell lymphoma subtypes by their protein expression profiles. <b>2012</b> , 11, 77-89	135
1633	Identification of glucose kinase-dependent and -independent pathways for carbon control of primary metabolism, development and antibiotic production in <i>Streptomyces coelicolor</i> by quantitative proteomics. <b>2012</b> , 86, 1490-507	41
1632	Lysine methylation of VCP by a member of a novel human protein methyltransferase family. <b>2012</b> , 3, 1038	93
1631	The protein composition of the digestive fluid from the venus flytrap sheds light on prey digestion mechanisms. <b>2012</b> , 11, 1306-19	63
1630	Proteomics-based identification of low-abundance signaling and regulatory protein complexes in native plant tissues. <b>2012</b> , 7, 2144-58	68
1629	Analyzing protein-protein interactions from affinity purification-mass spectrometry data with SAINT. <b>2012</b> , Chapter 8, Unit8.15	90
1628	ZIC-CHILIC as a fractionation method for sensitive and powerful shotgun proteomics. <b>2012</b> , 7, 2041-55	29
1627	SprayQc: a real-time LC-MS/MS quality monitoring system to maximize uptime using off the shelf components. <b>2012</b> , 11, 3458-66	51
1626	Measuring phosphorylation-specific changes in response to kinase inhibitors in mammalian cells using quantitative proteomics. <b>2012</b> , 795, 217-31	2
1625	Analysis of the <i>Plasmodium falciparum</i> proteasome using Blue Native PAGE and label-free quantitative mass spectrometry. <b>2012</b> , 43, 1119-29	15
1624	Quantitative mass spectrometry in proteomics: critical review update from 2007 to the present. <b>2012</b> , 404, 939-65	585
1623	Proteome alterations in primary human alveolar macrophages in response to influenza A virus infection. <b>2012</b> , 11, 4091-101	36

1622	The effect of the degree of sulfation of glycosaminoglycans on osteoclast function and signaling pathways. <b>2012</b> , 33, 8418-29	59
1621	Mass spectrometry-based proteomics for systems biology. <b>2012</b> , 23, 591-7	78
1620	Identification of peptide features in precursor spectra using Hardkl� and Kr�ik. <b>2012</b> , Chapter 13, Unit13.18	9
1619	SILAC for the study of mammalian cell lines and yeast protein complexes. <b>2012</b> , 893, 201-21	12
1618	MSQuant: a platform for stable isotope-based quantitative proteomics. <b>2012</b> , 893, 511-22	5
1617	Quantitative analysis of S-nitrosylated proteins. <b>2012</b> , 893, 405-16	6
1616	Polycomb PHF19 binds H3K36me3 and recruits PRC2 and demethylase NO66 to embryonic stem cell genes during differentiation. <b>2012</b> , 19, 1273-81	182
1615	Assignment of protein interactions from affinity purification/mass spectrometry data. <b>2012</b> , 11, 1462-74	34
1614	The Plasmodium falciparum schizont phosphoproteome reveals extensive phosphatidylinositol and cAMP-protein kinase A signaling. <b>2012</b> , 11, 5323-37	110
1613	Current challenges in software solutions for mass spectrometry-based quantitative proteomics. <b>2012</b> , 43, 1087-108	87
1612	Mass spectrometry-based phosphoproteomics in cancer research. <b>2012</b> , 7, 566-586	0
1611	Quantitative dynamics of phosphoproteome: the devil is in the details. <b>2012</b> , 84, 8431-6	2
1610	Targeted mutation of SLC4A5 induces arterial hypertension and renal metabolic acidosis. <b>2012</b> , 21, 1025-36	36
1609	Improved two-dimensional reversed phase-reversed phase LC-MS/MS approach for identification of peptide-protein interactions. <b>2012</b> , 11, 1175-83	23
1608	Quantitative Methods in Proteomics. <b>2012</b> ,	7
1607	Key issues in the acquisition and analysis of qualitative and quantitative mass spectrometry data for peptide-centric proteomic experiments. <b>2012</b> , 43, 1075-85	12
1606	Analysis of Protein (-RNA) Complexes by (Quantitative) Mass Spectrometric Analysis. <b>2012</b> , 366-379	
1605	A critical appraisal of techniques, software packages, and standards for quantitative proteomic analysis. <b>2012</b> , 16, 431-42	46

1604	Identifying chromatin readers using a SILAC-based histone peptide pull-down approach. <b>2012</b> , 512, 137-60	9
1603	Quantitative proteomics using stable isotope labeling with amino acids in cell culture reveals protein and pathway regulation in porcine circovirus type 2 infected PK-15 cells. <b>2012</b> , 11, 995-1008	33
1602	Quantitative maps of protein phosphorylation sites across 14 different rat organs and tissues. <b>2012</b> , 3, 876	248
1601	IsoQuant: a software tool for stable isotope labeling by amino acids in cell culture-based mass spectrometry quantitation. <b>2012</b> , 84, 4535-43	19
1600	Integrin and Cell Adhesion Molecules. <b>2012</b> ,	2
1599	Determining in vivo phosphorylation sites using mass spectrometry. <b>2012</b> , Chapter 18, Unit18.19.1-27	20
1598	Advances in quantitative phosphoproteomics. <b>2012</b> , 84, 735-46	78
1597	A cross-validation scheme for machine learning algorithms in shotgun proteomics. <b>2012</b> , 13 Suppl 16, S3	22
1596	1D and 2D annotation enrichment: a statistical method integrating quantitative proteomics with complementary high-throughput data. <b>2012</b> , 13 Suppl 16, S12	393
1595	Isotope pattern deconvolution for peptide mass spectrometry by non-negative least squares/least absolute deviation template matching. <b>2012</b> , 13, 291	9
1594	Analysis of two distinct mycelial populations in liquid-grown <i>Streptomyces</i> cultures using a flow cytometry-based proteomics approach. <b>2012</b> , 96, 1301-12	29
1593	Kinase Inhibitors. <b>2012</b> ,	2
1592	Label-free quantitative proteomics of CD133-positive liver cancer stem cells. <b>2012</b> , 10, 69	7
1591	Comprehensive analysis of the N and C terminus of endogenous serum peptides reveals a highly conserved cleavage site pattern derived from proteolytic enzymes. <b>2012</b> , 3, 669-74	9
1590	Mass spectrometric tools for systematic analysis of protein phosphorylation. <b>2012</b> , 106, 3-32	11
1589	Proteomic screening for Rho-kinase substrates by combining kinase and phosphatase inhibitors with 14-3-3 $\beta$ affinity chromatography. <b>2012</b> , 37, 39-48	22
1588	MiR-133b targets antiapoptotic genes and enhances death receptor-induced apoptosis. <b>2012</b> , 7, e35345	74
1587	Comparative SILAC proteomic analysis of <i>Trypanosoma brucei</i> bloodstream and procyclic lifecycle stages. <b>2012</b> , 7, e36619	122

1586	The adenomatous polyposis coli protein contributes to normal compaction of mitotic chromatin. <b>2012</b> , 7, e38102	10
1585	An improvement of shotgun proteomics analysis by adding next-generation sequencing transcriptome data in orange. <b>2012</b> , 7, e39494	14
1584	Short-chain 3-hydroxyacyl-coenzyme A dehydrogenase associates with a protein super-complex integrating multiple metabolic pathways. <b>2012</b> , 7, e35048	16
1583	Characterization of the Phosphoproteome in SLE Patients. <b>2012</b> , 7, e53129	6
1582	Dynamic Proteomics: Methodologies and Analysis. <b>2012</b> ,	1
1581	Quantitative Proteomics for Investigation of Secreted Factors: Focus on Muscle Secretome. <b>2012</b> ,	
1580	Analyzing LC-MS/MS data by spectral count and ion abundance: two case studies. <b>2012</b> , 5, 75-87	31
1579	Efficient enrichment of phosphopeptides by magnetic TiO <sub>2</sub> -coated carbon-encapsulated iron nanoparticles. <b>2012</b> , 12, 380-90	49
1578	pParse: a method for accurate determination of monoisotopic peaks in high-resolution mass spectra. <b>2012</b> , 12, 226-35	51
1577	Effect of mass spectrometric parameters on peptide and protein identification rates for shotgun proteomic experiments on an LTQ-orbitrap mass analyzer. <b>2012</b> , 12, 21-31	43
1576	Workflow for analysis of high mass accuracy salivary data set using MaxQuant and ProteinPilot search algorithm. <b>2012</b> , 12, 1726-30	15
1575	To label or not to label: applications of quantitative proteomics in neuroscience research. <b>2012</b> , 12, 736-47	52
1574	A quantitative proteomic analysis of lung epithelial (A549) cells infected with 2009 pandemic influenza A virus using stable isotope labelling with amino acids in cell culture. <b>2012</b> , 12, 1431-6	36
1573	Deep metaproteomic analysis of human salivary supernatant. <b>2012</b> , 12, 992-1001	63
1572	Two steps forward--one step back: advances in affinity purification mass spectrometry of macromolecular complexes. <b>2012</b> , 12, 1591-608	44
1571	Computational and informatics strategies for identification of specific protein interaction partners in affinity purification mass spectrometry experiments. <b>2012</b> , 12, 1639-55	66
1570	Direct comparison of MS-based label-free and SILAC quantitative proteome profiling strategies in primary retinal Müller cells. <b>2012</b> , 12, 1902-11	94
1569	Systems biology analysis of protein-drug interactions. <b>2012</b> , 6, 102-16	19



1568	SIRT1 negatively regulates the activities, functions, and protein levels of hMOF and TIP60. <b>2012</b> , 32, 2823-36	72
1567	Phosphoproteomic analysis of cells treated with longevity-related autophagy inducers. <b>2012</b> , 11, 1827-40	28
1566	Advancing cell biology through proteomics in space and time (PROSPECTS). <b>2012</b> , 11, O112.017731	52
1565	OCAP: an open comprehensive analysis pipeline for iTRAQ. <b>2012</b> , 28, 1404-5	8
1564	A redox-regulated SUMO/acetylation switch of HIPK2 controls the survival threshold to oxidative stress. <b>2012</b> , 46, 472-83	87
1563	Software tools for MS-based quantitative proteomics: a brief overview. <b>2012</b> , 893, 489-99	24
1562	Protein-protein interactions in plants. <b>2012</b> , 53, 617-25	32
1561	Applications of stable isotope dimethyl labeling in quantitative proteomics. <b>2012</b> , 404, 991-1009	57
1560	Symmetric dimethylation of H3R2 is a newly identified histone mark that supports euchromatin maintenance. <b>2012</b> , 19, 136-44	224
1559	DnaK functions as a central hub in the E. coli chaperone network. <b>2012</b> , 1, 251-64	233
1558	The transcription factor TFEB links mTORC1 signaling to transcriptional control of lysosome homeostasis. <b>2012</b> , 5, ra42	764
1557	Tissue proteomics by one-dimensional gel electrophoresis combined with label-free protein quantification. <b>2012</b> , 11, 3680-9	29
1556	Secretome protein enrichment identifies physiological BACE1 protease substrates in neurons. <b>2012</b> , 31, 3157-68	236
1555	Prospects for a statistical theory of LC/TOFMS data. <b>2012</b> , 23, 779-91	3
1554	Enhanced methylarginine characterization by post-translational modification-specific targeted data acquisition and electron-transfer dissociation mass spectrometry. <b>2012</b> , 23, 1376-89	32
1553	Phosphoproteomic analysis: an emerging role in deciphering cellular signaling in human embryonic stem cells and their differentiated derivatives. <b>2012</b> , 8, 16-31	9
1552	Gain and loss of extracellular molecules in sporadic inclusion body myositis and polymyositis--a proteomics-based study. <b>2012</b> , 22, 32-40	4
1551	Cold acclimation induces changes in Arabidopsis tonoplast protein abundance and activity and alters phosphorylation of tonoplast monosaccharide transporters. <b>2012</b> , 69, 529-41	92

1550	The proteome and gene expression profile of cementoblastic cells treated by bone morphogenetic protein-7 in vitro. <b>2012</b> , 39, 80-90	20
1549	The role of bFGF on the ability of MSC to activate endogenous regenerative mechanisms in an ectopic bone formation model. <b>2012</b> , 33, 2086-96	69
1548	Association between segments of zonula occludens proteins: live-cell FRET and mass spectrometric analysis. <b>2012</b> , 1257, 67-76	1
1547	Dual phosphoproteomics and chemical proteomics analysis of erlotinib and gefitinib interference in acute myeloid leukemia cells. <b>2012</b> , 75, 1343-56	64
1546	Systematic and quantitative comparison of digest efficiency and specificity reveals the impact of trypsin quality on MS-based proteomics. <b>2012</b> , 75, 1454-62	194
1545	Unraveling the human dendritic cell phagosome proteome by organellar enrichment ranking. <b>2012</b> , 75, 1547-62	24
1544	Optimized nLC-MS workflow for laser capture microdissected breast cancer tissue. <b>2012</b> , 75, 2844-54	39
1543	Proteomic analysis by SILAC and 2D-DIGE reveals radiation-induced endothelial response: four key pathways. <b>2012</b> , 75, 2319-30	36
1542	Cytosol protein regulation in H295R steroidogenesis model induced by the zearalenone metabolites, $\beta$ -zearalenol and $\alpha$ -zearalenol. <b>2012</b> , 59, 17-24	13
1541	A proteomics approach reveals divergent molecular responses to salinity in populations of European whitefish ( <i>Coregonus lavaretus</i> ). <b>2012</b> , 21, 3516-30	43
1540	Proteomics for biomedicine: a half-completed journey. <b>2012</b> , 4, 75-7	5
1539	Phosphorylation site localization in peptides by MALDI MS/MS and the Mascot Delta Score. <b>2012</b> , 402, 249-60	22
1538	Existing bioinformatics tools for the quantitation of post-translational modifications. <b>2012</b> , 42, 129-38	11
1537	Whole gel processing procedure for GeLC-MS/MS based proteomics. <b>2013</b> , 11, 17	59
1536	Alterations of Gab2 signalling complexes in imatinib and dasatinib treated chronic myeloid leukaemia cells. <b>2013</b> , 11, 30	13
1535	Angiogenin induces modifications in the astrocyte secretome: relevance to amyotrophic lateral sclerosis. <b>2013</b> , 91, 274-85	31
1534	Mapping gene activity of Arabidopsis root hairs. <b>2013</b> , 14, R67	71
1533	A de novo assembly of the newt transcriptome combined with proteomic validation identifies new protein families expressed during tissue regeneration. <b>2013</b> , 14, R16	85

1532	Identification of Post-Translational Modifications by Mass Spectrometry. <b>2013</b> , 66, 734	19
1531	Global proteome analysis of the NCI-60 cell line panel. <b>2013</b> , 4, 609-20	225
1530	Quantitative profiling of tyrosine phosphorylation revealed changes in the activity of the T cell receptor signaling pathway upon cisplatin-induced apoptosis. <b>2013</b> , 91, 344-57	12
1529	Sulfur amino acids regulate translational capacity and metabolic homeostasis through modulation of tRNA thiolation. <b>2013</b> , 154, 416-29	146
1528	Computational mass spectrometry for small molecules. <b>2013</b> , 5, 12	105
1527	Mass spectrometry-based identification and characterisation of lysine and arginine methylation in the human proteome. <b>2013</b> , 9, 2231-47	122
1526	Small-molecule modulation of Wnt signaling via modulating the Axin-LRP5/6 interaction. <b>2013</b> , 9, 579-85	58
1525	The RNA-binding protein repertoire of embryonic stem cells. <b>2013</b> , 20, 1122-30	320
1524	Molecular Dermatology. <b>2013</b> ,	2
1523	Cell-selective labeling using amino acid precursors for proteomic studies of multicellular environments. <b>2013</b> , 10, 768-73	38
1522	Cell Senescence. <b>2013</b> ,	3
1521	Latency-associated degradation of the MRP1 drug transporter during latent human cytomegalovirus infection. <b>2013</b> , 340, 199-202	112
1520	Regulation of miR-17-92a cluster processing by the microRNA binding protein SND1. <b>2013</b> , 587, 2405-11	19
1519	Characterization of a high field Orbitrap mass spectrometer for proteome analysis. <b>2013</b> , 13, 2552-62	9
1518	MultiAlign: a multiple LC-MS analysis tool for targeted omics analysis. <b>2013</b> , 14, 49	23
1517	MITEs in the promoters of effector genes allow prediction of novel virulence genes in <i>Fusarium oxysporum</i> . <b>2013</b> , 14, 119	130
1516	Characterization of a short isoform of the kidney protein podocin in human kidney. <b>2013</b> , 14, 102	13
1515	DMSO enhances electrospray response, boosting sensitivity of proteomic experiments. <b>2013</b> , 10, 989-91	170

1514	Gene Regulation. <b>2013</b> ,	1
1513	Analysis of the proteolysis of bioactive peptides using a peptidomics approach. <b>2013</b> , 8, 1730-42	23
1512	Increased proteome coverage by combining PAGE and peptide isoelectric focusing: comparative study of gel-based separation approaches. <b>2013</b> , 13, 2947-55	41
1511	Chronic high glucose induced INS-1 cell mitochondrial dysfunction: a comparative mitochondrial proteome with SILAC. <b>2013</b> , 13, 3030-9	14
1510	Sirtuins. <b>2013</b> ,	1
1509	Na <sup>+</sup> /K <sup>+</sup> -ATPase is a new interacting partner for the neuronal glycine transporter GlyT2 that downregulates its expression in vitro and in vivo. <b>2013</b> , 33, 14269-81	33
1508	A gain-of-function mutation in DHT synthesis in castration-resistant prostate cancer. <b>2013</b> , 154, 1074-1084	210
1507	Correlation between structure, protein composition, morphogenesis and cytopathology of Glossina pallidipes salivary gland hypertrophy virus. <b>2013</b> , 94, 193-208	16
1506	SILAC proteomics of planarians identifies Ncoa5 as a conserved component of pluripotent stem cells. <b>2013</b> , 5, 1142-55	34
1505	ComplexQuant: high-throughput computational pipeline for the global quantitative analysis of endogenous soluble protein complexes using high resolution protein HPLC and precision label-free LC/MS/MS. <b>2013</b> , 81, 102-11	14
1504	Lysine succinylation is a frequently occurring modification in prokaryotes and eukaryotes and extensively overlaps with acetylation. <b>2013</b> , 4, 842-51	452
1503	Quantitative proteomic analysis reveals the neuroprotective effects of huperzine A for amyloid beta treated neuroblastoma N2a cells. <b>2013</b> , 13, 1314-24	32
1502	Identification of proteomic biomarkers in M. Longissimus dorsi as potential predictors of pork quality. <b>2013</b> , 95, 679-87	31
1501	Global impact of Salmonella pathogenicity island 2-secreted effectors on the host phosphoproteome. <b>2013</b> , 12, 1632-43	28
1500	Detection and initial characterization of protein entities consisting of the HIV glycoprotein cytoplasmic C-terminal domain alone. <b>2013</b> , 441, 85-94	3
1499	Cleaning up the masses: exclusion lists to reduce contamination with HPLC-MS/MS. <b>2013</b> , 88, 92-103	74
1498	Comparative proteomics reveal diverse functions and dynamic changes of Bombyx mori silk proteins spun from different development stages. <b>2013</b> , 12, 5213-22	58
1497	Chronic hypoxia alters mitochondrial composition in human macrophages. <b>2013</b> , 1834, 2750-60	24

1496	Mass spectrometric protein maps for biomarker discovery and clinical research. <b>2013</b> , 13, 811-25	105
1495	Comparison of SILAC and mTRAQ quantification for phosphoproteomics on a quadrupole orbitrap mass spectrometer. <b>2013</b> , 12, 4089-100	28
1494	Honey bee protein atlas at organ-level resolution. <b>2013</b> , 23, 1951-60	42
1493	Radiation Proteomics. <b>2013</b> ,	3
1492	Evaluation of Drosophila metabolic labeling strategies for in vivo quantitative proteomic analyses with applications to early pupa formation and amino acid starvation. <b>2013</b> , 12, 2138-50	10
1491	Coupling of mitochondrial import and export translocases by receptor-mediated supercomplex formation. <b>2013</b> , 154, 596-608	96
1490	Systematic identification of proteins binding to chromatin-embedded ubiquitylated H2B reveals recruitment of SWI/SNF to regulate transcription. <b>2013</b> , 4, 601-8	62
1489	Golgi-dependent signaling: self-coordination of membrane trafficking. <b>2013</b> , 118, 359-82	2
1488	Quantitative proteomics by amino acid labeling in foot-and-mouth disease virus (FMDV)-infected cells. <b>2013</b> , 12, 363-77	20
1487	Quantitative interaction screen of telomeric repeat-containing RNA reveals novel TERRA regulators. <b>2013</b> , 23, 2149-57	52
1486	Involvement of mitochondrial dynamics in the segregation of mitochondrial matrix proteins during stationary phase mitophagy. <b>2013</b> , 4, 2789	76
1485	Asn3, a reliable, robust, and universal lock mass for improved accuracy in LC-MS and LC-MS/MS. <b>2013</b> , 85, 11054-60	10
1484	Affinity proteomics reveals human host factors implicated in discrete stages of LINE-1 retrotransposition. <b>2013</b> , 155, 1034-48	133
1483	Refined preparation and use of anti-diglycine remnant (K-EGG) antibody enables routine quantification of 10,000s of ubiquitination sites in single proteomics experiments. <b>2013</b> , 12, 825-31	219
1482	Integrated structural analysis of the human nuclear pore complex scaffold. <b>2013</b> , 155, 1233-43	273
1481	EMRE is an essential component of the mitochondrial calcium uniporter complex. <b>2013</b> , 342, 1379-82	433
1480	Recent progress using systems biology approaches to better understand molecular mechanisms of immunity. <b>2013</b> , 25, 201-8	16
1479	Expanded polyglutamine-containing N-terminal huntingtin fragments are entirely degraded by mammalian proteasomes. <b>2013</b> , 288, 27068-27084	51

1478	Differential proteomic profiling in human spermatozoa that did or did not result in pregnancy via IVF and AID. <b>2013</b> , 7, 850-8	36
1477	Direct proteomic quantification of the secretome of activated immune cells. <b>2013</b> , 340, 475-8	147
1476	Label-free quantitative proteomic analysis of right ventricular remodeling in infant Tetralogy of Fallot patients. <b>2013</b> , 84, 78-91	13
1475	The cellular interactome of the coronavirus infectious bronchitis virus nucleocapsid protein and functional implications for virus biology. <b>2013</b> , 87, 9486-500	59
1474	Data visualization in environmental proteomics. <b>2013</b> , 13, 2805-21	17
1473	Tunable signal processing through modular control of transcription factor translocation. <b>2013</b> , 339, 460-4	103
1472	Global quantitative SILAC phosphoproteomics reveals differential phosphorylation is widespread between the procyclic and bloodstream form lifecycle stages of <i>Trypanosoma brucei</i> . <b>2013</b> , 12, 2233-44	139
1471	The <i>Aeromonas salmonicida</i> subsp. <i>salmonicida</i> exoproteome: determination of the complete repertoire of Type-Three Secretion System effectors and identification of other virulence factors. <b>2013</b> , 11, 42	18
1470	Quantitative proteomics reveals regulatory differences in the chondrocyte secretome from human medial and lateral femoral condyles in osteoarthritic patients. <b>2013</b> , 11, 43	31
1469	The proteome of the calcified layer organic matrix of turkey ( <i>Meleagris gallopavo</i> ) eggshell. <b>2013</b> , 11, 40	35
1468	Quantitative proteomic analysis of cultured skin fibroblast cells derived from patients with triglyceride deposit cardiomyovascularopathy. <b>2013</b> , 8, 197	7
1467	The neuropeptide complement of the marine annelid <i>Platynereis dumerilii</i> . <b>2013</b> , 14, 906	91
1466	SACE_5599, a putative regulatory protein, is involved in morphological differentiation and erythromycin production in <i>Saccharopolyspora erythraea</i> . <b>2013</b> , 12, 126	15
1465	Comparative secretome analysis of <i>Trichoderma asperellum</i> S4F8 and <i>Trichoderma reesei</i> Rut C30 during solid-state fermentation on sugarcane bagasse. <b>2013</b> , 6, 172	61
1464	Identification of gene fusions from human lung cancer mass spectrometry data. <b>2013</b> , 14 Suppl 8, S5	21
1463	Urinary proteomic and non-prefractionation quantitative phosphoproteomic analysis during pregnancy and non-pregnancy. <b>2013</b> , 14, 777	25
1462	Proteomic strategies to characterize signaling pathways. <b>2013</b> , 1007, 359-77	9
1461	Determination of phosphorylation sites in the DivIVA cytoskeletal protein of <i>Streptomyces coelicolor</i> by targeted LC-MS/MS. <b>2013</b> , 12, 4187-92	9

1460	SILAC-based proteome analysis of <i>Starmerella bombicola</i> sophorolipid production. <b>2013</b> , 12, 4376-92	20
1459	Comparing immobilized kinase inhibitors and covalent ATP probes for proteomic profiling of kinase expression and drug selectivity. <b>2013</b> , 12, 1723-31	44
1458	Post-translational modifications and mass spectrometry detection. <b>2013</b> , 65, 925-941	80
1457	A Gro/TLE-NuRD corepressor complex facilitates Tbx20-dependent transcriptional repression. <b>2013</b> , 12, 5395-409	24
1456	Proteome-wide identification of poly(ADP-Ribosyl)ation targets in different genotoxic stress responses. <b>2013</b> , 52, 272-85	243
1455	TIMP-1 increases expression and phosphorylation of proteins associated with drug resistance in breast cancer cells. <b>2013</b> , 12, 4136-51	26
1454	Large-scale identification of ubiquitination sites by mass spectrometry. <b>2013</b> , 8, 1950-60	196
1453	Proteomic tools for environmental microbiology--a roadmap from sample preparation to protein identification and quantification. <b>2013</b> , 13, 2700-30	39
1452	Mutated desmoglein-2 proteins are incorporated into desmosomes and exhibit dominant-negative effects in arrhythmogenic right ventricular cardiomyopathy. <b>2013</b> , 34, 697-705	27
1451	Candidate biomarker discovery for angiogenesis by automatic integration of Orbitrap MS1 spectral- and X!Tandem MS2 sequencing information. <b>2013</b> , 11, 182-94	1
1450	Proteomic analysis of <i>Plasmodium falciparum</i> schizonts reveals heparin-binding merozoite proteins. <b>2013</b> , 12, 2185-93	24
1449	Probing the acetylation code of histone H4. <b>2013</b> , 13, 2989-97	11
1448	Comparison of Resins for Metal Oxide Affinity Chromatography with Mass Spectrometry Detection for the Determination of Phosphopeptides. <b>2013</b> , 46, 1505-1524	7
1447	The Hog1 stress-activated protein kinase targets nucleoporins to control mRNA export upon stress. <b>2013</b> , 288, 17384-98	29
1446	Identification of complex relationship between protein kinases and substrates during the cell cycle of HeLa cells by phosphoproteomic analysis. <b>2013</b> , 13, 1233-46	2
1445	SILAC-based proteomics of human primary endothelial cell morphogenesis unveils tumor angiogenic markers. <b>2013</b> , 12, 3599-611	50
1444	Rapid combinatorial ERLIC-SCX solid-phase extraction for in-depth phosphoproteome analysis. <b>2013</b> , 12, 5989-95	26
1443	Deep coverage of the <i>Escherichia coli</i> proteome enables the assessment of false discovery rates in simple proteogenomic experiments. <b>2013</b> , 12, 3420-30	60

1442	Smurf1-mediated Lys29-linked nonproteolytic polyubiquitination of axin negatively regulates Wnt/ $\beta$ -catenin signaling. <b>2013</b> , 33, 4095-105	59
1441	The transmission of nuclear pore complexes to daughter cells requires a cytoplasmic pool of Nsp1. <b>2013</b> , 203, 215-32	36
1440	Yeast ribosomal protein L7 and its homologue Rlp7 are simultaneously present at distinct sites on pre-60S ribosomal particles. <b>2013</b> , 41, 9461-70	20
1439	The cotranslational function of ribosome-associated Hsp70 in eukaryotic protein homeostasis. <b>2013</b> , 152, 196-209	177
1438	The proteomic investigation of chromatin functional domains reveals novel synergisms among distinct heterochromatin components. <b>2013</b> , 12, 764-80	46
1437	A proteomics search algorithm specifically designed for high-resolution tandem mass spectra. <b>2013</b> , 12, 1377-86	121
1436	PROTEINCHALLENGE: crowd sourcing in proteomics analysis and software development. <b>2013</b> , 88, 41-6	16
1435	Hydrophilic strong anion exchange (hSAX) chromatography for highly orthogonal peptide separation of complex proteomes. <b>2013</b> , 12, 2449-57	53
1434	Quantitative proteomic analysis revealed N'-nitrosonornicotine-induced down-regulation of nonmuscle myosin II and reduced cell migration in cultured human skin fibroblast cells. <b>2013</b> , 12, 1282-8	8
1433	Rif1 prevents resection of DNA breaks and promotes immunoglobulin class switching. <b>2013</b> , 339, 711-5	304
1432	Advances in characterizing ubiquitylation sites by mass spectrometry. <b>2013</b> , 17, 49-58	47
1431	STEPS: a grid search methodology for optimized peptide identification filtering of MS/MS database search results. <b>2013</b> , 13, 766-70	12
1430	Cyclic GMP-AMP synthase is a cytosolic DNA sensor that activates the type I interferon pathway. <b>2013</b> , 339, 786-91	2259
1429	Microbiota from the distal guts of lean and obese adolescents exhibit partial functional redundancy besides clear differences in community structure. <b>2013</b> , 15, 211-26	150
1428	A map of general and specialized chromatin readers in mouse tissues generated by label-free interaction proteomics. <b>2013</b> , 49, 368-78	128
1427	Redox proteomics: chemical principles, methodological approaches and biological/biomedical promises. <b>2013</b> , 113, 596-698	179
1426	An automated pipeline for high-throughput label-free quantitative proteomics. <b>2013</b> , 12, 1628-44	123
1425	High resolution quantitative proteomics of HeLa cells protein species using stable isotope labeling with amino acids in cell culture(SILAC), two-dimensional gel electrophoresis(2DE) and nano-liquid chromatography coupled to an LTQ-OrbitrapMass spectrometer. <b>2013</b> , 12, 529-38	84



1424	System-wide identification of RNA-binding proteins by interactome capture. <b>2013</b> , 8, 491-500	135
1423	Triacylglycerol synthesis enzymes mediate lipid droplet growth by relocating from the ER to lipid droplets. <b>2013</b> , 24, 384-99	485
1422	A Natural Product Inspired Tetrahydropyran Collection Yields Mitosis Modulators that Synergistically Target CSE1L and Tubulin. <b>2013</b> , 125, 428-432	18
1421	A natural product inspired tetrahydropyran collection yields mitosis modulators that synergistically target CSE1L and tubulin. <b>2013</b> , 52, 410-4	57
1420	Characterization and analysis of the composition and dynamics of the mammalian riboproteome. <b>2013</b> , 4, 1276-87	43
1419	A DNA-centric protein interaction map of ultraconserved elements reveals contribution of transcription factor binding hubs to conservation. <b>2013</b> , 5, 531-45	23
1418	Analysis of the STAT3 interactome using in-situ biotinylation and SILAC. <b>2013</b> , 94, 370-86	8
1417	Large precursor tolerance database search - a simple approach for estimation of the amount of spectra with precursor mass shifts in proteomic data. <b>2013</b> , 91, 375-84	
1416	CD74-dependent deregulation of the tumor suppressor scribble in human epithelial and breast cancer cells. <b>2013</b> , 15, 660-8	32
1415	Subpopulation-proteomics in prokaryotic populations. <b>2013</b> , 24, 79-87	32
1414	Tools for label-free peptide quantification. <b>2013</b> , 12, 549-56	171
1413	IDPQuantify: combining precursor intensity with spectral counts for protein and peptide quantification. <b>2013</b> , 12, 4111-21	16
1412	Initial quantitative proteomic map of 28 mouse tissues using the SILAC mouse. <b>2013</b> , 12, 1709-22	166
1411	Rapid and deep human proteome analysis by single-dimension shotgun proteomics. <b>2013</b> , 12, 3330-8	107
1410	Identification of lysine succinylation substrates and the succinylation regulatory enzyme CobB in Escherichia coli. <b>2013</b> , 12, 3509-20	165
1409	Dispersed sites of HIV Vif-dependent polyubiquitination in the DNA deaminase APOBEC3F. <b>2013</b> , 425, 1172-82	18
1408	Benchmarking stable isotope labeling based quantitative proteomics. <b>2013</b> , 88, 14-26	100
1407	Mitochondrial SIRT4-type proteins in Caenorhabditis elegans and mammals interact with pyruvate carboxylase and other acetylated biotin-dependent carboxylases. <b>2013</b> , 13, 705-20	12

1406	Current algorithmic solutions for peptide-based proteomics data generation and identification. <b>2013</b> , 24, 31-8	41
1405	The SH2 domain interaction landscape. <b>2013</b> , 3, 1293-305	89
1404	OTULIN restricts Met1-linked ubiquitination to control innate immune signaling. <b>2013</b> , 50, 818-830	157
1403	Comparative proteome approach demonstrates that platelet-derived growth factor C and D efficiently induce proliferation while maintaining multipotency of hMSCs. <b>2013</b> , 319, 2649-62	7
1402	Increased WD-repeat containing protein 1 in interstitial fluid from ovarian carcinomas shown by comparative proteomic analysis of malignant and healthy gynecological tissue. <b>2013</b> , 1834, 2347-59	21
1401	The proteome of Toll-like receptor 3-stimulated human immortalized fibroblasts: implications for susceptibility to herpes simplex virus encephalitis. <b>2013</b> , 131, 1157-66	11
1400	The LMNA mutation p.Arg321Ter associated with dilated cardiomyopathy leads to reduced expression and a skewed ratio of lamin A and lamin C proteins. <b>2013</b> , 319, 3010-9	17
1399	Quantitative analysis of global phosphorylation changes with high-resolution tandem mass spectrometry and stable isotopic labeling. <b>2013</b> , 61, 251-9	10
1398	Correlation of precursor and product ions in single-stage high resolution mass spectrometry. A tool for detecting diagnostic ions and improving the precursor elemental composition elucidation. <b>2013</b> , 772, 47-58	8
1397	Proteomic mapping of mitochondria in living cells via spatially restricted enzymatic tagging. <b>2013</b> , 339, 1328-1331	731
1396	Dynamic readers for 5-(hydroxy)methylcytosine and its oxidized derivatives. <b>2013</b> , 152, 1146-59	748
1395	Proteomic Analysis of Cellular Systems. <b>2013</b> , 3-25	13
1394	Deficiency of terminal ADP-ribose protein glycohydrolase TARG1/C6orf130 in neurodegenerative disease. <b>2013</b> , 32, 1225-37	215
1393	The Usp8 deubiquitination enzyme is post-translationally modified by tyrosine and serine phosphorylation. <b>2013</b> , 25, 919-30	16
1392	Detecting endogenous SUMO targets in mammalian cells and tissues. <b>2013</b> , 20, 525-31	155
1391	Next Generation Instruments and Methods for Proteomics. <b>2013</b> , 15-67	4
1390	Determining the calibration of confidence estimation procedures for unique peptides in shotgun proteomics. <b>2013</b> , 80, 123-31	32
1389	The coming age of complete, accurate, and ubiquitous proteomes. <b>2013</b> , 49, 583-90	294

1388	Postnatal cardiomyocyte growth and mitochondrial reorganization cause multiple changes in the proteome of human cardiomyocytes. <b>2013</b> , 9, 1210-9	30
1387	Protein analysis by shotgun/bottom-up proteomics. <b>2013</b> , 113, 2343-94	902
1386	Phosphoproteome analysis of an early onset mouse model (TgCRND8) of Alzheimer's disease reveals temporal changes in neuronal and glia signaling pathways. <b>2013</b> , 13, 1292-305	12
1385	Technologies and challenges in large-scale phosphoproteomics. <b>2013</b> , 13, 910-31	130
1384	Label-free quantitative analysis of the membrane proteome of Bace1 protease knock-out zebrafish brains. <b>2013</b> , 13, 1519-27	21
1383	Proteomic workflow for analysis of archival formalin-fixed and paraffin-embedded clinical samples to a depth of 10 000 proteins. <b>2013</b> , 7, 225-33	117
1382	In vivo SILAC-based proteomics reveals phosphoproteome changes during mouse skin carcinogenesis. <b>2013</b> , 3, 552-66	82
1381	Quantitative phosphoproteomics reveal mTORC1 activates de novo pyrimidine synthesis. <b>2013</b> , 339, 1320-3	345
1380	Shotgun proteomics of archival triple-negative breast cancer samples. <b>2013</b> , 7, 283-91	24
1379	Spatial regulation of VEGF receptor endocytosis in angiogenesis. <b>2013</b> , 15, 249-60	190
1378	Target identification for small bioactive molecules: finding the needle in the haystack. <b>2013</b> , 52, 2744-92	339
1377	Protein lysine acetylation analysis: current MS-based proteomic technologies. <b>2013</b> , 138, 1628-36	30
1376	Using ProtMAX to create high-mass-accuracy precursor alignments from label-free quantitative mass spectrometry data generated in shotgun proteomics experiments. <b>2013</b> , 8, 595-601	22
1375	Centrosome isolation and analysis by mass spectrometry-based proteomics. <b>2013</b> , 525, 371-93	9
1374	From cells to peptides: "one-stop" integrated proteomic processing using amphipols. <b>2013</b> , 12, 1512-9	21
1373	Applications of selected reaction monitoring (SRM)-mass spectrometry (MS) for quantitative measurement of signaling pathways. <b>2013</b> , 61, 313-22	42
1372	Proteomics and the analysis of proteomic data: 2013 overview of current protein-profiling technologies. <b>2013</b> , Chapter 13, Unit 13.21	11
1371	References. <b>2013</b> , 313-326	

1370	Proteomic survey of the <i>Streptomyces coelicolor</i> nucleoid. <b>2013</b> , 83, 37-46	7
1369	Identifying specific protein-DNA interactions using SILAC-based quantitative proteomics. <b>2013</b> , 977, 137-57	15
1368	Using guanidine-hydrochloride for fast and efficient protein digestion and single-step affinity-purification mass spectrometry. <b>2013</b> , 12, 1020-30	33
1367	QuaNCAT: quantitating proteome dynamics in primary cells. <b>2013</b> , 10, 343-6	117
1366	Secretome analyses of A $\beta$ (1-42) stimulated hippocampal astrocytes reveal that CXCL10 is involved in astrocyte migration. <b>2013</b> , 12, 832-43	18
1365	Label-free quantitative proteomics trends for protein-protein interactions. <b>2013</b> , 81, 91-101	47
1364	A proteomic characterization of factors enriched at nascent DNA molecules. <b>2013</b> , 3, 1105-16	87
1363	The p53/microRNA network in cancer: experimental and bioinformatics approaches. <b>2013</b> , 774, 77-101	54
1362	In vitro bioactivity and biocompatibility evaluation of bulk nanostructured titanium in osteoblast-like cells by quantitative proteomic analysis. <b>2013</b> , 1, 1926-1938	9
1361	In-depth proteomic analyses of exosomes isolated from expressed prostatic secretions in urine. <b>2013</b> , 13, 1667-1671	109
1360	Protein tyrosine phosphatase SHP2/PTPN11 mistargeting as a consequence of SH2-domain point mutations associated with Noonan Syndrome and leukemia. <b>2013</b> , 84, 132-47	11
1359	Bioinformatic progress and applications in metaproteogenomics for bridging the gap between genomic sequences and metabolic functions in microbial communities. <b>2013</b> , 13, 2786-804	39
1358	High performance computational analysis of large-scale proteome data sets to assess incremental contribution to coverage of the human genome. <b>2013</b> , 12, 2858-68	26
1357	Delineating the synovial fluid proteome: recent advancements and ongoing challenges in biomarker research. <b>2013</b> , 50, 51-63	18
1356	Exonuclease hDIS3L2 specifies an exosome-independent 3'-5' degradation pathway of human cytoplasmic mRNA. <b>2013</b> , 32, 1855-68	113
1355	Scanning of novel cancer/testis proteins by human testis proteomic analysis. <b>2013</b> , 13, 1200-10	47
1354	Combinatorial ligand libraries as a two-dimensional method for proteome analysis. <b>2013</b> , 1297, 106-12	17
1353	Dynamic adipocyte phosphoproteome reveals that Akt directly regulates mTORC2. <b>2013</b> , 17, 1009-1020	269

1352	Citric acid-assisted two-step enrichment with TiO <sub>2</sub> enhances the separation of multi- and monophosphorylated peptides and increases phosphoprotein profiling. <b>2013</b> , 12, 2467-76	27
1351	Displacement of N/Q-rich peptides on TiO <sub>2</sub> beads enhances the depth and coverage of yeast phosphoproteome analyses. <b>2013</b> , 12, 2905-13	23
1350	Computational proteomics pitfalls and challenges: HavanaBioinfo 2012 workshop report. <b>2013</b> , 87, 134-8	17
1349	Relative quantification of proteasome activity by activity-based protein profiling and LC-MS/MS. <b>2013</b> , 8, 1155-68	62
1348	A general molecular affinity strategy for global detection and proteomic analysis of lysine methylation. <b>2013</b> , 50, 444-56	122
1347	Quantitative cross-linking/mass spectrometry using isotope-labelled cross-linkers. <b>2013</b> , 88, 120-8	109
1346	β1- and β2-class integrins cooperate to regulate myosin II during rigidity sensing of fibronectin-based microenvironments. <b>2013</b> , 15, 625-36	307
1345	Absolute quantification of E1, ubiquitin-like proteins and Nedd8-MLN4924 adduct by mass spectrometry. <b>2013</b> , 67, 139-47	11
1344	Mass spectrometry-based proteomics: basic principles and emerging technologies and directions. <b>2013</b> , 990, 1-35	21
1343	Protein quantification by peptide quality control (PQPQ) of shotgun proteomics data. <b>2013</b> , 1023, 149-58	3
1342	PolyQ proteins interfere with nuclear degradation of cytosolic proteins by sequestering the Sis1p chaperone. <b>2013</b> , 154, 134-45	255
1341	Tightly anchored tissue-mimetic matrices as instructive stem cell microenvironments. <b>2013</b> , 10, 788-94	162
1340	Critical assessment of proteome-wide label-free absolute abundance estimation strategies. <b>2013</b> , 13, 2567-78	141
1339	Adaptation of a commonly used, chemically defined medium for human embryonic stem cells to stable isotope labeling with amino acids in cell culture. <b>2013</b> , 12, 3233-45	10
1338	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <b>2013</b> , 499, 74-8	563
1337	The anticancer drug AUY922 generates a proteomics fingerprint that is highly conserved among structurally diverse Hsp90 inhibitors. <b>2013</b> , 12, 3697-706	20
1336	Oncogene-induced cellular senescence elicits an anti-Warburg effect. <b>2013</b> , 13, 2585-96	33
1335	Comprehensive profiling of N-linked glycosylation sites in HeLa cells using hydrazide enrichment. <b>2013</b> , 12, 248-59	16

1334	Label-free quantification in clinical proteomics. <b>2013</b> , 1834, 1581-90	134
1333	LC-MS spectra processing. <b>2013</b> , 1007, 47-63	11
1332	Identification of LIN28B-bound mRNAs reveals features of target recognition and regulation. <b>2013</b> , 10, 1146-59	47
1331	Mass Spectrometry Data Analysis in Proteomics. <b>2013</b> ,	7
1330	Global protein phosphorylation dynamics during deoxynivalenol-induced ribotoxic stress response in the macrophage. <b>2013</b> , 268, 201-11	37
1329	Origin of monocytes and macrophages in a committed progenitor. <b>2013</b> , 14, 821-30	424
1328	The Low Molecular Weight Proteome. <b>2013</b> ,	
1327	Neutron encoded labeling for peptide identification. <b>2013</b> , 85, 5129-37	39
1326	Profiling of the kinome of cytomegalovirus-infected cells reveals the functional importance of host kinases Aurora A, ABL and AMPK. <b>2013</b> , 99, 139-48	35
1325	Molecular architecture of the chick vestibular hair bundle. <b>2013</b> , 16, 365-74	121
1324	Unbiased characterization of the senescence-associated secretome using SILAC-based quantitative proteomics. <b>2013</b> , 965, 175-84	10
1323	Phosphoproteomic analysis of aortic endothelial cells activated by oxidized phospholipids. <b>2013</b> , 1000, 53-69	3
1322	Changes in milk proteome and metabolome associated with dry period length, energy balance, and lactation stage in postparturient dairy cows. <b>2013</b> , 12, 3288-96	61
1321	Elucidation of in situ polycyclic aromatic hydrocarbon degradation by functional metaproteomics (protein-SIP). <b>2013</b> , 13, 2910-20	63
1320	Hexavalent chromium-induced alteration of proteomic landscape in human skin fibroblast cells. <b>2013</b> , 12, 3511-8	16
1319	Proteome profiling of human neutrophil granule subsets, secretory vesicles, and cell membrane: correlation with transcriptome profiling of neutrophil precursors. <b>2013</b> , 94, 711-21	151
1318	Mspire-Simulator: LC-MS shotgun proteomic simulator for creating realistic gold standard data. <b>2013</b> , 12, 5742-9	16
1317	Mass defect-based pseudo-isobaric dimethyl labeling for proteome quantification. <b>2013</b> , 85, 10658-63	38

1316	Characterization of the novel broad-spectrum kinase inhibitor CTx-0294885 as an affinity reagent for mass spectrometry-based kinome profiling. <b>2013</b> , 12, 3104-16	40
1315	Delayed times to tissue fixation result in unpredictable global phosphoproteome changes. <b>2013</b> , 12, 4424-34	24
1314	Aurora B suppresses microtubule dynamics and limits central spindle size by locally activating KIF4A. <b>2013</b> , 202, 605-21	93
1313	Mapping of the N-linked glycoproteome of human spermatozoa. <b>2013</b> , 12, 5750-9	44
1312	PhosSA: Fast and accurate phosphorylation site assignment algorithm for mass spectrometry data. <b>2013</b> , 11, S14	8
1311	6-thioguanine induces mitochondrial dysfunction and oxidative DNA damage in acute lymphoblastic leukemia cells. <b>2013</b> , 12, 3803-11	14
1310	FTDR 2.0: a tool to achieve sub-ppm level recalibrated accuracy in routine LC-MS analysis. <b>2013</b> , 12, 3857-64	2
1309	Proteome-wide discovery and characterizations of nucleotide-binding proteins with affinity-labeled chemical probes. <b>2013</b> , 85, 3198-206	23
1308	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. <b>2013</b> , 305, G348-56	86
1307	Subcellular proteomics reveals a role for nucleo-cytoplasmic trafficking at the DNA replication origin activation checkpoint. <b>2013</b> , 12, 1436-53	13
1306	Molecular fingerprinting of the podocyte reveals novel gene and protein regulatory networks. <b>2013</b> , 83, 1052-64	109
1305	Comparative secretome analysis of epithelial and mesenchymal subpopulations of head and neck squamous cell carcinoma identifies S100A4 as a potential therapeutic target. <b>2013</b> , 12, 3778-92	30
1304	Substrate specificity of clostridial glucosylating toxins and their function on colonocytes analyzed by proteomics techniques. <b>2013</b> , 12, 1604-18	40
1303	Assessment of global proteome dynamics in carp: a model for investigating environmental stress. <b>2013</b> , 12, 5246-52	6
1302	Correction of errors in tandem mass spectrum extraction enhances phosphopeptide identification. <b>2013</b> , 12, 5548-57	9
1301	Two birds with one stone: doing metabolomics with your proteomics kit. <b>2013</b> , 13, 3371-86	19
1300	Proteomic analysis of the SH2 domain-containing leukocyte protein of 76 kDa (SLP76) interactome in resting and activated primary mast cells [corrected]. <b>2013</b> , 12, 2874-89	10
1299	The sirtuin SIRT6 regulates stress granule formation in <i>C. elegans</i> and mammals. <b>2013</b> , 126, 5166-77	46

1298	A fast workflow for identification and quantification of proteomes. <b>2013</b> , 12, 2370-80	83
1297	Proteolytic post-translational modification of proteins: proteomic tools and methodology. <b>2013</b> , 12, 3532-42	98
1296	Unique protein signature of circulating microparticles in systemic lupus erythematosus. <b>2013</b> , 65, 2680-90	70
1295	SILAC-based phosphoproteomics reveals an inhibitory role of KSR1 in p53 transcriptional activity via modulation of DBC1. <b>2013</b> , 109, 2675-84	15
1294	Discovery of histone modification crosstalk networks by stable isotope labeling of amino acids in cell culture mass spectrometry (SILAC MS). <b>2013</b> , 12, 2048-59	31
1293	Quantitative proteome analysis of alveolar type-II cells reveals a connection of integrin receptor subunits beta 2/6 and WNT signaling. <b>2013</b> , 12, 5598-608	8
1292	Comparative analysis of dynamic proteomic profiles between in vivo and in vitro produced mouse embryos during postimplantation period. <b>2013</b> , 12, 3843-56	25
1291	Automated gas-phase purification for accurate, multiplexed quantification on a stand-alone ion-trap mass spectrometer. <b>2013</b> , 85, 2079-86	12
1290	Identification of a metabolizing enzyme in human kidney by proteomic correlation profiling. <b>2013</b> , 12, 2313-23	11
1289	RNA-binding protein GLD-1/quaking genetically interacts with the mir-35 and the let-7 miRNA pathways in <i>Caenorhabditis elegans</i> . <b>2013</b> , 3, 130151	14
1288	Quantification of the N-glycosylated secretome by super-SILAC during breast cancer progression and in human blood samples. <b>2013</b> , 12, 158-71	95
1287	Cell cycle regulation of microtubule interactomes: multi-layered regulation is critical for the interphase/mitosis transition. <b>2013</b> , 12, 3135-47	18
1286	Perturbations to the ubiquitin conjugate proteome in yeast <i>Ubx</i> mutants identify Ubx2 as a regulator of membrane lipid composition. <b>2013</b> , 12, 2791-803	24
1285	The mzQuantML data standard for mass spectrometry-based quantitative studies in proteomics. <b>2013</b> , 12, 2332-40	55
1284	Mouse urinary peptides provide a molecular basis for genotype discrimination by nasal sensory neurons. <b>2013</b> , 4, 1616	61
1283	Proteomic identification of novel secreted antibacterial toxins of the <i>Serratia marcescens</i> type VI secretion system. <b>2013</b> , 12, 2735-49	71
1282	Characterization of native protein complexes and protein isoform variation using size-fractionation-based quantitative proteomics. <b>2013</b> , 12, 3851-73	104
1281	Tools (Viewer, Library and Validator) that facilitate use of the peptide and protein identification standard format, termed mzIdentML. <b>2013</b> , 12, 3026-35	28



1280	A SILAC-based approach identifies substrates of caspase-dependent cleavage upon TRAIL-induced apoptosis. <b>2013</b> , 12, 1436-50	23
1279	Label-Free Quantitation and Mapping of the ErbB2 Tumor Receptor by Multiple Protease Digestion with Data-Dependent (MS1) and Data-Independent (MS2) Acquisitions. <b>2013</b> , 2013, 791985	20
1278	The Application of SILAC Mouse in Human Body Fluid Proteomics Analysis Reveals Protein Patterns Associated with IgA Nephropathy. <b>2013</b> , 2013, 275390	11
1277	HOT1 is a mammalian direct telomere repeat-binding protein contributing to telomerase recruitment. <b>2013</b> , 32, 1681-701	61
1276	Ube2W conjugates ubiquitin to amino groups of protein N-termini. <b>2013</b> , 453, 137-45	69
1275	Heterozygous Lmna <sup>ΔK32</sup> mice develop dilated cardiomyopathy through a combined pathomechanism of haploinsufficiency and peptide toxicity. <b>2013</b> , 22, 3152-64	45
1274	Systematic evaluation of reference protein normalization in proteomic experiments. <b>2013</b> , 4, 25	7
1273	Proteomic Profiling of Ex Vivo Expanded CD34-Positive Haematopoietic Cells Derived from Umbilical Cord Blood. <b>2013</b> , 2013, 245695	4
1272	A classifier based on accurate mass measurements to aid large scale, unbiased glycoproteomics. <b>2013</b> , 12, 1017-25	23
1271	A new cellular stress response that triggers centriolar satellite reorganization and ciliogenesis. <b>2013</b> , 32, 3029-40	90
1270	The chromodomain helicase Chd4 is required for Polycomb-mediated inhibition of astroglial differentiation. <b>2013</b> , 32, 1598-612	61
1269	NKT cell-TCR expression activates conventional T cells in vivo, but is largely dispensable for mature NKT cell biology. <b>2013</b> , 11, e1001589	29
1268	Phosphorylation variation during the cell cycle scales with structural propensities of proteins. <b>2013</b> , 9, e1002842	48
1267	Towards systematic discovery of signaling networks in budding yeast filamentous growth stress response using interventional phosphorylation data. <b>2013</b> , 9, e1003077	13
1266	Endonuclease G mediates synuclein cytotoxicity during Parkinson's disease. <b>2013</b> , 32, 3041-54	63
1265	Insm1 controls development of pituitary endocrine cells and requires a SNAG domain for function and for recruitment of histone-modifying factors. <b>2013</b> , 140, 4947-58	32
1264	Phosphoproteomic analyses reveal signaling pathways that facilitate lytic gammaherpesvirus replication. <b>2013</b> , 9, e1003583	19
1263	Sequestration by IFIT1 impairs translation of 2'O-unmethylated capped RNA. <b>2013</b> , 9, e1003663	139

1262	Mass spectrometry-based proteomics for the analysis of chromatin structure and dynamics. <b>2013</b> , 14, 5402-31	27
1261	The amidation step of diphthamide biosynthesis in yeast requires DPH6, a gene identified through mining the DPH1-DPH5 interaction network. <b>2013</b> , 9, e1003334	34
1260	Active transport and diffusion barriers restrict Joubert Syndrome-associated ARL13B/ARL-13 to an Inv-like ciliary membrane subdomain. <b>2013</b> , 9, e1003977	73
1259	Silicon era of carbon-based life: application of genomics and bioinformatics in crop stress research. <b>2013</b> , 14, 11444-83	7
1258	$\beta$ 1 integrins with individually disrupted cytoplasmic NPxY motifs are embryonic lethal but partially active in the epidermis. <b>2013</b> , 133, 2722-2731	12
1257	Mechanisms of human adenovirus inactivation by sunlight and UVC light as examined by quantitative PCR and quantitative proteomics. <b>2013</b> , 79, 1325-32	47
1256	Arabidopsis nanodomain-delimited ABA signaling pathway regulates the anion channel SLAH3. <b>2013</b> , 110, 8296-301	151
1255	Spatiotemporal organization of Aurora-B by APC/CCdh1 after mitosis coordinates cell spreading through FHOD1. <b>2013</b> , 126, 2845-56	27
1254	The centriolar satellite protein SSX2IP promotes centrosome maturation. <b>2013</b> , 202, 81-95	50
1253	The restricted metabolism of the obligate organohalide respiring bacterium Dehalobacter restrictus: lessons from tiered functional genomics. <b>2013</b> , 368, 20120325	54
1252	RNF111/Arkadia is a SUMO-targeted ubiquitin ligase that facilitates the DNA damage response. <b>2013</b> , 201, 797-807	110
1251	Unraveling sterol-dependent membrane phenotypes by analysis of protein abundance-ratio distributions in different membrane fractions under biochemical and endogenous sterol depletion. <b>2013</b> , 12, 3732-43	5
1250	Quantitative phosphoproteomics after auxin-stimulated lateral root induction identifies an SNX1 protein phosphorylation site required for growth. <b>2013</b> , 12, 1158-69	76
1249	Wnt3a-dependent and -independent protein interaction networks of chromatin-bound $\beta$ -catenin in mouse embryonic stem cells. <b>2013</b> , 12, 1980-94	14
1248	Proteomics of genetically engineered mouse mammary tumors identifies fatty acid metabolism members as potential predictive markers for cisplatin resistance. <b>2013</b> , 12, 1319-34	19
1247	Activated cyclin-dependent kinase 5 promotes microglial phagocytosis of fibrillar $\beta$ -amyloid by up-regulating lipoprotein lipase expression. <b>2013</b> , 12, 2833-44	42
1246	Predicting response to bevacizumab in ovarian cancer: a panel of potential biomarkers informing treatment selection. <b>2013</b> , 19, 5227-39	54
1245	A combined approach of quantitative interaction proteomics and live-cell imaging reveals a regulatory role for endoplasmic reticulum (ER) reticulon homology proteins in peroxisome biogenesis. <b>2013</b> , 12, 2408-25	65

1244	Distinct XPPX sequence motifs induce ribosome stalling, which is rescued by the translation elongation factor EF-P. <b>2013</b> , 110, 15265-70	123
1243	Global subcellular characterization of protein degradation using quantitative proteomics. <b>2013</b> , 12, 638-50	91
1242	PGE(2) induces macrophage IL-10 production and a regulatory-like phenotype via a protein kinase A-SIK-CRTC3 pathway. <b>2013</b> , 190, 565-77	155
1241	Sucrose-induced receptor kinase SIRK1 regulates a plasma membrane aquaporin in Arabidopsis. <b>2013</b> , 12, 2856-73	76
1240	Phosphorylation of Gβis crucial for efficient chemotropism in yeast. <b>2013</b> , 126, 2997-3009	12
1239	Early phosphoproteomic changes in the mouse spleen during deoxynivalenol-induced ribotoxic stress. <b>2013</b> , 135, 129-43	21
1238	Popular computational methods to assess multiprotein complexes derived from label-free affinity purification and mass spectrometry (AP-MS) experiments. <b>2013</b> , 12, 1-13	39
1237	Glycosyltransferases from oat (Avena) implicated in the acylation of avenacins. <b>2013</b> , 288, 3696-704	31
1236	Multiple RNA interactions position Mrd1 at the site of the small subunit pseudoknot within the 90S pre-ribosome. <b>2013</b> , 41, 1178-90	18
1235	Acetylation dynamics of human nuclear proteins during the ionizing radiation-induced DNA damage response. <b>2013</b> , 12, 1688-95	24
1234	The Escherichia coli peripheral inner membrane proteome. <b>2013</b> , 12, 599-610	61
1233	Burial of the polymorphic residue 129 in amyloid fibrils of prion stop mutants. <b>2013</b> , 288, 2994-3002	15
1232	Quantitative proteomic analysis reveals concurrent RNA-protein interactions and identifies new RNA-binding proteins in Saccharomyces cerevisiae. <b>2013</b> , 23, 1028-38	48
1231	Translating mRNAs strongly correlate to proteins in a multivariate manner and their translation ratios are phenotype specific. <b>2013</b> , 41, 4743-54	107
1230	Ionizing radiation effects on cells, organelles and tissues on proteome level. <b>2013</b> , 990, 37-48	19
1229	Interaction between AP-5 and the hereditary spastic paraplegia proteins SPG11 and SPG15. <b>2013</b> , 24, 2558-69	77
1228	Quantitative Measurements in Proteomics. <b>2013</b> , 135-150	
1227	Integrative analysis of miRNA and mRNA expression profiles in pheochromocytoma and paraganglioma identifies genotype-specific markers and potentially regulated pathways. <b>2013</b> , 20, 477-93	40

1226	Quantitative dissection and stoichiometry determination of the human SET1/MLL histone methyltransferase complexes. <b>2013</b> , 33, 2067-77	145
1225	Stoichiometry of chromatin-associated protein complexes revealed by label-free quantitative mass spectrometry-based proteomics. <b>2013</b> , 41, e28	183
1224	QARIP: a web server for quantitative proteomic analysis of regulated intramembrane proteolysis. <b>2013</b> , 41, W459-64	17
1223	A new strategy for gene targeting and functional proteomics using the DT40 cell line. <b>2013</b> , 41, e167	13
1222	F-actin asymmetry and the endoplasmic reticulum-associated TCC-1 protein contribute to stereotypic spindle movements in the <i>Caenorhabditis elegans</i> embryo. <b>2013</b> , 24, 2201-15	13
1221	A complex of Cox4 and mitochondrial Hsp70 plays an important role in the assembly of the cytochrome c oxidase. <b>2013</b> , 24, 2609-19	31
1220	Prolyl hydroxylase domain protein 2 (PHD2) binds a Pro-Xaa-Leu-Glu motif, linking it to the heat shock protein 90 pathway. <b>2013</b> , 288, 9662-9674	40
1219	Mitochondrial outer membrane proteome of <i>Trypanosoma brucei</i> reveals novel factors required to maintain mitochondrial morphology. <b>2013</b> , 12, 515-28	67
1218	Sulfur-34S stable isotope labeling of amino acids for quantification (SULAQ34) of proteomic changes in <i>Pseudomonas fluorescens</i> during naphthalene degradation. <b>2013</b> , 12, 2060-9	15
1217	Isotope coded protein labeling coupled immunoprecipitation (ICPL-IP): a novel approach for quantitative protein complex analysis from native tissue. <b>2013</b> , 12, 1395-406	7
1216	Novel proteomic approach (PUNCH-P) reveals cell cycle-specific fluctuations in mRNA translation. <b>2013</b> , 27, 1834-44	72
1215	Magnetic fractionation and proteomic dissection of cellular organelles occupied by the late replication complexes of Semliki Forest virus. <b>2013</b> , 87, 10295-312	36
1214	Current status and advances in quantitative proteomic mass spectrometry. <b>2013</b> , 2013, 180605	115
1213	Quantitative Proteomics via High Resolution MS Quantification: Capabilities and Limitations. <b>2013</b> , 2013, 674282	14
1212	The effect of proteasome inhibition on the generation of the human leukocyte antigen (HLA) peptidome. <b>2013</b> , 12, 1853-64	52
1211	Phosphoproteomic analysis reveals the effects of PilF phosphorylation on type IV pilus and biofilm formation in <i>Thermus thermophilus</i> HB27. <b>2013</b> , 12, 2701-13	18
1210	YidC occupies the lateral gate of the SecYEG translocon and is sequentially displaced by a nascent membrane protein. <b>2013</b> , 288, 16295-16307	78
1209	Protein synthesis rate is the predominant regulator of protein expression during differentiation. <b>2013</b> , 9, 689	150

1208	In-depth proteomic analysis of mouse microglia using a combination of FASP and StageTip-based, high pH, reversed-phase fractionation. <b>2013</b> , 13, 2984-8	27
1207	Global remodelling of cellular microenvironment due to loss of collagen VII. <b>2013</b> , 9, 657	71
1206	Properties of isotope patterns and their utility for peptide identification in large-scale proteomic experiments. <b>2013</b> , 27, 1067-75	3
1205	Proteome turnover in bacteria: current status for <i>Corynebacterium glutamicum</i> and related bacteria. <b>2013</b> , 6, 708-19	18
1204	Protein correlation profiles identify lipid droplet proteins with high confidence. <b>2013</b> , 12, 1115-26	107
1203	Enhanced recovery of lyophilized peptides in shotgun proteomics by using an LC-ESI-MS compatible surfactant. <b>2013</b> , 13, 751-5	15
1202	Mitochondrial translation factors of <i>Trypanosoma brucei</i> : elongation factor-Tu has a unique subdomain that is essential for its function. <b>2013</b> , 90, 744-55	21
1201	Molecular basis of the essential S phase function of the rad53 checkpoint kinase. <b>2013</b> , 33, 3202-13	17
1200	Molecular deconvolution of the monoclonal antibodies that comprise the polyclonal serum response. <b>2013</b> , 110, 2993-8	107
1199	Quantitative measurement of phosphoproteome response to osmotic stress in arabidopsis based on Library-Assisted eXtracted Ion Chromatogram (LAXIC). <b>2013</b> , 12, 2354-69	55
1198	FMN2 is a novel regulator of the cyclin-dependent kinase inhibitor p21. <b>2013</b> , 12, 2348-54	9
1197	Initiation with elongator tRNAs. <b>2013</b> , 195, 4202-9	16
1196	Cleansing of Mass Spectrometry Data for Protein Identification and Quantification. <b>2013</b> , 59-76	
1195	Mutant p53 enhances MET trafficking and signalling to drive cell scattering and invasion. <b>2013</b> , 32, 1252-65	144
1194	JMJD1C demethylates MDC1 to regulate the RNF8 and BRCA1-mediated chromatin response to DNA breaks. <b>2013</b> , 20, 1425-33	73
1193	Comparative proteomics of two life cycle stages of stable isotope-labeled <i>Trypanosoma brucei</i> reveals novel components of the parasite's host adaptation machinery. <b>2013</b> , 12, 172-9	67
1192	Identification of CRM1-dependent Nuclear Export Cargos Using Quantitative Mass Spectrometry. <b>2013</b> , 12, 664-78	69
1191	Quantitative proteomics with siRNA screening identifies novel mechanisms of trastuzumab resistance in HER2 amplified breast cancers. <b>2013</b> , 12, 180-93	37

1190	Consistency of the proteome in primary human keratinocytes with respect to gender, age, and skin localization. <b>2013</b> , 12, 2509-21	29
1189	Determination of an angiotensin II-regulated proteome in primary human kidney cells by stable isotope labeling of amino acids in cell culture (SILAC). <b>2013</b> , 288, 24834-47	24
1188	Native SILAC: metabolic labeling of proteins in prototroph microorganisms based on lysine synthesis regulation. <b>2013</b> , 12, 1995-2005	43
1187	Identification of mRNAs bound and regulated by human LIN28 proteins and molecular requirements for RNA recognition. <b>2013</b> , 19, 613-26	110
1186	The heme a synthase Cox15 associates with cytochrome c oxidase assembly intermediates during Cox1 maturation. <b>2013</b> , 33, 4128-37	38
1185	Quantitative mass spectrometry-based proteomics in angiogenesis. <b>2013</b> , 7, 464-76	4
1184	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. <b>2013</b> , 7, 273-82	39
1183	Proteomics. <b>2013</b> , 83-106	2
1182	The <i>Aeromonas salmonicida</i> subsp. <i>salmonicida</i> exoproteome: global analysis, moonlighting proteins and putative antigens for vaccination against furunculosis. <b>2013</b> , 11, 44	28
1181	Identifizierung der Zielproteine bioaktiver Verbindungen: Die Suche nach der Nadel im Heuhaufen. <b>2013</b> , 125, 2808-2859	43
1180	Exosomal Proteome Profiling: A Potential Multi-Marker Cellular Phenotyping Tool to Characterize Hypoxia-Induced Radiation Resistance in Breast Cancer. <b>2013</b> , 1, 87-108	39
1179	Visual analytics of phosphorylation time-series data on insulin response. <b>2013</b> ,	2
1178	Global screening of CK2 kinase substrates by an integrated phosphoproteomics workflow. <b>2013</b> , 3, 3460	61
1177	Identification of dynamic changes in proteins associated with the cellular cytoskeleton after exposure to okadaic acid. <b>2013</b> , 11, 1763-82	23
1176	Comparison of preservation methods for bacterial cells in cytomics and proteomics. <b>2013</b> , 3,	3
1175	Cell cycle-regulated protein abundance changes in synchronously proliferating HeLa cells include regulation of pre-mRNA splicing proteins. <b>2013</b> , 8, e58456	11
1174	<i>Photobacterium profundum</i> under pressure: a MS-based label-free quantitative proteomics study. <b>2013</b> , 8, e60897	22
1173	Novel binding partners and differentially regulated phosphorylation sites clarify Eps8 as a multi-functional adaptor. <b>2013</b> , 8, e61513	10

1172	Metabolic turnover of synaptic proteins: kinetics, interdependencies and implications for synaptic maintenance. <b>2013</b> , 8, e63191	130
1171	Identification of critical regions in human SAMHD1 required for nuclear localization and Vpx-mediated degradation. <b>2013</b> , 8, e66201	23
1170	Direct detection of alternative open reading frames translation products in human significantly expands the proteome. <b>2013</b> , 8, e70698	135
1169	Expansion of multipotent stem cells from the adult human brain. <b>2013</b> , 8, e71334	36
1168	Structure-activity relationship of nerve-highlighting fluorophores. <b>2013</b> , 8, e73493	21
1167	Multivalent engagement of TFIID to nucleosomes. <b>2013</b> , 8, e73495	14
1166	Ran GTPase-activating protein 1 is a therapeutic target in diffuse large B-cell lymphoma. <b>2013</b> , 8, e79863	12
1165	A novel pulse-chase SILAC strategy measures changes in protein decay and synthesis rates induced by perturbation of proteostasis with an Hsp90 inhibitor. <b>2013</b> , 8, e80423	31
1164	Dynamic impacts of the inhibition of the molecular chaperone Hsp90 on the T-cell proteome have implications for anti-cancer therapy. <b>2013</b> , 8, e80425	31
1163	Comparative proteomics analysis of placenta from pregnant women with intrahepatic cholestasis of pregnancy. <b>2013</b> , 8, e83281	19
1162	Dynamic changes in mucus thickness and ion secretion during <i>Citrobacter rodentium</i> infection and clearance. <b>2013</b> , 8, e84430	34
1161	MAVS recruits multiple ubiquitin E3 ligases to activate antiviral signaling cascades. <b>2013</b> , 2, e00785	227
1160	Design and Statistical Analysis of Mass Spectrometry-Based Quantitative Proteomics Data. <b>2013</b> , 179-204	
1159	Proteomic Tools to Characterize Non-Thermal Plasma Effects in Eukaryotic Cells. <b>2013</b> , 3, 81-95	15
1158	Proteomic analysis of C2C12 myoblast and myotube exosome-like vesicles: a new paradigm for myoblast-myotube cross talk?. <b>2014</b> , 9, e84153	95
1157	The probabilistic convolution tree: efficient exact Bayesian inference for faster LC-MS/MS protein inference. <b>2014</b> , 9, e91507	11
1156	Alteration of protein levels during influenza virus H1N1 infection in host cells: a proteomic survey of host and virus reveals differential dynamics. <b>2014</b> , 9, e94257	29
1155	Quantitative-proteomic comparison of alpha and Beta cells to uncover novel targets for lineage reprogramming. <b>2014</b> , 9, e95194	10

1154	Genome-wide binding of MBD2 reveals strong preference for highly methylated loci. <b>2014</b> , 9, e99603	34
1153	Hijacking of host cellular functions by an intracellular parasite, the microsporidian <i>Anncaliia algerae</i> . <b>2014</b> , 9, e100791	19
1152	Stepwise splitting of ribosomal proteins from yeast ribosomes by LiCl. <b>2014</b> , 9, e101561	7
1151	Human stefin B role in cell's response to misfolded proteins and autophagy. <b>2014</b> , 9, e102500	11
1150	Phosphorylation site dynamics of early T-cell receptor signaling. <b>2014</b> , 9, e104240	46
1149	Profound impact of Hfq on nutrient acquisition, metabolism and motility in the plant pathogen <i>Agrobacterium tumefaciens</i> . <b>2014</b> , 9, e110427	24
1148	The ~ 16 kDa C-terminal sequence of clathrin assembly protein AP180 is essential for efficient clathrin binding. <b>2014</b> , 9, e110557	5
1147	HSP90 inhibition enhances antimetabolic drug-induced mitotic arrest and cell death in preclinical models of non-small cell lung cancer. <b>2014</b> , 9, e115228	10
1146	Quantitative proteomics analysis identifies mitochondria as therapeutic targets of multidrug-resistance in ovarian cancer. <b>2014</b> , 4, 1164-75	25
1145	[Analysis of oncogenic signaling induced by tyrosine kinases in tumors by SILAC-based quantitative proteomic approach]. <b>2014</b> , 30, 558-66	
1144	Proteogenomics in microbiology: taking the right turn at the junction of genomics and proteomics. <b>2014</b> , 14, 2360-675	24
1143	Inducing autophagy: a comparative phosphoproteomic study of the cellular response to ammonia and rapamycin. <b>2014</b> , 10, 339-55	57
1142	Proteomic analysis of effects by x-rays and heavy ion in HeLa cells. <b>2014</b> , 48, 142-54	10
1141	The membrane proteome of sensory cilia to the depth of olfactory receptors. <b>2014</b> , 13, 1828-43	33
1140	Identification of importin $\beta$ specific transport cargoes using a proteomic screening approach. <b>2014</b> , 13, 1286-98	16
1139	The mRNAs associated to a zinc finger protein from <i>Trypanosoma cruzi</i> shift during stress conditions. <b>2014</b> , 11, 921-33	21
1138	A substrate trapping approach identifies proteins regulated by reversible S-nitrosylation. <b>2014</b> , 13, 2573-83	26
1137	Parkin is activated by PINK1-dependent phosphorylation of ubiquitin at Ser65. <b>2014</b> , 460, 127-39	529



1136	Using SILAC proteomics to investigate the effect of the mycotoxin, alternariol, in the human H295R steroidogenesis model. <b>2014</b> , 30, 361-76	6
1135	A simple peak detection and label-free quantitation algorithm for chromatography-mass spectrometry. <b>2014</b> , 15, 376	9
1134	iTRAQ-based quantitative proteome and phosphoprotein characterization reveals the central metabolism changes involved in wheat grain development. <b>2014</b> , 15, 1029	68
1133	Casein kinase 1 $\Phi$ phosphorylates the Wnt regulator Jade-1 and modulates its activity. <b>2014</b> , 289, 26344-26356	11
1132	Human METTL20 methylates lysine residues adjacent to the recognition loop of the electron transfer flavoprotein in mitochondria. <b>2014</b> , 289, 24640-51	38
1131	C9orf72 FTLD/ALS-associated Gly-Ala dipeptide repeat proteins cause neuronal toxicity and Unc119 sequestration. <b>2014</b> , 128, 485-503	217
1130	A trimeric lipoprotein assists in trimeric autotransporter biogenesis in enterobacteria. <b>2014</b> , 289, 7388-98	20
1129	Defective Tibetan PHD2 binding to p23 links high altitude adaption to altered oxygen sensing. <b>2014</b> , 289, 14656-65	52
1128	A complex of Cas proteins 5, 6, and 7 is required for the biogenesis and stability of clustered regularly interspaced short palindromic repeats (crispr)-derived rnas (crnas) in <i>Haloferax volcanii</i> . <b>2014</b> , 289, 7164-7177	55
1127	The miR-206/133b cluster is dispensable for development, survival and regeneration of skeletal muscle. <b>2014</b> , 4, 23	62
1126	Ultradeep human phosphoproteome reveals a distinct regulatory nature of Tyr and Ser/Thr-based signaling. <b>2014</b> , 8, 1583-94	616
1125	Molecular signatures that correlate with induction of lens regeneration in newts: lessons from proteomic analysis. <b>2014</b> , 8, 22	12
1124	The Cdc42 guanine nucleotide exchange factor FGD6 coordinates cell polarity and endosomal membrane recycling in osteoclasts. <b>2014</b> , 289, 18347-59	42
1123	Proteomic survey reveals altered energetic patterns and metabolic failure prior to retinal degeneration. <b>2014</b> , 34, 2797-812	17
1122	Overexpression of Q-rich prion-like proteins suppresses polyQ cytotoxicity and alters the polyQ interactome. <b>2014</b> , 111, 18219-24	38
1121	Global phosphoproteome analysis of human bone marrow reveals predictive phosphorylation markers for the treatment of acute myeloid leukemia with quizartinib. <b>2014</b> , 28, 716-9	23
1120	Advantages and Applications of Gel-Free Proteomic Approaches in the Study of Prokaryotes. <b>2014</b> , 64, 157-200	1
1119	Dynamic proteomic profiles of in vivo- and in vitro-produced mouse postimplantation extraembryonic tissues and placentas. <b>2014</b> , 91, 155	22

1118	Proteogenomic analysis and global discovery of posttranslational modifications in prokaryotes. <b>2014</b> , 111, E5633-42	40
1117	SILAC-based proteomic quantification of chemoattractant-induced cytoskeleton dynamics on a second to minute timescale. <b>2014</b> , 5, 3319	15
1116	SILVER: an efficient tool for stable isotope labeling LC-MS data quantitative analysis with quality control methods. <b>2014</b> , 30, 586-7	18
1115	Redox regulation of Arabidopsis mitochondrial citrate synthase. <b>2014</b> , 7, 156-69	67
1114	Antimicrobial targets localize to the extracellular vesicle-associated proteome of <i>Pseudomonas aeruginosa</i> grown in a biofilm. <b>2014</b> , 5, 464	26
1113	Proteomics of a fuzzy organelle: interphase chromatin. <b>2014</b> , 33, 648-64	41
1112	The yeast Sks1p kinase signaling network regulates pseudohyphal growth and glucose response. <b>2014</b> , 10, e1004183	25
1111	The RSF1 histone-remodelling factor facilitates DNA double-strand break repair by recruiting centromeric and Fanconi Anaemia proteins. <b>2014</b> , 12, e1001856	33
1110	A combination of SILAC and nucleotide acyl phosphate labelling reveals unexpected targets of the Rsk inhibitor BI-D1870. <b>2014</b> , 34,	10
1109	TET-mediated oxidation of methylcytosine causes TDG or NEIL glycosylase dependent gene reactivation. <b>2014</b> , 42, 8592-604	69
1108	The Arabidopsis class II sirtuin is a lysine deacetylase and interacts with mitochondrial energy metabolism. <b>2014</b> , 164, 1401-14	73
1107	A role for eisosomes in maintenance of plasma membrane phosphoinositide levels. <b>2014</b> , 25, 2797-806	28
1106	Plasma membrane lipid-protein interactions affect signaling processes in sterol-biosynthesis mutants in <i>Arabidopsis thaliana</i> . <b>2014</b> , 5, 78	21
1105	Phytoplasma effector SAP54 hijacks plant reproduction by degrading MADS-box proteins and promotes insect colonization in a RAD23-dependent manner. <b>2014</b> , 12, e1001835	122
1104	Suicidal autointegration of sleeping beauty and piggyBac transposons in eukaryotic cells. <b>2014</b> , 10, e1004103	27
1103	StableIsotope Labeling with Amino Acids in Cell Culture (SILAC)-based strategy for proteome-wide thermodynamic analysis of protein-ligand binding interactions. <b>2014</b> , 13, 1800-13	47
1102	Bioinformatic Approaches to Increase Proteome Coverage. <b>2014</b> , 385-419	1
1101	Sphingosine kinase 1 isoform-specific interactions in breast cancer. <b>2014</b> , 28, 1899-915	20

1100	A systems-wide screen identifies substrates of the SCF <sup>TrCP</sup> ubiquitin ligase. <b>2014</b> , 7, rs8	35
1099	Quantitative proteomics analysis of altered protein expression in the placental villous tissue of early pregnancy loss using isobaric tandem mass tags. <b>2014</b> , 2014, 647143	10
1098	Comparative proteome analysis revealing an 11-protein signature for aggressive triple-negative breast cancer. <b>2014</b> , 106, djt376	62
1097	A novel mechanism inducing genome instability in Kaposi's sarcoma-associated herpesvirus infected cells. <b>2014</b> , 10, e1004098	46
1096	In-vivo quantitative proteomics reveals a key contribution of post-transcriptional mechanisms to the circadian regulation of liver metabolism. <b>2014</b> , 10, e1004047	260
1095	Radiosensitization of human leukemic HL-60 cells by ATR kinase inhibitor (VE-821): phosphoproteomic analysis. <b>2014</b> , 15, 12007-26	20
1094	Combining affinity proteomics and network context to identify new phosphatase substrates and adapters in growth pathways. <b>2014</b> , 5, 115	12
1093	Phosphoinositide metabolism links cGMP-dependent protein kinase G to essential Ca <sup>2+</sup> signals at key decision points in the life cycle of malaria parasites. <b>2014</b> , 12, e1001806	136
1092	Detecting differential protein expression in large-scale population proteomics. <b>2014</b> , 30, 2741-6	13
1091	Analysis of T4SS-induced signaling by H. pylori using quantitative phosphoproteomics. <b>2014</b> , 5, 356	16
1090	Quantitative phosphoproteomics of cytotoxic T cells to reveal protein kinase d 2 regulated networks. <b>2014</b> , 13, 3544-57	15
1089	Membrane protein profiling of human colon reveals distinct regional differences. <b>2014</b> , 13, 2277-87	26
1088	Host factors that interact with the pestivirus N-terminal protease, Npro, are components of the ribonucleoprotein complex. <b>2014</b> , 88, 10340-53	15
1087	Use of quantitative mass spectrometric analysis to elucidate the mechanisms of phospho-priming and auto-activation of the checkpoint kinase Rad53 in vivo. <b>2014</b> , 13, 551-65	12
1086	A horizontally acquired transcription factor coordinates Salmonella adaptations to host microenvironments. <b>2014</b> , 5, e01727-14	15
1085	An unbiased proteomic screen reveals caspase cleavage is positively and negatively regulated by substrate phosphorylation. <b>2014</b> , 13, 1184-97	28
1084	The Haemophilus ducreyi LspA1 protein inhibits phagocytosis by using a new mechanism involving activation of C-terminal Src kinase. <b>2014</b> , 5, e01178-14	9
1083	Quantitative proteomic analysis of compartmentalized signaling networks. <b>2014</b> , 535, 309-25	2

1082	Data set for the proteomics analysis of the endomembrane system from the unicellular <i>Entamoeba histolytica</i> . <b>2014</b> , 1, 29-36	5
1081	The virion of Cafeteria roenbergensis virus (CroV) contains a complex suite of proteins for transcription and DNA repair. <b>2014</b> , 466-467, 82-94	24
1080	Copy number analysis of the murine platelet proteome spanning the complete abundance range. <b>2014</b> , 13, 3435-45	138
1079	Global mass spectrometry and transcriptomics array based drug profiling provides novel insight into glucosamine induced endoplasmic reticulum stress. <b>2014</b> , 13, 3294-307	25
1078	Systematic analysis of the phosphoproteome and kinase-substrate networks in the mouse testis. <b>2014</b> , 13, 3626-38	27
1077	JUMP: a tag-based database search tool for peptide identification with high sensitivity and accuracy. <b>2014</b> , 13, 3663-73	80
1076	Identification of candidate substrates for the Golgi Tul1 E3 ligase using quantitative diGly proteomics in yeast. <b>2014</b> , 13, 2871-82	25
1075	A comprehensive proteomic view of responses of A549 type II alveolar epithelial cells to human respiratory syncytial virus infection. <b>2014</b> , 13, 3250-69	24
1074	A chromatin activity-based chemoproteomic approach reveals a transcriptional repressome for gene-specific silencing. <b>2014</b> , 5, 5733	21
1073	BRCA2 diffuses as oligomeric clusters with RAD51 and changes mobility after DNA damage in live cells. <b>2014</b> , 207, 599-613	42
1072	Combining pulsed SILAC labeling and click-chemistry for quantitative secretome analysis. <b>2014</b> , 1174, 101-14	21
1071	Analytical utility of mass spectral binning in proteomic experiments by SPectral Immonium Ion Detection (SPIID). <b>2014</b> , 13, 1914-24	15
1070	A holin and an endopeptidase are essential for chitinolytic protein secretion in <i>Serratia marcescens</i> . <b>2014</b> , 207, 615-26	24
1069	The COP9 signalosome is involved in the regulation of lipid metabolism and of transition metals uptake in <i>Saccharomyces cerevisiae</i> . <b>2014</b> , 281, 175-90	13
1068	Detecting envelope stress by monitoring $\alpha$ -barrel assembly. <b>2014</b> , 159, 1652-64	118
1067	Quantitative proteomic analysis of exosome protein content changes induced by hepatitis B virus in Huh-7 cells using SILAC labeling and LC-MS/MS. <b>2014</b> , 13, 5391-402	51
1066	Proteome and phosphoproteome characterization reveals new response and defense mechanisms of <i>Brachypodium distachyon</i> leaves under salt stress. <b>2014</b> , 13, 632-52	103
1065	Chemoproteomics demonstrates target engagement and exquisite selectivity of the clinical phosphodiesterase 10A inhibitor MP-10 in its native environment. <b>2014</b> , 9, 2823-32	20

1064	USP17- and SCF <sup>TrCP</sup> --regulated degradation of DEC1 controls the DNA damage response. <b>2014</b> , 34, 4177-85	18
1063	microRNA-mediated regulation of mTOR complex components facilitates discrimination between activation and anergy in CD4 T cells. <b>2014</b> , 211, 2281-95	49
1062	Isolation and characterization of a prokaryotic cell organelle from the anammox bacterium <i>Kuenenia stuttgartiensis</i> . <b>2014</b> , 94, 794-802	58
1061	Assessment of serum protein dynamics by native SILAC flooding (SILflood). <b>2014</b> , 86, 11033-7	9
1060	Protter: interactive protein feature visualization and integration with experimental proteomic data. <b>2014</b> , 30, 884-6	666
1059	CDK5 is a major regulator of the tumor suppressor DLC1. <b>2014</b> , 207, 627-42	41
1058	In situ visualization of newly synthesized proteins in environmental microbes using amino acid tagging and click chemistry. <b>2014</b> , 16, 2568-90	129
1057	In-depth proteomic analysis of whole testis tissue from the adult rhesus macaque. <b>2014</b> , 14, 1393-402	11
1056	The Q Exactive HF, a Benchtop mass spectrometer with a pre-filter, high-performance quadrupole and an ultra-high-field Orbitrap analyzer. <b>2014</b> , 13, 3698-708	229
1055	MBD5 and MBD6 interact with the human PR-DUB complex through their methyl-CpG-binding domain. <b>2014</b> , 14, 2179-89	61
1054	In vitro characterization of bacterial and chloroplast Hsp70 systems reveals an evolutionary optimization of the co-chaperones for their Hsp70 partner. <b>2014</b> , 460, 13-24	13
1053	Establishment of a proteomic profile associated with gonocyte and spermatogonial stem cell maturation and differentiation in neonatal mice. <b>2014</b> , 14, 274-85	20
1052	Accurate proteome-wide label-free quantification by delayed normalization and maximal peptide ratio extraction, termed MaxLFQ. <b>2014</b> , 13, 2513-26	2578
1051	Cell-type-resolved quantitative proteomics of murine liver. <b>2014</b> , 20, 1076-87	106
1050	SNF5/INI1 deficiency redefines chromatin remodeling complex composition during tumor development. <b>2014</b> , 12, 1574-85	19
1049	Integrated omic analysis of lung cancer reveals metabolism proteome signatures with prognostic impact. <b>2014</b> , 5, 5469	67
1048	Deep proteomic evaluation of primary and cell line motoneuron disease models delineates major differences in neuronal characteristics. <b>2014</b> , 13, 3410-20	40
1047	Integration of mass spectrometry and RNA-Seq data to confirm human ab initio predicted genes and lncRNAs. <b>2014</b> , 14, 2760-8	16

1046	Proteomics analysis of adult testis from <i>Bombyx mori</i> . <b>2014</b> , 14, 2345-9	5
1045	MapZ marks the division sites and positions FtsZ rings in <i>Streptococcus pneumoniae</i> . <b>2014</b> , 516, 259-262	138
1044	Rapid and deep proteomes by faster sequencing on a benchtop quadrupole ultra-high-field Orbitrap mass spectrometer. <b>2014</b> , 13, 6187-95	134
1043	Comprehensive assessment of proteins regulated by dexamethasone reveals novel effects in primary human peripheral blood mononuclear cells. <b>2014</b> , 13, 5989-6000	41
1042	Structural basis for microtubule recognition by the human kinetochore Ska complex. <b>2014</b> , 5, 2964	66
1041	Global profiling of co- and post-translationally N-myristoylated proteomes in human cells. <b>2014</b> , 5, 4919	148
1040	Proteomics for systems toxicology. <b>2014</b> , 11, 73-90	45
1039	Peptide handling by HLA-B27 subtypes influences their biological behavior, association with ankylosing spondylitis and susceptibility to endoplasmic reticulum aminopeptidase 1 (ERAP1). <b>2014</b> , 13, 3367-80	30
1038	Quantitative proteome analyses identify PrfA-responsive proteins and phosphoproteins in <i>Listeria monocytogenes</i> . <b>2014</b> , 13, 6046-57	21
1037	Off-line high-pH reversed-phase fractionation for in-depth phosphoproteomics. <b>2014</b> , 13, 6176-86	194
1036	Proteomic analysis of human fetal atria and ventricle. <b>2014</b> , 13, 5869-78	23
1035	In-depth quantitative proteomic analysis of de novo protein synthesis induced by brain-derived neurotrophic factor. <b>2014</b> , 13, 5707-14	35
1034	ICan: an optimized ion-current-based quantification procedure with enhanced quantitative accuracy and sensitivity in biomarker discovery. <b>2014</b> , 13, 5888-97	21
1033	The p38 $\alpha$ mitogen-activated protein kinase possesses an intrinsic autophosphorylation activity, generated by a short region composed of the $\alpha$ helix and MAPK insert. <b>2014</b> , 289, 23546-56	30
1032	Protein acetylation affects acetate metabolism, motility and acid stress response in <i>Escherichia coli</i> . <b>2014</b> , 10, 762	98
1031	Construction and assessment of individualized proteogenomic databases for large-scale analysis of nonsynonymous single nucleotide variants. <b>2014</b> , 14, 2699-708	13
1030	eIF2B is a decameric guanine nucleotide exchange factor with a $\alpha\beta$ tetrameric core. <b>2014</b> , 5, 3902	52
1029	The neuroendocrine phenotype of gastric myofibroblasts and its loss with cancer progression. <b>2014</b> , 35, 1798-806	16

1028	Identification of lipid synthesis and secretion proteins in bovine milk. <b>2014</b> , 81, 65-72	20
1027	Alterations in the cerebellar (Phospho)proteome of a cyclic guanosine monophosphate (cGMP)-dependent protein kinase knockout mouse. <b>2014</b> , 13, 2004-16	11
1026	Global absolute quantification reveals tight regulation of protein expression in single <i>Xenopus</i> eggs. <b>2014</b> , 42, 9880-91	47
1025	Systems genomics evaluation of the SH-SY5Y neuroblastoma cell line as a model for Parkinson's disease. <b>2014</b> , 15, 1154	87
1024	The translation initiation complex eIF3 in trypanosomatids and other pathogenic excavates--identification of conserved and divergent features based on orthologue analysis. <b>2014</b> , 15, 1175	29
1023	RNA-seq reveals the pan-transcriptomic impact of attenuating the gliotoxin self-protection mechanism in <i>Aspergillus fumigatus</i> . <b>2014</b> , 15, 894	35
1022	Human post-mortem synapse proteome integrity screening for proteomic studies of postsynaptic complexes. <b>2014</b> , 7, 88	39
1021	Class I and IIa histone deacetylases have opposite effects on sclerostin gene regulation. <b>2014</b> , 289, 24995-5009	34
1020	The mzTab data exchange format: communicating mass-spectrometry-based proteomics and metabolomics experimental results to a wider audience. <b>2014</b> , 13, 2765-75	96
1019	Carpal tunnel syndrome is associated with high fibrinogen and fibrinogen deposits. <b>2014</b> , 75, 276-85; discussion 285	1
1018	Microbial-induced meprin $\alpha$ cleavage in MUC2 mucin and a functional CFTR channel are required to release anchored small intestinal mucus. <b>2014</b> , 111, 12396-401	130
1017	Linear mtDNA fragments and unusual mtDNA rearrangements associated with pathological deficiency of MGME1 exonuclease. <b>2014</b> , 23, 6147-62	50
1016	Architecture and ssDNA interaction of the Timeless-Tipin-RPA complex. <b>2014</b> , 42, 12912-27	16
1015	Proteomic Approach to the Reprogramming Machinery of the Mouse Oocyte. <b>2014</b> , 407-417	
1014	Translational stalling at polyproline stretches is modulated by the sequence context upstream of the stall site. <b>2014</b> , 42, 10711-9	63
1013	PIQMle: a web server for semi-quantitative proteomics data management and analysis. <b>2014</b> , 42, W100-6	7
1012	Proteomics of <i>Toxoplasma gondii</i> . <b>2014</b> , 731-754	0
1011	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. <b>2014</b> , 15, 6265-85	10

1010	An integrated approach for genome annotation of the eukaryotic thermophile <i>Chaetomium thermophilum</i> . <b>2014</b> , 42, 13525-33	40
1009	Orders of magnitude extension of the effective dynamic range of TDC-based TOFMS data through maximum likelihood estimation. <b>2014</b> , 25, 1824-7	4
1008	Inhibition of Cyclooxygenase-2 Prevents Chronic and Recurrent Cystitis. <b>2014</b> , 1, 46-57	61
1007	Analysis of expressed genes of the bacterium ' <i>Candidatus phytoplasma Mali</i> ' highlights key features of virulence and metabolism. <b>2014</b> , 9, e94391	23
1006	E-cadherin interactome complexity and robustness resolved by quantitative proteomics. <b>2014</b> , 7, rs7	114
1005	ROCK1 is a potential combinatorial drug target for BRAF mutant melanoma. <b>2014</b> , 10, 772	38
1004	Time-resolved dissection of early phosphoproteome and ensuing proteome changes in response to TGF- $\beta$ <b>2014</b> , 7, rs5	32
1003	Probing SH2-domains using Inhibitor Affinity Purification (IAP). <b>2014</b> , 12, 41	10
1002	Glycoproteomic analysis identifies human glycoproteins secreted from HIV latently infected T cells and reveals their presence in HIV+ plasma. <b>2014</b> , 11, 9	19
1001	Proteome analysis and conditional deletion of the EAAT2 glutamate transporter provide evidence against a role of EAAT2 in pancreatic insulin secretion in mice. <b>2014</b> , 289, 1329-44	37
1000	Proteomic and functional consequences of hexokinase deficiency in glucose-repressible <i>Kluyveromyces lactis</i> . <b>2014</b> , 13, 860-75	8
999	Insights into the activation of the helicase Prp43 by biochemical studies and structural mass spectrometry. <b>2014</b> , 42, 1162-79	50
998	Proteome-wide identification of SUMO2 modification sites. <b>2014</b> , 7, rs2	142
997	Systems Analysis of Chromatin-Related Protein Complexes in Cancer. <b>2014</b> ,	
996	Plasma proteome profiling of atherosclerotic disease manifestations reveals elevated levels of the cytoskeletal protein vinculin. <b>2014</b> , 101, 141-53	29
995	The phosphoproteome and its physiological dynamics in <i>Staphylococcus aureus</i> . <b>2014</b> , 304, 121-32	40
994	Proteomic investigation of cultivated fibroblasts from patients with mitochondrial short-chain acyl-CoA dehydrogenase deficiency. <b>2014</b> , 111, 360-368	19
993	Cytosolic calcium, hydrogen peroxide and related gene expression and protein modulation in <i>Arabidopsis thaliana</i> cell cultures respond immediately to altered gravitation: parabolic flight data. <b>2014</b> , 16 Suppl 1, 120-8	45



992	A proteomics strategy for the identification of FAT10-modified sites by mass spectrometry. <b>2014</b> , 13, 268-76	18
991	Computational proteomics: designing a comprehensive analytical strategy. <b>2014</b> , 19, 266-74	15
990	O-linked glycosylation sites profiling in Mycobacterium tuberculosis culture filtrate proteins. <b>2014</b> , 97, 296-306	38
989	Quantitative proteomics identifies the membrane-associated peroxidase GPx8 as a cellular substrate of the hepatitis C virus NS3-4A protease. <b>2014</b> , 59, 423-33	35
988	Proteomics of larval hemolymph in Bombyx mori reveals various nutrient-storage and immunity-related proteins. <b>2014</b> , 46, 1021-31	34
987	Dengue. <b>2014</b> ,	5
986	Herpes Simplex Virus. <b>2014</b> ,	1
985	A site-specific phosphorylation of the focal adhesion kinase controls the formation of spheroid cell clusters. <b>2014</b> , 39, 1199-205	9
984	Loss of glutathione peroxidase 7 promotes TNF- $\alpha$ -induced NF- $\kappa$ B activation in Barrett's carcinogenesis. <b>2014</b> , 35, 1620-8	24
983	What can proteomics tell us about platelets?. <b>2014</b> , 114, 1204-19	76
982	In vitro assembly and activity of an archaeal CRISPR-Cas type I-A Cascade interference complex. <b>2014</b> , 42, 5125-38	48
981	Epithelial-mesenchymal transition-associated secretory phenotype predicts survival in lung cancer patients. <b>2014</b> , 35, 1292-300	31
980	Stoichiometry of Saccharomyces cerevisiae lysine methylation: insights into non-histone protein lysine methyltransferase activity. <b>2014</b> , 13, 1744-56	19
979	Phosphoregulation of the human SMN complex. <b>2014</b> , 93, 106-17	17
978	Quantitative shotgun proteomics: considerations for a high-quality workflow in immunology. <b>2014</b> , 15, 112-7	72
977	Experimental and computational tools for analysis of signaling networks in primary cells. <b>2014</b> , 104, 11.11.1-11.11.1.23	1.23
976	DNA-aptamer/protein interaction as a cause of apoptosis and arrest of proliferation in Ehrlich ascites adenocarcinoma cells. <b>2014</b> , 8, 60-72	6
975	ADAM17 mediates OSCC development in an orthotopic murine model. <b>2014</b> , 13, 24	15

974	Heart regeneration: opportunities and challenges for drug discovery with novel chemical and therapeutic methods or agents. <b>2014</b> , 53, 4056-75	32
973	PA28 $\beta$ reduces size and increases hydrophilicity of 20S immunoproteasome peptide products. <b>2014</b> , 21, 470-480	41
972	Minimal, encapsulated proteomic-sample processing applied to copy-number estimation in eukaryotic cells. <b>2014</b> , 11, 319-24	977
971	Large-scale quantification of single amino-acid variations by a variation-associated database search strategy. <b>2014</b> , 13, 241-8	20
970	Direction pathway analysis of large-scale proteomics data reveals novel features of the insulin action pathway. <b>2014</b> , 30, 808-14	20
969	Bioinformatics tools to identify and quantify proteins using mass spectrometry data. <b>2014</b> , 94, 1-17	9
968	Proteomic profiles of human lung adeno and squamous cell carcinoma using super-SILAC and label-free quantification approaches. <b>2014</b> , 14, 795-803	24
967	Metaproteomics of our microbiome - developing insight in function and activity in man and model systems. <b>2014</b> , 97, 3-16	87
966	Proteasome-dependent degradation of transcription factor activating enhancer-binding protein 4 (TFAP4) controls mitotic division. <b>2014</b> , 289, 7730-7	18
965	Nascent chromatin capture proteomics determines chromatin dynamics during DNA replication and identifies unknown fork components. <b>2014</b> , 16, 281-93	225
964	Initial steps in RNA processing and ribosome assembly occur at mitochondrial DNA nucleoids. <b>2014</b> , 19, 618-29	79
963	Dynamic changes in ribosome-associated proteome and phosphoproteome during deoxynivalenol-induced translation inhibition and ribotoxic stress. <b>2014</b> , 138, 217-33	28
962	Proteomic analysis of cerebrospinal fluid extracellular vesicles: a comprehensive dataset. <b>2014</b> , 106, 191-204	172
961	Liposome-based assays to study membrane-associated protein networks. <b>2014</b> , 534, 223-43	5
960	Comparative interactomes of SIRT6 and SIRT7: Implication of functional links to aging. <b>2014</b> , 14, 1610-22	59
959	Monomethylarsonous acid inhibited endogenous cholesterol biosynthesis in human skin fibroblasts. <b>2014</b> , 277, 21-9	7
958	Shotgun Proteomics. <b>2014</b> ,	5
957	Comparative ribosome profiling reveals extensive translational complexity in different <i>Trypanosoma brucei</i> life cycle stages. <b>2014</b> , 42, 3623-37	107

956	Natural product proteomining, a quantitative proteomics platform, allows rapid discovery of biosynthetic gene clusters for different classes of natural products. <b>2014</b> , 21, 707-18	43
955	Deletion of 30 murine cytochrome p450 genes results in viable mice with compromised drug metabolism. <b>2014</b> , 42, 1022-30	21
954	Proteomic analysis of mouse astrocytes and their secretome by a combination of FASP and StageTip-based, high pH, reversed-phase fractionation. <b>2014</b> , 14, 1604-9	56
953	Phosphorus deficiency affects multiple macromolecular biosynthesis pathways of <i>Thalassiosira weissflogii</i> . <b>2014</b> , 33, 85-91	10
952	Prereplicative complexes assembled in vitro support origin-dependent and independent DNA replication. <b>2014</b> , 33, 605-20	62
951	Prosurvival function of the cellular apoptosis susceptibility/importin- $\beta$ transport cycle is repressed by p53 in liver cancer. <b>2014</b> , 60, 884-95	25
950	Coordinated activation of PTA-ACS and TCA cycles strongly reduces overflow metabolism of acetate in <i>Escherichia coli</i> . <b>2014</b> , 98, 5131-43	26
949	CoreFlow: a computational platform for integration, analysis and modeling of complex biological data. <b>2014</b> , 100, 167-73	8
948	Autoubiquitination of the 26S proteasome on Rpn13 regulates breakdown of ubiquitin conjugates. <b>2014</b> , 33, 1159-76	116
947	Molecular characterization and functional analyses of ZtWor1, a transcriptional regulator of the fungal wheat pathogen <i>Zymoseptoria tritici</i> . <b>2014</b> , 15, 394-405	38
946	The pea seedling mitochondrial N <sup>ε</sup> -lysine acetylome. <b>2014</b> , 19 Pt B, 154-65	34
945	Mass-spectrometry-based draft of the human proteome. <b>2014</b> , 509, 582-7	1332
944	Quantitative phosphoproteomics unravels biased phosphorylation of serotonin 2A receptor at Ser280 by hallucinogenic versus nonhallucinogenic agonists. <b>2014</b> , 13, 1273-85	38
943	Composition of isolated synaptic boutons reveals the amounts of vesicle trafficking proteins. <b>2014</b> , 344, 1023-8	453
942	Accurate label-free protein quantitation with high- and low-resolution mass spectrometers. <b>2014</b> , 13, 1034-1044	90
941	Quantitative accuracy in mass spectrometry based proteomics of complex samples: the impact of labeling and precursor interference. <b>2014</b> , 96, 133-44	61
940	SILAC peptide ratio calculator: a tool for SILAC quantitation of peptides and post-translational modifications. <b>2014</b> , 13, 506-16	4
939	Quantitative proteomic dissection of a native 14-3-3 $\sigma$ -interacting protein complex associated with hepatocellular carcinoma. <b>2014</b> , 46, 841-52	4

938	Guanylate binding protein 1-mediated interaction of T cell antigen receptor signaling with the cytoskeleton. <b>2014</b> , 192, 771-81	29
937	Resolution of the type material of the Asian elephant, <i>Elephas maximus</i> Linnaeus, 1758 (Proboscidea, Elephantidae). <b>2014</b> , 170, 222-232	24
936	Gene Function Analysis. <b>2014</b> ,	1
935	Introduction to opportunities and pitfalls in functional mass spectrometry based proteomics. <b>2014</b> , 1844, 12-20	24
934	Glutamine methylation in histone H2A is an RNA-polymerase-I-dedicated modification. <b>2014</b> , 505, 564-8	149
933	Citrullination regulates pluripotency and histone H1 binding to chromatin. <b>2014</b> , 507, 104-8	264
932	Trypsin-catalyzed N-terminal labeling of peptides with stable isotope-coded affinity tags for proteome analysis. <b>2014</b> , 86, 1170-7	8
931	Rapid profiling of protein kinase inhibitors by quantitative proteomics. <b>2014</b> , 5, 363-369	17
930	Secretome analysis of human mesenchymal stem cells undergoing chondrogenic differentiation. <b>2014</b> , 13, 1045-54	32
929	Proteins and Proteomics of Leishmania and Trypanosoma. <b>2014</b> ,	5
928	Collective migration of cancer-associated fibroblasts is enhanced by overexpression of tight junction-associated proteins claudin-11 and occludin. <b>2014</b> , 8, 178-95	37
927	Proteomic analysis of gliosomes from mouse brain: identification and investigation of glial membrane proteins. <b>2014</b> , 13, 5918-27	20
926	Architecture of the <i>Saccharomyces cerevisiae</i> SAGA transcription coactivator complex. <b>2014</b> , 33, 2534-46	78
925	Circadian clock-dependent and -independent rhythmic proteomes implement distinct diurnal functions in mouse liver. <b>2014</b> , 111, 167-72	227
924	A pipeline for determining protein-protein interactions and proximities in the cellular milieu. <b>2014</b> , 13, 2824-35	33
923	Using in vivo biotinylated ubiquitin to describe a mitotic exit ubiquitome from human cells. <b>2014</b> , 13, 2411-25	29
922	The INA complex facilitates assembly of the peripheral stalk of the mitochondrial F1Fo-ATP synthase. <b>2014</b> , 33, 1624-38	26
921	Comparative proteomic analysis of outer membrane vesicles from <i>Shigella flexneri</i> under different culture conditions. <b>2014</b> , 453, 696-702	12

920	Over 10,000 peptide identifications from the HeLa proteome by using single-shot capillary zone electrophoresis combined with tandem mass spectrometry. <b>2014</b> , 53, 13931-3	74
919	Quantitative proteomics reveals the dynamics of protein changes during Drosophila oocyte maturation and the oocyte-to-embryo transition. <b>2014</b> , 111, 16023-8	42
918	Huntingtin is associated with cytomatrix proteins at the presynaptic terminal. <b>2014</b> , 63, 96-100	12
917	Exploring intercellular signaling by proteomic approaches. <b>2014</b> , 14, 498-512	13
916	Phosphoproteome profiling of the macrophage response to different toll-like receptor ligands identifies differences in global phosphorylation dynamics. <b>2014</b> , 13, 5185-97	24
915	Proteome profiling of breast cancer biopsies reveals a wound healing signature of cancer-associated fibroblasts. <b>2014</b> , 13, 4773-82	28
914	Quantitative proteomics reveals novel therapeutic and diagnostic markers in hypertension. <b>2014</b> , 2, 79-87	20
913	A "proteomic ruler" for protein copy number and concentration estimation without spike-in standards. <b>2014</b> , 13, 3497-506	324
912	Characterization of early autophagy signaling by quantitative phosphoproteomics. <b>2014</b> , 10, 356-71	26
911	Using in-solution digestion, peptide fractionation, and a Q exactive mass spectrometer to analyze the proteome of clathrin-coated vesicles. <b>2014</b> , 2014, 1192-5	6
910	Using in-gel digestion and an Orbitrap mass spectrometer to analyze the proteome of clathrin-coated vesicles. <b>2014</b> , 2014, 1188-91	4
909	Long-term effects of repeated superovulation on ovarian structure and function in rhesus monkeys. <b>2014</b> , 102, 1452-1457.e1	16
908	General statistical framework for quantitative proteomics by stable isotope labeling. <b>2014</b> , 13, 1234-47	100
907	Proteomic analysis of intact flagella of procyclic Trypanosoma brucei cells identifies novel flagellar proteins with unique sub-localization and dynamics. <b>2014</b> , 13, 1769-86	83
906	Affinity purification-mass spectrometry and network analysis to understand protein-protein interactions. <b>2014</b> , 9, 2539-54	110
905	Protein interaction screening for the ankyrin repeats and suppressor of cytokine signaling (SOCS) box (ASB) family identify Asb11 as a novel endoplasmic reticulum resident ubiquitin ligase. <b>2014</b> , 289, 2043-54	30
904	Fractionation profiling: a fast and versatile approach for mapping vesicle proteomes and protein-protein interactions. <b>2014</b> , 25, 3178-94	35
903	Selective VPS34 inhibitor blocks autophagy and uncovers a role for NCOA4 in ferritin degradation and iron homeostasis in vivo. <b>2014</b> , 16, 1069-79	370

902	Label-free quantitative proteomic analysis of the YAP/TAZ interactome. <b>2014</b> , 306, C805-18	49
901	Ubiquitin-dependent regulation of MEKK2/3-MEK5-ERK5 signaling module by XIAP and cIAP1. <b>2014</b> , 33, 1784-801	22
900	Cleavage of E-cadherin and $\beta$ -catenin by calpain affects Wnt signaling and spheroid formation in suspension cultures of human pluripotent stem cells. <b>2014</b> , 13, 990-1007	41
899	More than a pore: ion channel signaling complexes. <b>2014</b> , 34, 15159-69	45
898	Proteomic analysis of protein deamidation. <b>2014</b> , 78, 24.5.1-24.5.14	6
897	Unravelling the proteome of adult rhesus monkey ovaries. <b>2014</b> , 10, 653-62	9
896	Comparison of alternative MS/MS and bioinformatics approaches for confident phosphorylation site localization. <b>2014</b> , 13, 1128-37	34
895	Protein turnover forms one of the highest maintenance costs in <i>Lactococcus lactis</i> . <b>2014</b> , 160, 1501-1512	30
894	Proteome-wide enrichment of proteins modified by lysine methylation. <b>2014</b> , 9, 37-50	57
893	Protein inference using Peptide quantification patterns. <b>2014</b> , 13, 3191-9	10
892	Uncovering global SUMOylation signaling networks in a site-specific manner. <b>2014</b> , 21, 927-36	314
891	Systematic nucleo-cytoplasmic trafficking of proteins following exposure of MCF7 breast cancer cells to estradiol. <b>2014</b> , 13, 1112-27	15
890	A normative study of the synovial fluid proteome from healthy porcine knee joints. <b>2014</b> , 13, 4377-87	48
889	Advancements of Mass Spectrometry in Biomedical Research. <b>2014</b> ,	4
888	A COFRADIC protocol to study protein ubiquitination. <b>2014</b> , 13, 3107-13	41
887	Quantitative proteomics reveals the kinetics of trypsin-catalyzed protein digestion. <b>2014</b> , 406, 6247-56	19
886	Disclosure of selective advantages in the "modern" sublineage of the <i>Mycobacterium tuberculosis</i> Beijing genotype family by quantitative proteomics. <b>2014</b> , 13, 2632-45	23
885	$\text{CaMKII}$ shuttles $\text{Ca}^{2+}$ /CaM to the nucleus to trigger CREB phosphorylation and gene expression. <b>2014</b> , 159, 281-94	160

884	Quantitative analysis of the Escherichia coli proteome. <b>2014</b> , 1, 7-11	20
883	Application of SILAC labeling to primary bone marrow-derived dendritic cells reveals extensive GM-CSF-dependent arginine metabolism. <b>2014</b> , 13, 752-62	6
882	PIM2 kinase is induced by cisplatin in ovarian cancer cells and limits drug efficacy. <b>2014</b> , 13, 4970-82	17
881	Cd <sup>2+</sup> -induced alteration of the global proteome of human skin fibroblast cells. <b>2014</b> , 13, 1677-87	10
880	In vivo proximity labeling for the detection of protein-protein and protein-RNA interactions. <b>2014</b> , 13, 6135-43	17
879	Systematic assessment of survey scan and MS2-based abundance strategies for label-free quantitative proteomics using high-resolution MS data. <b>2014</b> , 13, 2069-79	38
878	Exploring skyline for both MS(E) -based label-free proteomics and HRMS quantitation of small molecules. <b>2014</b> , 14, 169-80	11
877	Comparing SILAC- and stable isotope dimethyl-labeling approaches for quantitative proteomics. <b>2014</b> , 13, 4164-74	82
876	Comparative phosphoproteome analysis of the developing grains in bread wheat ( <i>Triticum aestivum</i> L.) under well-watered and water-deficit conditions. <b>2014</b> , 13, 4281-97	48
875	Structural model of a CRISPR RNA-silencing complex reveals the RNA-target cleavage activity in Cmr4. <b>2014</b> , 56, 43-54	112
874	Systematic analysis of missing proteins provides clues to help define all of the protein-coding genes on human chromosome 1. <b>2014</b> , 13, 114-25	21
873	Overview of peptide and protein analysis by mass spectrometry. <b>2014</b> , 108, 10.21.1-30	20
872	In situ sample processing approach (iSPA) for comprehensive quantitative phosphoproteome analysis. <b>2014</b> , 13, 3896-904	12
871	SAHA regulates histone acetylation, Butyrylation, and protein expression in neuroblastoma. <b>2014</b> , 13, 4211-9	22
870	Quantitative proteomic analysis of host-virus interactions reveals a role for Golgi brefeldin A resistance factor 1 (GBF1) in dengue infection. <b>2014</b> , 13, 2836-54	36
869	Transcriptomics and proteomics in stem cell research. <b>2014</b> , 8, 433-44	5
868	Quantitative phosphoproteomics reveals novel phosphorylation events in insulin signaling regulated by protein phosphatase 1 regulatory subunit 12A. <b>2014</b> , 109, 63-75	17
867	Decreasing the amount of trypsin in in-gel digestion leads to diminished chemical noise and improved protein identifications. <b>2014</b> , 109, 16-25	38

866	Multi-enzyme digestion FASP and the 'Total Protein Approach'-based absolute quantification of the <i>Escherichia coli</i> proteome. <b>2014</b> , 109, 322-31	121
865	Label-free proteomic analysis of environmental acidification-influenced <i>Streptococcus pyogenes</i> secretome reveals a novel acid-induced protein histidine triad protein A (HtpA) involved in necrotizing fasciitis. <b>2014</b> , 109, 90-103	13
864	The <i>Entamoeba histolytica</i> Dnmt2 homolog (Ehmeth) confers resistance to nitrosative stress. <b>2014</b> , 13, 494-503	24
863	AKT1 and AKT2 induce distinct phosphorylation patterns in HL-1 cardiac myocytes. <b>2014</b> , 13, 4232-45	14
862	Structural insight into how <i>Streptomyces coelicolor</i> maltosyl transferase GlgE binds $\alpha$ -maltose 1-phosphate and forms a maltosyl-enzyme intermediate. <b>2014</b> , 53, 2494-504	27
861	Deciphering the role of the ADAM17-dependent secretome in cell signaling. <b>2014</b> , 13, 2080-93	33
860	Absolute proteome and phosphoproteome dynamics during the cell cycle of <i>Schizosaccharomyces pombe</i> (Fission Yeast). <b>2014</b> , 13, 1925-36	103
859	Proteomic analysis of arginine methylation sites in human cells reveals dynamic regulation during transcriptional arrest. <b>2014</b> , 13, 2072-88	61
858	Degradation of the deubiquitinating enzyme USP33 is mediated by p97 and the ubiquitin ligase HERC2. <b>2014</b> , 289, 19789-98	18
857	Performance of super-SILAC based quantitative proteomics for comparison of different acute myeloid leukemia (AML) cell lines. <b>2014</b> , 14, 1971-6	28
856	Loss of the Timp gene family is sufficient for the acquisition of the CAF-like cell state. <b>2014</b> , 16, 889-901	139
855	pQuant improves quantitation by keeping out interfering signals and evaluating the accuracy of calculated ratios. <b>2014</b> , 86, 5286-94	58
854	Enhanced identification of zero-length chemical cross-links using label-free quantitation and high-resolution fragment ion spectra. <b>2014</b> , 13, 898-914	15
853	Deep proteomic profiling of human carotid atherosclerotic plaques using multidimensional LC-MS/MS. <b>2014</b> , 8, 631-5	15
852	Family-wide analysis of poly(ADP-ribose) polymerase activity. <b>2014</b> , 5, 4426	286
851	Regulation of nonribosomal peptide synthesis: bis-thiomethylation attenuates gliotoxin biosynthesis in <i>Aspergillus fumigatus</i> . <b>2014</b> , 21, 999-1012	56
850	Characterization of amyloid in equine recurrent uveitis as AA amyloid. <b>2014</b> , 151, 228-33	7
849	Metaproteomics: Evaluation of protein extraction from activated sludge. <b>2014</b> , 14, 2535-9	38



848	Priming of protein expression in the defence response of <i>Zantedeschia aethiopica</i> to <i>Pectobacterium carotovorum</i> . <b>2014</b> , 15, 364-78	11
847	Protein-to-mRNA ratios are conserved between <i>Pseudomonas aeruginosa</i> strains. <b>2014</b> , 13, 2370-80	17
846	Insights into the lysine acetylproteome of human sperm. <b>2014</b> , 109, 199-211	38
845	Improved bottom-up strategy to efficiently separate hypermodified histone peptides through ultra-HPLC separation on a bench top Orbitrap instrument. <b>2014</b> , 14, 2212-25	25
844	Proteomics meets genetics: SILAC labeling of <i>Drosophila melanogaster</i> larvae and cells for in vivo functional studies. <b>2014</b> , 1188, 293-311	3
843	Proteomic approaches to dissect neuronal signaling pathways. <b>2014</b> , 806, 499-508	1
842	Mass spectrometric analysis of post-translational modifications (PTMs) and protein-protein interactions (PPIs). <b>2014</b> , 806, 205-35	14
841	A type VI secretion-related pathway in <i>Bacteroidetes</i> mediates interbacterial antagonism. <b>2014</b> , 16, 227-236	205
840	Quantitative proteomic analysis of the influenza A virus nonstructural proteins NS1 and NS2 during natural cell infection identifies PACT as an NS1 target protein and antiviral host factor. <b>2014</b> , 88, 9038-48	40
839	Phosphoproteome analysis reveals new drought response and defense mechanisms of seedling leaves in bread wheat ( <i>Triticum aestivum</i> L.). <b>2014</b> , 109, 290-308	110
838	Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC). <b>2014</b> ,	1
837	Annotation of loci from genome-wide association studies using tissue-specific quantitative interaction proteomics. <b>2014</b> , 11, 868-74	50
836	The NBS1-Treacle complex controls ribosomal RNA transcription in response to DNA damage. <b>2014</b> , 16, 792-803	90
835	DeMix workflow for efficient identification of cofragmented peptides in high resolution data-dependent tandem mass spectrometry. <b>2014</b> , 13, 3211-23	44
834	Quantitative proteomics in cardiovascular research: global and targeted strategies. <b>2014</b> , 8, 488-505	17
833	Effect of embryonic development on the chicken egg yolk plasma proteome after 12 days of incubation. <b>2014</b> , 62, 2531-40	24
832	Elution profile analysis of SDS-induced subcomplexes by quantitative mass spectrometry. <b>2014</b> , 13, 1382-91	23
831	Immunoproteomics using polyclonal antibodies and stable isotope-labeled affinity-purified recombinant proteins. <b>2014</b> , 13, 1611-24	22

830	Regulation of the histone deacetylase Hst3 by cyclin-dependent kinases and the ubiquitin ligase SCFCdc4. <b>2014</b> , 289, 13186-96	9
829	Identification of regulatory networks in HSCs and their immediate progeny via integrated proteome, transcriptome, and DNA methylome analysis. <b>2014</b> , 15, 507-522	320
828	Dissecting the subcellular compartmentation of proteins and metabolites in arabidopsis leaves using non-aqueous fractionation. <b>2014</b> , 13, 2246-59	38
827	Decoration of outer membrane vesicles with multiple antigens by using an autotransporter approach. <b>2014</b> , 80, 5854-65	68
826	OPA1-dependent cristae modulation is essential for cellular adaptation to metabolic demand. <b>2014</b> , 33, 2676-91	224
825	A high-throughput siRNA screen identifies genes that regulate mannose 6-phosphate receptor trafficking. <b>2014</b> , 127, 5079-92	12
824	Evaluation of proteomic search engines for the analysis of histone modifications. <b>2014</b> , 13, 4470-8	25
823	Diverse sulfate-reducing bacteria of the Desulfosarcina/Desulfococcus clade are the key alkane degraders at marine seeps. <b>2014</b> , 8, 2029-44	134
822	Convergence of ubiquitylation and phosphorylation signaling in rapamycin-treated yeast cells. <b>2014</b> , 13, 1979-92	42
821	Automated peptide mapping and protein-topographical annotation of proteomics data. <b>2014</b> , 15, 207	7
820	Large-scale phosphoproteome analysis in seedling leaves of <i>Brachypodium distachyon</i> L. <b>2014</b> , 15, 375	29
819	The reduced kinome of <i>Ostreococcus tauri</i> : core eukaryotic signalling components in a tractable model species. <b>2014</b> , 15, 640	14
818	The <i>Lottia gigantea</i> shell matrix proteome: re-analysis including MaxQuant iBAQ quantitation and phosphoproteome analysis. <b>2014</b> , 12, 28	44
817	Identification of psoriatic arthritis mediators in synovial fluid by quantitative mass spectrometry. <b>2014</b> , 11, 27	41
816	N-glycosylation site occupancy in human prostaglandin H synthases expressed in <i>Pichia pastoris</i> . <b>2014</b> , 3, 436	2
815	Integration of proteomic and transcriptomic profiles identifies a novel PDGF-MYC network in human smooth muscle cells. <b>2014</b> , 12, 44	19
814	Nasal and ocular amyloidosis in a 15-year-old horse. <b>2014</b> , 56, 50	7
813	Heterologous expression of <i>Gaeumannomyces graminis</i> lipoxygenase in <i>Aspergillus nidulans</i> . <b>2014</b> , 4, 65	4

812	Subpopulation-proteomics reveal growth rate, but not cell cycling, as a major impact on protein composition in <i>Pseudomonas putida</i> KT2440. <b>2014</b> , 4, 71	13
811	Crux: rapid open source protein tandem mass spectrometry analysis. <b>2014</b> , 13, 4488-91	93
810	Regional diversity and developmental dynamics of the AMPA-receptor proteome in the mammalian brain. <b>2014</b> , 84, 41-54	149
809	Label-free quantitative proteomic analysis of human plasma-derived microvesicles to find protein signatures of abdominal aortic aneurysms. <b>2014</b> , 8, 620-5	19
808	Membrane-assisted isoelectric focusing device as a micropreparative fractionator for two-dimensional shotgun proteomics. <b>2014</b> , 86, 5728-32	9
807	The <i>Caenorhabditis elegans</i> pericentriolar material components SPD-2 and SPD-5 are monomeric in the cytoplasm before incorporation into the PCM matrix. <b>2014</b> , 25, 2984-92	26
806	Integrative network analysis of the signaling cascades in seedling leaves of bread wheat by large-scale phosphoproteomic profiling. <b>2014</b> , 13, 2381-95	31
805	Single-step enrichment by Ti4+-IMAC and label-free quantitation enables in-depth monitoring of phosphorylation dynamics with high reproducibility and temporal resolution. <b>2014</b> , 13, 2426-34	80
804	Assessing the citrullinome in rheumatoid arthritis synovial fluid with and without enrichment of citrullinated peptides. <b>2014</b> , 13, 2867-73	58
803	A role for the Cajal-body-associated SUMO isopeptidase USPL1 in snRNA transcription mediated by RNA polymerase II. <b>2014</b> , 127, 1065-78	36
802	Characterization and Prediction of miRNA Targets. <b>2014</b> , 833-860	
801	Statistical approach to protein quantification. <b>2014</b> , 13, 666-77	23
800	Proteomic profiling of the acid stress response in <i>Lactobacillus plantarum</i> 423. <b>2014</b> , 13, 4028-39	58
799	Investigating the applicability of antibodies generated within the human protein atlas as capture agents in immunoenrichment coupled to mass spectrometry. <b>2014</b> , 13, 4424-35	7
798	The quantitative nuclear matrix proteome as a biochemical snapshot of nuclear organization. <b>2014</b> , 13, 3940-56	31
797	APols-aided protein precipitation: a rapid method for concentrating proteins for proteomic analysis. <b>2014</b> , 247, 941-7	14
796	The nature and extent of contributions by defective ribosome products to the HLA peptidome. <b>2014</b> , 111, E1591-9	68
795	Transcriptomics assisted proteomic analysis of <i>Nicotiana occidentalis</i> infected by <i>Candidatus Phytoplasma mali</i> strain AT. <b>2014</b> , 14, 1882-9	34

794	Increased interaction with insulin receptor substrate 1, a novel abnormality in insulin resistance and type 2 diabetes. <b>2014</b> , 63, 1933-47	39
793	Toward understanding ubiquitin-modifying enzymes: from pharmacological targeting to proteomics. <b>2014</b> , 35, 187-207	35
792	Environmental proteomics: A long march in the pedosphere. <b>2014</b> , 69, 34-37	14
791	Structure of the pseudokinase domain of BIR2, a regulator of BAK1-mediated immune signaling in Arabidopsis. <b>2014</b> , 186, 112-21	40
790	Determining protein subcellular localization in mammalian cell culture with biochemical fractionation and iTRAQ 8-plex quantification. <b>2014</b> , 1156, 157-74	11
789	Quantitative, time-resolved proteomic analysis by combining bioorthogonal noncanonical amino acid tagging and pulsed stable isotope labeling by amino acids in cell culture. <b>2014</b> , 13, 1352-8	49
788	Deep proteomics of the <i>Xenopus laevis</i> egg using an mRNA-derived reference database. <b>2014</b> , 24, 1467-1475	158
787	MS Amanda, a universal identification algorithm optimized for high accuracy tandem mass spectra. <b>2014</b> , 13, 3679-84	262
786	High confidence proteomic analysis of yeast LDs identifies additional droplet proteins and reveals connections to dolichol synthesis and sterol acetylation. <b>2014</b> , 55, 1465-77	67
785	Proteomic analysis of the epidermal growth factor receptor (EGFR) interactome and post-translational modifications associated with receptor endocytosis in response to EGF and stress. <b>2014</b> , 13, 1644-58	71
784	Characterization of the pigmented shell-forming proteome of the common grove snail <i>Cepaea nemoralis</i> . <b>2014</b> , 15, 249	62
783	Characterization of the membrane proteome and N-glycoproteome in BV-2 mouse microglia by liquid chromatography-tandem mass spectrometry. <b>2014</b> , 15, 95	14
782	Characterization of the RNase R association with ribosomes. <b>2014</b> , 14, 34	20
781	Molecular mechanisms of nutlin-3 involve acetylation of p53, histones and heat shock proteins in acute myeloid leukemia. <b>2014</b> , 13, 116	22
780	On the extent and role of the small proteome in the parasitic eukaryote <i>Trypanosoma brucei</i> . <b>2014</b> , 12, 14	14
779	Bioinformatic analysis of proteomics data. <b>2014</b> , 8 Suppl 2, S3	93
778	Quantitative proteomics reveals ER-involvement in CD146-induced epithelial-mesenchymal transition in breast cancer cells. <b>2014</b> , 103, 153-69	21
777	High-confidence glycosome proteome for procyclic form <i>Trypanosoma brucei</i> by epitope-tag organelle enrichment and SILAC proteomics. <b>2014</b> , 13, 2796-806	72

776	In vivo quantitative proteomics for the study of oncometabolism. <b>2014</b> , 543, 235-59	2
775	Mass spectrometric analysis of histone proteoforms. <b>2014</b> , 7, 113-28	49
774	Chromatin enrichment for proteomics. <b>2014</b> , 9, 2090-9	53
773	Global analysis of muscle-specific kinase signaling by quantitative phosphoproteomics. <b>2014</b> , 13, 1993-2003	9
772	HGF induces epithelial-to-mesenchymal transition by modulating the mammalian hippo/MST2 and ISG15 pathways. <b>2014</b> , 13, 2874-86	55
771	Quantitative phosphoproteomics of murine Fmr1-KO cell lines provides new insights into FMRP-dependent signal transduction mechanisms. <b>2014</b> , 13, 4388-97	23
770	Polysome profiling shows the identity of human adipose-derived stromal/stem cells in detail and clearly distinguishes them from dermal fibroblasts. <b>2014</b> , 23, 2791-802	9
769	Mcdas localizes at centrioles and controls centriole numbers through PLK4-dependent phosphorylation.	0
768	Direct capture, inhibition and crystal structure of HsaD (Rv3569c) from M. tuberculosis.	0
767	Decoupling of mRNA and protein expression in aging brains reveals the age-dependent adaptation of specific gene subsets.	0
766	A Parallelization Strategy for the Time Efficient Analysis of Thousands of LC/MS Runs in High-Performance Computing Environment.	1
765	Data-Processing Workflow for Relative Quantification from Label-Free and Isobaric Labeling-Based Untargeted Shotgun Proteomics: From Database Search to Differential Expression Analysis. <b>2022</b> , 65-119	0
764	Two independent respiratory chains adapt OXPHOS performance to glycolytic switch. <b>2022</b> ,	0
763	The TRIPLE PHD FINGERS proteins are required for SWI/SNF complex-mediated $\pm 1$ nucleosome positioning and transcription start site determination in Arabidopsis.	0
762	Denitrifying bradyrhizobia retain strong N <sub>2</sub> O reduction during periods of starvation.	0
761	Peptide mapping of proteins by capillary electromigration methods.	1
760	A membrane integral methyltransferase catalysing N-terminal histidine methylation of lytic polysaccharide monooxygenases.	0
759	Convergent evolution of plant pattern recognition receptors sensing cysteine-rich patterns from three microbial kingdoms.	0

758	Identification of Plant ProteinMetabolite Interactions by Limited Proteolysis-Coupled Mass Spectrometry (LiP-MS). <b>2023</b> , 47-67	0
757	Leveraging the CSF proteome toward minimally-invasive diagnostics surveillance of brain malignancies.	0
756	A pathway for chitin oxidation in marine bacteria. <b>2022</b> , 13,	1
755	Structure of V-ATPase from citrus fruit. <b>2022</b> , 30, 1403-1410.e4	2
754	Thermosensation in <i>Caenorhabditis elegans</i> is linked to ubiquitin-dependent protein turnover via insulin and calcineurin signalling. <b>2022</b> , 13,	0
753	PEP7 acts as a peptide ligand for the receptor kinase SIK1 to regulate aquaporin-mediated water influx and lateral root growth. <b>2022</b> , 15, 1615-1631	0
752	<i>Rosmarinus officinalis</i> reduces the ochratoxin A production by <i>Aspergillus westerdijkiae</i> in a dry-cured fermented sausage-based medium. <b>2022</b> , 109436	1
751	Yeast $\beta$ -Glucan Improves Insulin Sensitivity and Hepatic Lipid Metabolism in Mice Humanized with Obese Type 2 Diabetic Gut Microbiota. 2100819	0
750	PROMIS: Co-fractionation Mass Spectrometry for Analysis of ProteinMetabolite Interactions. <b>2023</b> , 141-153	0
749	mtDNA breaks compromise mitochondrial membrane ultrastructure and trigger an integrated stress response.	0
748	Organ-specific metabolic pathways distinguish prediabetes, type 2 diabetes, and normal tissues. <b>2022</b> , 100763	0
747	Hox -driven conditional immortalization of myeloid and lymphoid progenitors: Uses, advantages, and future potential.	0
746	Secretome analysis of an environmental isolate <i>Enterobacter</i> sp. S-33 identifies proteins related to pathogenicity. <b>2022</b> , 204,	0
745	MICAL1 activation by PAK1 mediates actin filament disassembly. <b>2022</b> , 41, 111442	2
744	Parallel Analysis of ProteinProtein and ProteinMetabolite Complexes Using a Single-Step Affinity Purification. <b>2023</b> , 107-122	1
743	Crystal structure and biochemical analysis suggest that YjdB ATPase is a putative substrate-specific molecular chaperone. <b>2022</b> , 119,	0
742	The human disease gene LYSET is essential for lysosomal enzyme transport and viral infection. <b>2022</b> , 378,	4
741	Optimized protocol for obtaining and characterizing primary neuron-enriched cultures from embryonic chicken brains. <b>2022</b> , 3, 101753	0

740	Activation of CD44/PAK1/AKT signaling promotes resistance to FGFR1 inhibition in squamous-cell lung cancer. <b>2022</b> , 6,	0
739	Statistical Analysis of Quantitative Peptidomics and Peptide-Level Proteomics Data with Prostar. <b>2023</b> , 163-196	0
738	Divergent polo boxes in KKT2 and KKT3 initiate the kinetochore assembly cascade in <i>Trypanosoma brucei</i> .	0
737	PepWise: Peptide Identification Algorithms for Tandem Mass Spectrometry Based on the Weight of Pair Amino Acid Fracture. 14, 231-238	0
736	Structural basis for specific inhibition of the deubiquitinase UCHL1. <b>2022</b> , 13,	0
735	Raw milk kefir: microbiota, bioactive peptides, and immune modulation.	0
734	<i>Clostridioides difficile</i> Modifies its Aromatic Compound Metabolism in Response to Amidochelecardin-Induced Membrane Stress. <b>2022</b> , 7,	0
733	Global landscape of the host response to SARS-CoV-2 variants reveals viral evolutionary trajectories.	0
732	Branched-chain ketoacids derived from cancer cells modulate macrophage polarization and metabolic reprogramming. 13,	1
731	Molecular Mechanisms Mediating the Transfer of Disease-Associated Proteins and Effects on Neuronal Activity. <b>2022</b> , 1-26	1
730	Selective immunocapture reveals neoplastic human mast cells secrete distinct microvesicle- and exosome-like populations of KIT-containing extracellular vesicles. <b>2022</b> , 11, 12272	1
729	A high-content endogenous GLUT4 trafficking assay reveals new aspects of adipocyte biology. <b>2023</b> , 6, e202201585	0
728	Nuclear Proteomics of Induced Leukemia Cell Differentiation. <b>2022</b> , 11, 3221	0
727	Self-assembly and Hydrogelation Properties of Peptides Derived from Peptic Cleavage of Aggregation-prone Regions of Ovalbumin. <b>2022</b> , 8, 641	0
726	Cytomegalovirus US28 regulates cellular EphA2 to maintain viral latency. <b>2022</b> , 8,	1
725	Open modification searching of SARS-CoV-2 human protein interaction data reveals novel viral modification sites. <b>2022</b> , 100425	2
724	Electroneutral Polymer Nanodiscs Enable Interference-Free Probing of Membrane Proteins in a Lipid-Bilayer Environment. 2202492	2
723	Knockdown of METTL16 disrupts learning and memory by reducing the stability of MAT2A mRNA. <b>2022</b> , 8,	0

722	Proteomic and miRNA Profiles of Exosomes Derived from Myometrial Tissue in Laboring Women. <b>2022</b> , 23, 12343	0
721	Lipid and protein content profiling of isolated native autophagic vesicles.	2
720	Synergistic Combined-proteomics Guided Mapping strategy identifies mTOR mediated phosphorylation of LARP1 in nutrient responsiveness and dilated cardiomyopathy.	0
719	Hypoxia promotes osteogenesis by facilitating acetyl-CoA -mediated mitochondrial nuclear communication.	1
718	Tryptase regulation of joint lubrication and inflammation via proteoglycan-4 in osteoarthritis.	0
717	An Abundance of Free Proteasomal Regulatory (19S) Particles Regulate Neuronal Synapses Independent of the Proteasome.	0
716	Proteome effects of genome-wide single gene perturbations. <b>2022</b> , 13,	0
715	Fucosylation of HLA-DRB1 regulates CD4+T cell-mediated anti-melanoma immunity and enhances immunotherapy efficacy.	0
714	Zasp52 strengthens whole embryo tissue integrity through supracellular actomyosin networks.	0
713	A universal database reduction method based on the sequence tag strategy to facilitate large-scale database search in proteomics. <b>2022</b> , 116966	0
712	The human milk proteome and allergy of mother and child: Exploring associations with protein abundances and protein network connectivity. 13,	0
711	Algal photosystem I dimer and high-resolution model of PSI-plastocyanin complex. <b>2022</b> , 8, 1191-1201	2
710	Proteomic dataset comparing strains of <i>Leptospira borgpetersenii</i> serovar Hardjo cultured at different temperatures. <b>2022</b> , 108713	0
709	GNL3 regulates replication origin firing and protects stalled replication forks.	0
708	Glomerular proteomic profiling of kidney biopsies with hypertensive nephropathy reveals a signature of disease progression.	0
707	mTORC2 Interactome and Localization Determine Aggressiveness of High-Grade Glioma Cells through Association with Gelsolin.	0
706	MRPS36 provides a missing link in the eukaryotic 2-oxoglutarate dehydrogenase complex for recruitment of E3 to the E2 core.	0
705	The cholesterol transport protein GRAMD1C regulates autophagy initiation and mitochondrial bioenergetics. <b>2022</b> , 13,	0



704	Snf1/AMPK fine-tunes TORC1 signaling in response to glucose starvation.	0
703	NIMA-related kinase 9 regulates the phosphorylation of the essential myosin light chain in the heart. <b>2022</b> , 13,	0
702	Translational reprogramming in response to accumulating stressors ensures critical threshold levels of Hsp90 for mammalian life. <b>2022</b> , 13,	1
701	NADPH Oxidase 5 (NOX5) Overexpression Promotes Endothelial Dysfunction via Cell Apoptosis, Migration, and Metabolic Alterations in Human Brain Microvascular Endothelial Cells (hCMEC/D3). <b>2022</b> , 11, 2147	0
700	Metabolic engineering enables <i>Bacillus licheniformis</i> to grow on the marine polysaccharide ulvan. <b>2022</b> , 21,	0
699	Defining the Functional Interactome of Spliceosome-Associated G-patch Protein Gpl1 in the Fission Yeast <i>Schizosaccharomyces pombe</i> . <b>2022</b> , 23, 12800	0
698	AI-guided cryo-EM probes a thermophilic cell-free system with succinyl-coA manufacturing capability.	0
697	Immunopeptidomics-based design of mRNA vaccine formulations against <i>Listeria monocytogenes</i> . <b>2022</b> , 13,	2
696	Combined analysis of the transcriptome and proteome of <i>Eucommia ulmoides</i> Oliv. (Duzhong) in response to <i>Fusarium oxysporum</i> . 10,	0
695	The metabolite-controlled ubiquitin conjugase Ubc8 promotes mitochondrial protein import. <b>2023</b> , 6, e202201526	0
694	The Proteomic and Transcriptomic Landscapes Altered by Rgg2/3 Activity in <i>Streptococcus pyogenes</i> .	0
693	A DARPIn-based molecular toolset to probe gephyrin and inhibitory synapse biology. 11,	0
692	Integrated Omic Approaches Reveal Molecular Mechanisms of Tolerance during Soybean and <i>Meloidogyne incognita</i> Interactions. <b>2022</b> , 11, 2744	0
691	Integrative transcriptomic and proteomic analysis show circulating osteoprogenitors to have a mixed immune and mesenchymal progenitor function in humans.	0
690	In-cell chemical crosslinking identifies hotspots for p62-IBB $\alpha$ interaction that underscore a critical role of p62 in limiting NF- $\kappa$ B activation through IBB $\alpha$ stabilization.	0
689	The CRL4B E3 ligase regulates mitosis by recruiting phospho-specific DCAFs.	0
688	Changes of Protein Expression after CRISPR/Cas9 Knockout of miRNA-142 in Cell Lines Derived from Diffuse Large B-Cell Lymphoma. <b>2022</b> , 14, 5031	0
687	Metabolic rewiring of mitochondria in senescence revealed by time-resolved analysis of the mitochondrial proteome.	0

- 686 Environmental gradients reveal stress hubs predating plant terrestrialization. o
- 685 Synaptic proteomics reveal distinct molecular signatures of cognitive change and C9ORF72 repeat expansion in the human ALS cortex. **2022**, 10, 2
- 684 In Vitro Anti-Proliferative and Apoptotic Effects of Hydroxytyrosyl Oleate on SH-SY5Y Human Neuroblastoma Cells. **2022**, 23, 12348 5
- 683 Genome-centric insight into metabolically active microbial population in shallow-sea hydrothermal vents. **2022**, 10, o
- 682 TopFD - A Proteoform Feature Detection Tool for Top-Down Proteomics. o
- 681 Multi-Omics Analysis Revealed a Significant Alteration of Critical Metabolic Pathways Due to Sorafenib-Resistance in Hep3B Cell Lines. **2022**, 23, 11975 o
- 680 AUTS2 Controls Neuronal Lineage Choice Through a Novel PRC1-Independent Complex and BMP Inhibition. o
- 679 Proteomic identification and structural basis for the interaction between sorting nexin SNX17 and PDLIM family proteins. **2022**, o
- 678 Mapping Proteome and Lipidome Changes in Early-Onset Non-Alcoholic Fatty Liver Disease Using Hepatic 3D Spheroids. **2022**, 11, 3216 o
- 677 GPC3-Unc5 receptor complex structure and role in cell migration. **2022**, 185, 3931-3949.e26 o
- 676 Structure and functionality of a multimeric human COQ7:COQ9 complex. **2022**, o
- 675 Glycosylation Analysis of Feline Small Intestine Following Toxoplasma gondii Infection. **2022**, 12, 2858 o
- 674 A pilot study to show that asymptomatic sexually transmitted infections alter the foreskin epithelial proteome. 13, o
- 673 Chemical proteomics reveals interactors of the alarmone diadenosine triphosphate in the cancer cell line H1299. o
- 672 An apical membrane complex for triggering rhoptry exocytosis and invasion in Toxoplasma. o
- 671 Mammalian oocytes store mRNAs in a mitochondria-associated membraneless compartment. **2022**, 378, 2
- 670 Cross-linking of the endolysosomal system reveals potential flotillin structures and cargo. **2022**, 13, o
- 669 A cross-species proteomic map of synapse development reveals neoteny during human postsynaptic density maturation. o

- 668 Establishment of in vivo proximity labeling with biotin using TurboID in the filamentous fungus *Sordaria macrospora*. **2022**, 12, ○
- 667 Multiomics surface receptor profiling of the NCI-60 tumor cell panel uncovers novel theranostics for cancer immunotherapy. **2022**, 22, ○
- 666 Evidence for a fragile X messenger ribonucleoprotein 1 ( FMR1 ) mRNA gain-of-function toxicity mechanism contributing to the pathogenesis of fragile X-associated premature ovarian insufficiency. **2022**, 36, ○
- 665 The kinesin motor KIF1C is a putative transporter of the exon junction complex in neuronal cells. rna.079426.122 ○
- 664 Cell-specific bioorthogonal tagging of glycoproteins. **2022**, 13, 1
- 663 Peroxynitrite in the tumor microenvironment changes the profile of antigens allowing escape from cancer immunotherapy. **2022**, 40, 1173-1189.e6 ○
- 662 Proteome alterations during clonal isolation of established human pancreatic cancer cell lines. **2022**, 79, ○
- 661 Formation of toxic oligomers of polyQ-expanded Huntingtin by prion-mediated cross-seeding. **2022**, ○
- 660 Circulating osteoprogenitors have a mixed immune and mesenchymal progenitor function in humans. ○
- 659 Characterization of peptide-protein relationships in protein ambiguity groups via bipartite graphs. **2022**, 17, e0276401 ○
- 658 The Small RNA Teg41 Is a Pleiotropic Regulator of Virulence in *Staphylococcus aureus*. ○
- 657 Lipids mediate supramolecular outer membrane protein assembly in bacteria. **2022**, 8, 1
- 656 Ultra-sensitive platelet proteome maps the O-glycosylation landscape and charts the response to thrombin dosage. ○
- 655 Synchro-PASEF allows precursor-specific fragment ion extraction and interference removal in data-independent acquisition. ○
- 654 Genome-wide base editor screen identifies regulators of protein abundance in yeast. 11, 1
- 653 Refactored genetic codes enable bidirectional genetic isolation. **2022**, 378, 516-523 ○
- 652 Extracellular Vesicles in Diffuse Large B Cell Lymphoma: Characterization and Diagnostic Potential. **2022**, 23, 13327 ○
- 651 Mitochondrial Aconitase ACO2 Links Iron Homeostasis with Tumorigenicity in NonSmall Cell Lung Cancer. OF1-OF15 ○

- 650 Activated abscisic acid pathway and C4 pathway, inhibited cell cycle progression, responses of *Ulva prolifera* to short term high temperature elucidated by multi-omics. **2022**, 105796 ○
- 649 A comparative proteomics analysis identified differentially expressed proteins in pancreatic cancer-associated stellate cell small extracellular vesicles. **2022**, 100438 ○
- 648 Correlation between biological responses in vitro and in vivo to Ca-doped sol-gel coatings assessed using proteomic analysis. **2022**, 220, 112962 ○
- 647 Generation of cell-type-specific proteomes of neurodevelopment from human cerebral organoids. **2022**, 3, 101774 ○
- 646 Potential functionality of  $\beta$ -conglycinin with subunit deficiencies: soy protein may regulate glucose and lipid metabolism. ○
- 645 Analysis of the p53/microRNA Network in Cancer. **2022**, 187-228 1
- 644 Integrated multi-omics reveals minor spliceosome inhibition causes molecular stalling and developmental delay of the mouse forelimb. ○
- 643 The C-terminal region of phytoene synthase is a key element to control carotenoid biosynthesis in the haloarchaeon *Haloferax volcanii*. ○
- 642 FAP106 is an interaction hub required for stable assembly of conserved and lineage-specific proteins at the cilium inner junction. ○
- 641 DNA sequence and chromatin modifiers cooperate to confer epigenetic bistability at imprinting control regions. **2022**, 54, 1702-1710 ○
- 640 SEPeQuant enables comprehensive protein isoform characterization in shotgun proteomics. ○
- 639 IGF2BP2 is Induced by Stress in the Heart and Mediates Dilated Cardiomyopathy. ○
- 638 Time-Resolved Proteomics of Germinating Spores of *Bacillus cereus*. **2022**, 23, 13614 1
- 637 Foxd1 is Required for 3d Patterning of the Kidney Interstitial Matrix. ○
- 636 Host diet shapes functionally differentiated gut microbiomes in sympatric speciation of blind mole rats in Upper Galilee, Israel. 13, ○
- 635 A Mineral-Doped Micromodel Platform Demonstrates Fungal Bridging of Carbon Hot Spots and Hyphal Transport of Mineral-Derived Nutrients. ○
- 634 Targeting UGCG overcomes resistance to lysosomal autophagy inhibition.. ○
- 633 Light acclimation interacts with thylakoid ion transport to govern the dynamics of photosynthesis in *Arabidopsis*. ○

632	Proximity labeling facilitates defining the proteome neighborhood of photosystem II oxygen evolution complex in a model cyanobacterium. <b>2022</b> , 100440	o
631	Heavy Methyl SILAC Metabolic Labeling of Human Cell Lines for High-Confidence Identification of R/K-Methylated Peptides by High-Resolution Mass Spectrometry. <b>2023</b> , 173-186	o
630	Dynamic SILAC to Determine Protein Turnover in Neurons and Glia. <b>2023</b> , 1-17	o
629	SUMOylation regulates Lem2 function in centromere clustering and silencing.	o
628	TENT5 cytoplasmic noncanonical poly(A) polymerases regulate the innate immune response in animals. <b>2022</b> , 8,	1
627	Ubiquitin-based pathway acts inside chloroplasts to regulate photosynthesis. <b>2022</b> , 8,	1
626	IL-33 induces granzyme C expression in murine mast cells via an MSK1/2-CREB dependent pathway..	o
625	Power and optimal study design in iPSC-based brain disease modelling.	o
624	Assessment of infant outgrowth of cow's milk allergy in relation to the faecal microbiome and metaproteome.	o
623	Virulence Induction in <i>Pseudomonas aeruginosa</i> under Inorganic Phosphate Limitation: a Proteomics Perspective.	1
622	SILAC-Based Quantitative Proteomic Analysis of <i>Drosophila</i> Embryos. <b>2023</b> , 187-198	o
621	Fluid flow structures gut microbiota biofilm communities by distributing public goods.	o
620	Integrated Omics Reveal Time-Resolved Insights into T4 Phage Infection of <i>E. coli</i> on Proteome and Transcriptome Levels. <b>2022</b> , 14, 2502	o
619	A Cyanophage MarR-Type Transcription Factor Regulates Host RNase E Expression during Infection. <b>2022</b> , 10, 2245	o
618	Lipid nanoparticles with erythrocyte cell-membrane proteins. <b>2022</b> , 120791	o
617	Post-GWAS multiomic functional investigation of the TNIP1 locus in Alzheimer's disease implicates mediation through GPX3.	o
616	SUMO2 Protects Against Tau-induced Synaptic and Cognitive Dysfunction.	o
615	Connecting multiple microenvironment proteomes uncovers the biology in head and neck cancer. <b>2022</b> , 13,	o

614	SILAC-IodoTMT for Assessment of the Cellular Proteome and Its Redox Status. <b>2023</b> , 259-268	0
613	Monitoring Functional Post-Translational Modifications Using a Data-Driven Proteome Informatic Pipeline Based on PEIMAN2.	0
612	SILAC-based quantitative proteomics and microscopy analysis of cancer cells treated with the N-glycolyl GM3-specific anti-tumor antibody 14F7. 13,	0
611	Legionella pneumophila modulates host cytoskeleton by an effector of transglutaminase activity.	0
610	Label-free quantitative proteomics and immunoblotting identifies immunoreactive and other excretory-secretory (E/S) proteins of Anoplocephala perfoliata. 13,	0
609	Application of Machine Learning in Spatial Proteomics.	0
608	Identification of fungal lignocellulose-degrading biocatalysts secreted by Phanerochaete chrysosporium via activity-based protein profiling. <b>2022</b> , 5,	0
607	Targeted hydrolysis of native potato protein: A novel workflow for obtaining hydrolysates with improved interfacial properties. <b>2022</b> , 108299	1
606	Structure of Escherichia coli heat shock protein Hsp15 in complex with the ribosomal 50S subunit bearing peptidyl-tRNA.	0
605	Workflow for Quantitative Proteomic Analysis of Intestinal Organoids Using SILAC. <b>2023</b> , 151-161	0
604	SILAC-Based Proteomic Analysis of Meiosis in the Fission Yeast Schizosaccharomyces pombe. <b>2023</b> , 19-29	0
603	Coronary Artery Disease and Aortic Valve Stenosis: A Urine Proteomics Study. <b>2022</b> , 23, 13579	0
602	The deubiquitinase OTUD1 regulates immunoglobulin production and proteasome inhibitor sensitivity in multiple myeloma. <b>2022</b> , 13,	1
601	Spatial analysis of the glioblastoma proteome reveals specific molecular signatures and markers of survival. <b>2022</b> , 13,	2
600	The Proteome of Neuromelanin Granules in Dementia with Lewy Bodies. <b>2022</b> , 11, 3538	0
599	Functional annotation of proteins for signaling network inference in non-model species.	0
598	Mapping of the podocin proximity-dependent proteome reveals novel components of the kidney podocyte foot process.	0
597	Use of Nuclear and Chromatin Enrichment Procedures for Quantitation of Yeast DNA Replication Proteins Using SILAC. <b>2023</b> , 209-218	0

596	IKK $\alpha$ primes inflammasome formation by recruiting NLRP3 to the trans-Golgi network. <b>2022</b> ,	1
595	Chemoproteomic profiling to identify activity changes and functional inhibitors of DNA-binding proteins. <b>2022</b> ,	o
594	Dominant complementation of biological pathways in maize hybrid lines is associated with heterosis. <b>2022</b> , 256,	o
593	Short-Term Omega-3 Supplementation Modulates Novel Neurovascular and Fatty Acid Metabolic Proteome Changes in the Retina and Ophthalmic Artery of Mice with Targeted Cyp2c44 Gene Deletion. <b>2022</b> , 11, 3494	o
592	PARP1 proximity proteomics reveals interaction partners at stressed replication forks.	o
591	Integrative analysis of differentially expressed mRNAs and proteins induced by PGC-1 $\alpha$ in breast cancer cells. <b>2022</b> , 637, 73-82	o
590	MS-proteomics provides insight into the host responses towards alginate microspheres. <b>2022</b> , 17, 100490	o
589	Salivary Biomarker Evaluation of Chronic Pancreatitis Patients Reveals Alterations in Human Proteins, Cytokines, Prostaglandin E2 Levels, and Bacterial Diversity. <b>2022</b> , 51, 723-732	o
588	Neoadjuvant chemotherapy is associated with an altered metabolic profile and increased cancer stemness in patients with pancreatic ductal adenocarcinoma.	1
587	LC-MS / MS -Based Proteomics Methods for Quantifying Drug-Metabolizing Enzymes and Transporters. <b>2022</b> , 143-176	o
586	Identification of putative reader proteins of 5-methylcytosine and its derivatives in <i>Caenorhabditis elegans</i> RNA. 7, 282	o
585	Unscheduled DNA replication in G1 causes genome instability and damage signatures indicative of replication collisions. <b>2022</b> , 13,	o
584	DNAJB6-Containing Extracellular Vesicles as Chaperone Delivery Systems: A Proteomic Analysis. <b>2022</b> , 14, 2485	o
583	Expanded Proteomic Survey of the Human Parasite <i>Leishmania major</i> Focusing on Changes in Null Mutants of the Golgi GDP-Mannose/Fucose/Arabinopyranose Transporter LPG2 and of the Mitochondrial Fucosyltransferase FUT1.	o
582	Evidence for a putative isoprene reductase in <i>Acetobacterium wieringae</i> .	o
581	Pentatricopeptide Protein PTC2 Regulates COIII Translation in Mitochondria of the HeLa Cell Line. <b>2022</b> , 23, 14241	o
580	The Heterochromatin protein 1 is a regulator in RNA splicing precision deficient in ulcerative colitis. <b>2022</b> , 13,	1
579	Proteomics uncover EPHA2 as a potential novel therapeutic target in colorectal cancer cell lines with acquired cetuximab resistance.	o

578	Impact of inherent biases built into proteomic techniques: Proximity labeling and affinity capture compared. <b>2022</b> , 102726	0
577	The non-apoptotic function of Caspase-8 in negatively regulating the CDK9-mediated Ser2 phosphorylation of RNA polymerase II in cervical cancer. <b>2022</b> , 79,	0
576	Cryo-Electron Microscopy Snapshots of Eukaryotic Membrane Proteins in Native Lipid-Bilayer Nanodiscs.	2
575	Cross-Linking Mass Spectrometry Data Analysis. <b>2022</b> , 339-370	0
574	The permanently chaperone-active small heat shock protein Hsp17 from <i>Caenorhabditis elegans</i> exhibits topological separation of its N-terminal regions. <b>2023</b> , 299, 102753	0
573	Proteome Remodeling of the Eye Lens at 50 Years Identified With Data-Independent Acquisition. <b>2023</b> , 22, 100453	0
572	Magnetic enrichment of immuno-specific extracellular vesicles for mass spectrometry using biofilm-derived iron oxide nanowires.	1
571	Proteins in Tumor-Derived Plasma Extracellular Vesicles Indicate Tumor Origin. <b>2023</b> , 22, 100476	0
570	Recent advances in machine learning applications in metabolic engineering. <b>2023</b> , 62, 108069	1
569	Quantification of lactoferrin in human milk using monolithic cation exchange HPLC. <b>2023</b> , 1214, 123548	1
568	An alkali-resistant zirconium-biligand organic framework with dual-metal centers for highly selective capture of phosphopeptides. <b>2022</b> , 148, 85-94	0
567	Site-Specific Activity-Based Protein Profiling Using Phosphonate Handles. <b>2023</b> , 22, 100455	0
566	A multi-omics based anti-inflammatory immune signature characterizes long COVID-19 syndrome. <b>2023</b> , 26, 105717	0
565	Proteomics analysis indicates the involvement of immunity and inflammation in the onset stage of SOD1-G93A mouse model of ALS. <b>2023</b> , 272, 104776	0
564	How to dissect viral infections and their interplay with the host-proteome by immunoaffinity and mass spectrometry: A tutorial. <b>2023</b> , 186, 108323	0
563	Cms1 coordinates stepwise local 90S pre-ribosome assembly with timely snR83 release. <b>2022</b> , 41, 111684	0
562	VPS34-dependent control of apical membrane function of proximal tubule cells and nutrient recovery by the kidney. <b>2022</b> , 15,	0
561	SnRK1 inhibits anthocyanin biosynthesis through both transcriptional regulation and direct phosphorylation and dissociation of the MYB/bHLH/TTG1 MBW complex.	0



560	EVAnalyzer: High content imaging for rigorous characterisation of single extracellular vesicles using standard laboratory equipment and a new open-source ImageJ/Fiji plugin. <b>2022</b> , 11, 12282	0
559	Proteomic profiling of sweat in patients with cystic fibrosis provides new insights into epidermal homeostasis.	0
558	In vitro studies of the protein-interaction network of cell-wall lytic transglycosylase RlpA of <i>Pseudomonas aeruginosa</i> . <b>2022</b> , 5,	0
557	Proteomics reveals unique identities of human TGF- $\beta$ -induced and thymus-derived CD4+ regulatory T cells. <b>2022</b> , 12,	0
556	Transparent Exploration of Machine Learning for Biomarker Discovery from Proteomics and Omics Data.	0
555	Study of SarA by DNA Affinity Capture Assay (DACA) Employing Three Promoters of Key Virulence and Resistance Genes in Methicillin-Resistant <i>Staphylococcus aureus</i> . <b>2022</b> , 11, 1714	0
554	AlphaPeptDeep: a modular deep learning framework to predict peptide properties for proteomics. <b>2022</b> , 13,	4
553	Scalable Generation of Nanovesicles from Human-Induced Pluripotent Stem Cells for Cardiac Repair. <b>2022</b> , 23, 14334	3
552	Phosphoproteomic dysregulation in Huntington's disease mice is rescued by environmental enrichment. <b>2022</b> , 4,	0
551	A Mass Spectrometry-Based Strategy for Mapping Modification Sites for the Ubiquitin-Like Modifier NEDD8. <b>2023</b> , 137-149	0
550	Mitotic bookmarking redundancy by nuclear receptors mediates robust post-mitotic reactivation of the pluripotency network.	0
549	Thermostable Proteins from HaCaT Keratinocytes Identify a Wide Breadth of Intrinsically Disordered Proteins and Candidates for Liquid-Liquid Phase Separation. <b>2022</b> , 23, 14323	0
548	Carbon nanoparticles induce DNA repair and PARP inhibitor resistance associated with nanozyme activity in cancer cells. <b>2022</b> , 13,	1
547	EMC3 regulates mesenchymal cell survival via control of the mitotic spindle assembly. <b>2022</b> , 105667	0
546	Neuron-specific protein network mapping of autism risk genes identifies shared biological mechanisms and disease-relevant pathologies. <b>2022</b> , 41, 111678	1
545	Golgi-IP, a novel tool for multimodal analysis of Golgi molecular content.	0
544	GltS regulates biofilm formation in methicillin-resistant <i>Staphylococcus aureus</i> . <b>2022</b> , 5,	0
543	Differential requirements of IQUB for the assembly of radial spoke 1 and the motility of mouse cilia and flagella. <b>2022</b> , 41, 111683	0

- 542 Remodelled Ribosomes Synthesise a Specific Proteome in Proliferating Plant Tissue during Cold. o
- 541 Marine bacteroidetes use a conserved enzymatic cascade to digest diatom  $\beta$ -mannan. o
- 540 Tandem Mass Tag-Based Phosphoproteomics in Plants. **2023**, 309-319 o
- 539 Chromatin Enrichment for Proteomics in Plants (ChEP-P). **2023**, 285-293 o
- 538 Proteomic analysis of plasma to identify novel biomarkers for intra-amniotic infection and/or inflammation in preterm premature rupture of membranes. o
- 537 DNA methylation-based classification of sinonasal tumors. **2022**, 13, 1
- 536 Lysosomal damage drives mitochondrial proteome remodelling and reprograms macrophage immunometabolism. **2022**, 13, o
- 535 Collagen constitutes about twelve percent in females and seventeen percent in males of the total protein in mice. o
- 534 MYC multimers shield stalled replication forks from RNA polymerase. **2022**, 612, 148-155 o
- 533 Proteomic analysis reveals that aging rabbit vocal folds are more vulnerable to changes caused by systemic dehydration. **2022**, 23, o
- 532 Factors governing attachment of *Rhizobium leguminosarum* to legume roots. o
- 531 Multiomics of Colorectal Cancer Organoids Reveals Putative Mediators of Cancer Progression Resulting from SMAD4 Inactivation. o
- 530 Integrated Multi-omics Analyses of NFKB1 patients B cells points towards an up regulation of NF- $\kappa$ B network inhibitors. o
- 529 Temporal landscape of mitochondrial proteostasis governed by the UPRmt. o
- 528 Small leucine-rich proteoglycans inhibit CNS regeneration by modifying the structural and mechanical properties of the lesion environment. 1
- 527 LZTR1 mutation mediates oncogenesis through stabilization of EGFR and AXL. o
- 526 Inflammation-related citrullination of matrisome proteins in human cancer. 12, o
- 525 Proteome profiles during early stage of somatic embryogenesis of two *Eucalyptus* species. **2022**, 22, o

- 524 Ckb and Ybx2 interact with Ribc2 and are necessary for the ciliary beating of multi-cilia. o
- 523 Proteomic analysis of *Sarcoptes scabiei* reveals that proteins differentially expressed between eggs and female adult stages are involved predominantly in genetic information processing, metabolism and/or host-parasite interactions. **2022**, 16, e0010946 o
- 522 Protein-Peptide Turnover Profiling reveals the order of PTM addition and removal during protein maturation. **2022**, 13, o
- 521 Lysine Succinylation of VBS Contributes to Sclerotia Development and Aflatoxin Biosynthesis in *Aspergillus flavus*. **2022**, 100490 o
- 520 Endometrial small extracellular vesicles regulate human trophoctodermal cell invasion by reprogramming the phosphoproteome landscape. 10, 1
- 519 A database of accurate electrophoretic migration patterns for human proteins. **2022**, 167933 o
- 518 The Arabidopsis TIR-NBS-LRR protein CSA1 guards BAK1-BIR3 homeostasis and mediates convergence of pattern- and effector-induced immune responses. **2022**, 30, 1717-1731.e6 o
- 517 Application of ALFA-Tagging in the Nematode Model Organisms *Caenorhabditis elegans* and *Pristionchus pacificus*. **2022**, 11, 3875 o
- 516 *Toxoplasma gondii* virulence factor ROP1 reduces parasite susceptibility to murine and human innate immune restriction. **2022**, 18, e1011021 o
- 515 CPPA: A Web Tool for Exploring Proteomic and Phosphoproteomic Data in Cancer. o
- 514 Primary Focal Segmental Glomerulosclerosis Plasmas Increase Lipid Droplet Formation and Perilipin-2 Expression in Human Podocytes. **2023**, 24, 194 o
- 513 Molecular anatomy of eosinophil activation by IL5 and IL33. o
- 512 Motif-Targeting Phosphoproteome Analysis of Cancer Cells for Profiling Kinase Inhibitors. **2023**, 15, 78 o
- 511 The Mba1 homologue of *Trypanosoma brucei* is involved in the biogenesis of oxidative phosphorylation complexes. o
- 510 Structural basis for the assembly of the type V CRISPR-associated transposon complex. **2022**, 185, 4999-5010.e17
- 509 New metabolic signature for Chagas disease reveals sex steroid perturbation in humans and mice. **2022**, 8, e12380 o
- 508 Slow growing behavior in African trypanosomes during adipose tissue colonization. **2022**, 13, o
- 507 Aminolipids elicit functional trade-offs between competitiveness and bacteriophage attachment in *Ruegeria pomeroyi*. o

- 506 Characterization of an RNA binding protein interactome reveals a context-specific post-transcriptional landscape of MYC-amplified medulloblastoma. **2022**, 13, ○
- 505 The Highly Potent AhR Agonist Picoberin Modulates Hh-Dependent Osteoblast Differentiation. **2022**, 65, 16268-16289 ○
- 504 A critical period of translational control during brain development at codon resolution. **2022**, 29, 1277-1290 1
- 503 Phosphoproteomic Analysis of Dopamine D2 Receptor Signaling Reveals Interplay of G Protein- and  $\beta$ -Arrestin-Mediated Effects. ○
- 502 A Dual Detergent Strategy to Capture a Bacterial Outer Membrane Proteome in Peptidiscs for Characterization by Mass Spectrometry and Binding Assays. ○
- 501 Plasma proteome profiling of healthy subjects undergoing bed rest reveals unloading-dependent changes linked to muscle atrophy. ○
- 500 Cardiovirus leader proteins retarget RSK kinases toward alternative substrates to perturb nucleocytoplasmic traffic. **2022**, 18, e1011042 ○
- 499 Horizontal Transfer of Bacteriocin Biosynthesis Genes Requires Metabolic Adaptation To Improve Compound Production and Cellular Fitness. ○
- 498 TBC1D15 potentiates lysosomal regeneration from damaged membranes. ○
- 497 TurboID reveals the proximiomes of CGE1, VIPP1, and VIPP2 in *Chlamydomonas reinhardtii*. ○
- 496 Mass Spectrometric Methods for Non-Targeted Screening of Metabolites: A Future Perspective for the Identification of Unknown Compounds in Plant Extracts. **2022**, 9, 415 ○
- 495 The protein phosphatase 2A holoenzyme is a key regulator of starch metabolism and bradyzoite differentiation in *Toxoplasma gondii*. **2022**, 13, ○
- 494 Extensive proteome and functional genomic profiling of variability between genetically identical human B-lymphoblastoid cells. **2022**, 9, ○
- 493 Lysine deserts prevent adventitious ubiquitylation of ubiquitin-proteasome components. ○
- 492 Tumor PKC $\delta$  instigates immune exclusion in EGFR-mutated non-small cell lung cancer. **2022**, 20, ○
- 491 Excessive proteostasis contributes to pathology in fragile X syndrome. **2022**, ○
- 490 Native size exclusion chromatography-based mass spectrometry (SEC-MS) reveals new components of the early Heat Shock Protein 90 inhibition response among limited global changes. **2022**, 100485 ○
- 489 Combining Metabolic Pulse Labeling and Quantitative Proteomics to Monitor Protein Synthesis Upon Viral Infection. **2023**, 149-165 ○

- 488 Mice Placental ECM Components May Provide A Three-Dimensional Placental Microenvironment. **2023**, 10, 16 ○
- 487 Classification of Extracellular Vesicles Based on Surface Glycan Structures by Spongy-like Separation Media. **2022**, 94, 18025-18033 ○
- 486 Synchro-PASEF allows precursor-specific fragment ion extraction and interference removal in data-independent acquisition. **2022**, 100489 ○
- 485 High-content screening identifies a critical role for P pili in early adhesion of uropathogenic *Escherichia coli* to bladder cells. ○
- 484 The cyanobacterial Extracellular Polypeptide Phycocyanobilin inhibits cysteine protease legumain. ○
- 483 Proteomic profiling reveals mitochondrial dysfunction in the cerebellum of transgenic mice overexpressing DYRK1A, a Down syndrome candidate gene. 15, ○
- 482 Structural mechanism of extranucleosomal DNA readout by the INO80 complex. **2022**, 8, 1
- 481 The Alarmone Diadenosine Tetraphosphate as a Cosubstrate for Protein AMPylation. ○
- 480 High-quality and robust protein quantification in large clinical/pharmaceutical cohorts with IonStar proteomics investigation. ○
- 479 Oncogenic deubiquitination controls tyrosine kinase signaling and therapy response in acute lymphoblastic leukemia. **2022**, 8, ○
- 478 Typic: A Practical and Robust Tool to Rank Proteotypic Peptides for Targeted Proteomics. ○
- 477 Human SLFN5 and its *Xenopus Laevis* ortholog regulate entry into mitosis and oocyte meiotic resumption. **2022**, 8, ○
- 476 pGlycoQuant with a deep residual network for quantitative glycoproteomics at intact glycopeptide level. **2022**, 13, 1
- 475 Comprehensive Evaluation of Rapamycin Specificity as an mTOR Inhibitor. ○
- 474 AKTIP loss is enriched in ER-positive breast cancer for tumorigenesis and confers endocrine resistance. **2022**, 41, 111821 ○
- 473 The phase separated CO<sub>2</sub>-fixing pyrenoid proteome determined by TurboID. ○
- 472 Synaptic activity-dependent changes in the hippocampal palmitoylome. **2022**, 15, 1
- 471 MATRIX platform to analyze translation machinery remodeling in glioblastoma cells. **2022**, 3, 101919 ○

- 470 What doesn't kill you makes you live longer - Longevity of a social host linked to parasite proteins. o
- 469 Proteomic repository data submission, dissemination, and reuse: key messages. 1-14 o
- 468 Epigenetic reprogramming shapes the cellular landscape of schwannoma. o
- 467 Bidirectional promoter activity from expression cassettes can drive off-target repression of neighboring gene translation. 11, o
- 466 Dynamics and composition of small heat shock protein condensates and aggregates. o
- 465 A transcriptional switch controls sex determination in *Plasmodium falciparum*. **2022**, 612, 528-533 o
- 464 Acetic Acid Ion Pairing Additive for Reversed-Phase HPLC Improves Detection Sensitivity in Bottom-up Proteomics Compared to Formic Acid. o
- 463 Moonlighting chaperone activity of the enzyme PqsE contributes to RhlR-controlled virulence of *Pseudomonas aeruginosa*. **2022**, 13, 1
- 462 Synovial Fluid in Knee Osteoarthritis Extends Proinflammatory Niche for Macrophage Polarization. **2022**, 11, 4115 o
- 461 Translation factor eIF5a is essential for IFN $\gamma$  production and cell cycle regulation in primary CD8+ T lymphocytes. **2022**, 13, o
- 460 Expression of Synj2bp in mouse liver regulates the extent of wrapER-mitochondria contact to maintain hepatic lipid homeostasis. **2022**, 17, 1
- 459 Epidermal stratification requires retromer-mediated desmoglein-1 recycling. **2022**, 57, 2683-2698.e8 o
- 458 Fibroblasts-derived extracellular vesicles contain SFRP1 and mediate pulmonary fibrosis. o
- 457 Affinity-Based Interactome Analysis of Endogenous LINE-1 Macromolecules. **2023**, 215-256 o
- 456 Parkin-dependent mitophagy occurs via proteasome-dependent steps sequentially targeting separate mitochondrial sub-compartments for autophagy. **2022**, 1, 576-602 o
- 455 A metabolite sensor subunit of the Atg1/ULK complex regulates selective autophagy. o
- 454 MS-DAP Platform for Downstream Data Analysis of Label-Free Proteomics Uncovers Optimal Workflows in Benchmark Data Sets and Increased Sensitivity in Analysis of Alzheimer's Biomarker Data. o
- 453 Fibroblast inflammatory priming determines regenerative versus fibrotic skin repair in reindeer. **2022**, 185, 4717-4736.e25 2

452	Previously Unidentified Histone H1-Like Protein Is Involved in Cell Division and Ribosome Biosynthesis in <i>Toxoplasma gondii</i> . <b>2022</b> , 7,	0
451	Absolute quantification of cellular levels of photosynthesis-related proteins in <i>Synechocystis</i> sp. PCC 6803.	0
450	Development of SOS1 Inhibitor-Based Degraders to Target KRAS-Mutant Colorectal Cancer. <b>2022</b> , 65, 16432-16450	2
449	Non-targeted metabolomics identifies erythronate accumulation in cancer cells.	0
448	Analysis of proteome adaptation reveals a key role of the bacterial envelope in starvation survival. <b>2022</b> , 18,	0
447	Benchmarking tools for detecting longitudinal differential expression in proteomics data allows establishing a robust reproducibility optimization regression approach. <b>2022</b> , 13,	0
446	A quantitative and site-specific atlas of the in vivo citrullinome reveals widespread existence of citrullination.	0
445	Remodeling of algal photosystem I through phosphorylation.	0
444	c-Abl Regulates the Pathological Deposition of TDP-43 via Tyrosine 43 Phosphorylation. <b>2022</b> , 11, 3972	0
443	Exploiting effector - host interactions using TurboID-based proximity labeling.	0
442	Proteome analysis of <i>Ehrlichia chaffeensis</i> containing phagosome membranes revealed the presence of numerous bacterial and host proteins. 12,	1
441	Flotillin-2 regulates epidermal growth factor receptor activation, degradation by Cbl-mediated ubiquitination, and cancer growth. <b>2022</b> , 102766	0
440	Peptide collision cross sections of 22 post-translational modifications.	0
439	Evaluation of the Potential Risk of Analyzing Phosphopeptides with Easy-nLC 1200-Coupled Mass Spectrometers. <b>2022</b> , 7, 47806-47811	0
438	HNF1 $\alpha$ -associated cyst development and electrolyte disturbances are not explained by BAIAP2L2 expression. <b>2023</b> , 37,	0
437	Hippo-released WWC1 facilitates AMPA receptor regulatory complexes for hippocampal learning. <b>2022</b> , 41, 111766	0
436	Exploring functional protein covariation across single cells using nPOP. <b>2022</b> , 23,	1
435	The Alarmone Diadenosine Tetraphosphate as a Cosubstrate for Protein AMPylation.	0

- 434 Synapse integrity and function: Dependence on protein synthesis and identification of potential failure points. 15, ○
- 433 Membrane Protein Modification Modulates Big and Small Extracellular Vesicle Biodistribution and Tumorigenic Potential in Breast Cancers in vivo. 2208966 ○
- 432 Proteomics to study cancer immunity and improve treatment. ○
- 431 Basal cell adhesion molecule promotes metastasis-associated processes in ovarian cancer. **2023**, 13, ○
- 430 In-cell chemical crosslinking identifies hotspots for SQSTM-1/p62-IB interaction that underscore a critical role of p62 in limiting NF- $\kappa$ B activation through IB stabilization. **2023**, 100495 ○
- 429 Integrative proteogenomics using ProteomeGenerator2. ○
- 428 An E3 ligase network engages GCN1 to promote the degradation of translation factors on stalled ribosomes. **2023**, 1 ○
- 427 Pathway-guided monitoring of the disease course in bladder cancer with longitudinal urine proteomics. **2023**, 3, ○
- 426 Direct and cost-effective method for histone isolation from cultured mammalian cells. 1-14 ○
- 425 Glucose dissociates DDX21 dimers to regulate mRNA splicing and tissue differentiation. **2023**, 186, 80-97.e26 ○
- 424 Legionella - and host-driven lipid flux at LCV-ER membrane contact sites promotes vacuole remodeling. 1
- 423 Proteomic and in silico analyses of dextran synthesis influence on *Leuconostoc lactis* AV1n adaptation to temperature change. 13, ○
- 422 GlnH, a Novel Antigen That Offers Partial Protection against Verocytotoxigenic *Escherichia coli* Infection. **2023**, 11, 175 ○
- 421 SPECC1L binds the myosin phosphatase complex MYPT1/PP1 and can regulate its distribution between microtubules and filamentous actin. **2023**, 102893 ○
- 420 Massive solubility changes of neuronal proteins upon simulated traumatic brain injury reveal the role of shockwave in irreversible damage. ○
- 419 Advancements in Oncoproteomics Technologies: Treading toward Translation into Clinical Practice. **2023**, 11, 2 1
- 418 A high-confidence Physcomitrium patens plasmodesmata proteome by iterative scoring and validation reveals diversification of cell wall proteins during evolution. ○
- 417 E4F1 and ZNF148 are transcriptional activators of the A57C and wildtype TERT promoter. ○



- 416 Pitfalls and Solutions in Mass Spectrometry-Based Identification of Protein Glycation. o
- 415 ROP39 is an Irgb10-specific parasite effector that modulates acute *Toxoplasma gondii* virulence. **2023**, 19, e1011003 o
- 414 TopPICR: A Companion R Package for Top-Down Proteomics Data Analysis. o
- 413 Gene-by-gene screen of the unknown proteins encoded on *Plasmodium falciparum* chromosome 3. **2023**, 14, 9-23.e7 o
- 412 Rapid Multi-Omics Sample Preparation for Mass Spectrometry. o
- 411 Uptake-independent killing of macrophages by extracellular aggregates of *Mycobacterium tuberculosis* ESX-1 and PDIM-dependent. o
- 410 Mechanism of ribosome-associated mRNA degradation during tubulin autoregulation. o
- 409 Proteomics separates adult-type diffuse high-grade gliomas in metabolic subgroups independent of 1p/19q codeletion and across IDH mutational status. **2023**, 4, 100877 o
- 408 TOBF1 modulates mouse embryonic stem cell fate through co-transcriptional regulation of alternative splicing. o
- 407 Modulation of cellular transcriptome and proteome composition by azidohomoalanine □ implications on click chemistry based secretome analysis. o
- 406 Monitoring mitochondrial translation by pulse SILAC. **2023**, 102865 o
- 405 A deeply conserved protease, acylamino acid-releasing enzyme (AARE), acts in ageing in *Physcomitrella* and *Arabidopsis*. **2023**, 6, o
- 404 Transcriptome and Proteome Analysis Revealed the Influence of High-Molecular-Weight Glutenin Subunits (HMW-GSs) Deficiency on Expression of Storage Substances and the Potential Regulatory Mechanism of HMW-GSs. **2023**, 12, 361 o
- 403 Identifying and characterising Thrp3, Bclaf1 and Erh interactions using cross-linking mass spectrometry. 6, 260 o
- 402 PML mutants resistant to arsenic induced degradation fail to generate the appropriate SUMO and ubiquitin signals required for RNF4 and p97 recruitment. o
- 401 Characterisation of N-linked protein glycosylation in the bacterial pathogen *Campylobacter hepaticus*. **2023**, 13, o
- 400 MSstatsShiny: A GUI for Versatile, Scalable, and Reproducible Statistical Analyses of Quantitative Proteomic Experiments. o
- 399 Metabolic rewiring of the probiotic bacterium *Lactococcus rhamnosus* GG contributes to cell-wall remodeling and antimicrobials production. o

- 398 The Crux Toolkit for Analysis of Bottom-Up Tandem Mass Spectrometry Proteomics Data. o
- 397 Production of  $\beta$ -PheRS fragments correlates with food avoidance and slow growth, and is suppressed by the appetite-inducing hormone CCHa2. o
- 396 Non-enzymatic acetylation inhibits glycolytic enzymes in *Escherichia coli*. **2023**, 42, 111950 o
- 395 Comparative Proteomics of Outer Membrane Vesicles from Polymyxin-Susceptible and Extremely Drug-Resistant *Klebsiella pneumoniae*. o
- 394 Deep learning-driven fragment ion series classification enables highly precise and sensitive de novo peptide sequencing. o
- 393 Benchmarking commonly used software suites and analysis workflows for DIA proteomics and phosphoproteomics. **2023**, 14, o
- 392 Hemisynthetic alkaloids derived from trilobine are antimalarials with sustained activity in multidrug resistant *Plasmodium falciparum*. **2023**, 105940 o
- 391 Multi-layered chromatin proteomics identifies cell vulnerabilities in DNA repair. o
- 390 Mass Spectrometry-Based Proteomics Workflows in Cancer Research: The Relevance of Choosing the Right Steps. **2023**, 15, 555 o
- 389 Global profiling of protein lysine lactylation and potential target modified protein analysis in hepatocellular carcinoma. 2200432 o
- 388 Comparative proteomics study of mitochondrial electron transport system modulation in SH-SY5Y cells following MPP+ versus 6-OHDA-induced neurodegeneration. **2023**, 14, o
- 387 An epithelial-to-mesenchymal transition induced extracellular vesicle prognostic signature in non-small cell lung cancer. **2023**, 6, 1
- 386 A CRISPR/Cas9-mediated screen identifies determinants of early plasma cell differentiation. 13, o
- 385 ONE-HELIX PROTEIN 2 is not required for the synthesis of photosystem II subunit D1 in *Chlamydomonas*. o
- 384 Combination of automated sample preparation and micro-flow LCMS for high-throughput plasma proteomics. **2023**, 20, o
- 383 Genetic code expansion reveals aminoacylated lysine ubiquitination mediated by UBE2W. 1
- 382 Deep learning prediction boosts phosphoproteomics-based discoveries through improved phosphopeptide identification. o
- 381 PDE6D Mediates Trafficking of Prenylated Proteins NIM1K and UBL3 to Primary Cilia. **2023**, 12, 312 o

- 380 Translation initiation of leaderless and polycistronic transcripts in mammalian mitochondria. o
- 379 Chemical Proteomics with Novel Fully Functionalized Fragments and Stringent Target Prioritization Identifies the Glutathione-Dependent Isomerase GSTZ1 as a Lung Cancer Target. o
- 378 Lipopolysaccharide Primes Human Macrophages for Noncanonical Inflammasome-Induced Extracellular Vesicle Secretion. **2023**, 210, 322-334 o
- 377 P-Rex1 is a novel substrate of the E3 ubiquitin ligase Malin associated with Lafora disease. **2023**, 177, 105998 1
- 376 Bump-and-hole engineering of human polypeptide N-acetylgalactosamine transferases to dissect their protein substrates and glycosylation sites in cells. **2023**, 4, 101974 o
- 375 Proteomics-based trapping with single or multiple inactive mutants reproducibly profiles histone deacetylase 1 substrates. **2023**, 274, 104807 o
- 374 A Multi-Omics Approach Reveals Features That Permit Robust and Widespread Regulation of IFN-Inducible Antiviral Effectors. **2022**, 209, 1930-1941 o
- 373 Differentiated extracts from freshwater and terrestrial mollusks inhibit virulence factor production in *Cryptococcus neoformans*. o
- 372 Toward structural-omics of the bovine retinal pigment epithelium. **2022**, 41, 111876 o
- 371 Phosphoproteomic analysis identifies supervillin as an ERK3 substrate regulating cytokinesis and cell ploidy. o
- 370 Desmosomal cell cohesion and epidermal differentiation are modulated by dolichol phosphate mannosyltransferase 1 (DPM1) through SERPINB5-dependent mechanisms. o
- 369 Evolution of Rev7 interactions in eukaryotic TLS DNA polymerase Pol $\eta$  **2022**, 102859 o
- 368 Heritability of Protein and Metabolite Biomarkers Associated with COVID-19 Severity: A Metabolomics and Proteomics Analysis. **2023**, 13, 46 o
- 367 TBK1 phosphorylation activates LIR-dependent degradation of the inflammation repressor TNIP1. **2023**, 222, 2 2
- 366 Genetic and phosphoproteomic basis of LysM-mediated immune signaling in *Marchantia polymorpha* highlights conserved elements and new aspect of pattern-triggered immunity in land plants. o
- 365 Npl3 functions in mRNP assembly by recruitment of mRNP components to the transcription site and their transfer onto the mRNA. o
- 364 Rho-Kinase/ROCK Phosphorylates PSD-93 Downstream of NMDARs to Orchestrate Synaptic Plasticity. **2023**, 24, 404 2
- 363 Deep Learning Based MS2 Feature Detection for Data-Independent Shotgun Proteomics. **2022**, o

- 362 Proteomics of High-Grade Serous Ovarian Cancer Models Identifies Cancer-Associated Fibroblast Markers Associated with Clinical Outcomes. **2023**, 13, 75 ○
- 361 Multi-omics profiling visualizes dynamics of cardiac development and functions. **2022**, 41, 111891 ○
- 360 Prevention of Noise-Induced Hearing Loss In Vivo: Continuous Application of Insulin-like Growth Factor 1 and Its Effect on Inner Ear Synapses, Auditory Function and Perilymph Proteins. **2023**, 24, 291 1
- 359 Integrated View of Baseline Protein Expression in Human Tissues. 1
- 358 The p97/VCP segregase is essential for arsenic-induced degradation of PML and PML-RARA. **2023**, 222, ○
- 357 Multi-omics Analysis of the Role of PHGDH in Colon Cancer. **2023**, 22, 153303382211459 ○
- 356 sLORFinder: a tool to detect open reading frames resulting from trans-splicing of spliced leader sequences. **2023**, 24, ○
- 355 Mesothelioma-associated fibroblasts enhance proliferation and migration of pleural mesothelioma cells via c-Met/PI3K and WNT signaling but do not protect against cisplatin. **2023**, 42, ○
- 354 CHalf: Folding Stability Made Simple. **2023**, 22, 605-614 ○
- 353 Probing the sub-cellular mechanisms of LCA5-Leber Congenital Amaurosis and associated gene therapy with expansion microscopy. ○
- 352 A simple non-invasive method to collect soft tick saliva reveals differences in Ornithodoros moubata saliva composition between ticks infected and uninfected with Borrelia duttonii spirochetes. 13, ○
- 351 Characterization of the preferred cation cofactors of chloroplast protein kinases in Arabidopsis thaliana. ○
- 350 Defining the lipidome of Arabidopsis leaf mitochondria: Specific lipid complement and biosynthesis capacity. ○
- 349 ChIP-MS reveals the local chromatin composition by label-free quantitative proteomics. ○
- 348 New panel of biomarkers to discriminate between amelanotic and melanotic metastatic melanoma. 12, 1
- 347 Genomic and proteomic analysis of Bacillus subtilis as microplastic bioremediation agents. **2023**, ○
- 346 Ciliopathy-associated missense mutations in IFT140 are hypomorphic and have edgetic effects on protein interaction networks. ○
- 345 Immunoreactivity against SLC3A2 in high grade gliomas displays positive correlation with glioblastoma patient survival: Potential target for glioma diagnosis and therapy. ○

344	Integrating Transcriptomics and Metabolomics to Explore the Novel Pathway of <i>Fusobacterium nucleatum</i> Invading Colon Cancer Cells. <b>2023</b> , 12, 201	0
343	An Isobaric Labeling Approach to Enhance Detection and Quantification of Tissue-Derived Plasma Proteins as Potential Early Disease Biomarkers. <b>2023</b> , 13, 215	0
342	<i>Verticillium dahliae</i> Vta3 promotes ELV1 virulence factor gene expression in xylem sap, but tames MtF1-mediated late stages of fungus-plant interactions and microsclerotia formation. <b>2023</b> , 19, e1011100	0
341	Human mitochondria require mtRF1 for translation termination at non-canonical stop codons. <b>2023</b> , 14,	0
340	Fucosylation of HLA-DRB1 regulates CD4+ T cell-mediated anti-melanoma immunity and enhances immunotherapy efficacy.	0
339	Low level of antioxidant capacity biomarkers but not target overexpression predicts vulnerability to ROS-inducing drugs.	0
338	Nematode gene annotation by machine-learning-assisted proteotranscriptomics enables proteome-wide evolutionary analysis. <b>2023</b> , 33, 112-128	0
337	A novel class of sulphonamides potently block malaria transmission by targeting a <i>Plasmodium</i> vacuole membrane protein. <b>2023</b> , 16,	1
336	Hypolipidemic Effects of Beetroot Juice in SHR-CRP and HHTg Rat Models of Metabolic Syndrome: Analysis of Hepatic Proteome. <b>2023</b> , 13, 192	0
335	Identification of levoglucosan degradation pathways in bacteria and sequence similarity network analysis.	0
334	Photo-ANA enables profiling of hostBacteria protein interactions during infection.	0
333	piRNA processing by a trimeric Schlafen-domain nuclease.	0
332	Multiple oxidative post-translational modifications of human glutamine synthetase mediate peroxynitrite-dependent enzyme inactivation and aggregation. <b>2023</b> , 102941	0
331	A targeted multi-proteomics approach generates a blueprint of the ciliary ubiquitinome. 11,	0
330	Visualization of translation and protein biogenesis at the ER membrane. <b>2023</b> , 614, 160-167	1
329	MitoStores: chaperone-controlled protein granules store mitochondrial precursors in the cytosol.	2
328	Revealing determinants of translation efficiency via whole-gene codon randomization and machine learning.	1
327	SPRTN-dependent DPC degradation precedes repair of damaged DNA: a proof of concept revealed by the STAR assay.	0

- 326 Proteomic analysis of canine vaccines. **2023**, 1-7 o
- 325 Raw milk kefir: microbiota, bioactive peptides, and immune modulation. **2023**, 14, 1648-1661 o
- 324 Glycoproteome remodelling and granule-specific N-glycosylation accompany neutrophil granulopoiesis. o
- 323 Taspase1 Facilitates Topoisomerase II $\beta$ -Mediated DNA Double-Strand Breaks Driving Estrogen-Induced Transcription. **2023**, 12, 363 o
- 322 The Mycobacterium tuberculosis protein O-phosphorylation landscape. o
- 321 Structure of the Commander endosomal trafficking complex linked to X-linked intellectual disability/Ritscher-Schinzel syndrome. o
- 320 Exploration of the Nuclear Proteomes in the Ciliate Oxytricha trifallax. **2023**, 11, 343 o
- 319 Protein interaction studies in human induced neurons indicate convergent biology underlying autism spectrum disorders. **2023**, 100250 o
- 318 Cervical Fluids Are a Source of Protein Biomarkers for Early, Non-Invasive Endometrial Cancer Diagnosis. **2023**, 15, 911 o
- 317 MS1Connect: a mass spectrometry run similarity measure. **2023**, 39, o
- 316 Mitochondrial complexome reveals quality-control pathways of protein import. **2023**, 614, 153-159 o
- 315 Silent recognition of flagellins from human gut commensal bacteria by Toll-like receptor 5. **2023**, 8, o
- 314 The Impact of Low-Temperature Inactivation of Protease AprX from Pseudomonas on Its Proteolytic Capacity and Specificity: A Peptidomic Study. **2023**, 4, 150-166 o
- 313 Establishment and characterization of canine mammary tumoroids for translational research. **2023**, 21, o
- 312 Analysis of Yeast Peroxisomes via Spatial Proteomics. **2023**, 13-31 o
- 311 Identification of N-degrons and N-recognins using peptide pull-downs combined with quantitative mass spectrometry. **2023**, o
- 310 Quantitative analysis of high-throughput biological data. o
- 309 Comparative proteomics of vesicles essential for the egress of Plasmodium falciparum gametocytes from red blood cells. o

308	Mechanical loading is required for initiation of extracellular matrix deposition at the developing murine myotendinous junction. <b>2023</b> , 116, 28-48	o
307	PerTurboID: A targeted in situ method to measure changes in a local protein environment reveals the impact of kinase deletion on cytoadhesion in malaria causing parasites.	o
306	Alternative polyadenylation alters protein dosage by switching between intronic and 3'UTR sites. <b>2023</b> , 9,	o
305	Frontiers in mass spectrometryBased clinical proteomics for cancer diagnosis and treatment.	o
304	Integrative proteomics highlight presynaptic alterations and c-Jun misactivation as convergent pathomechanisms in ALS.	o
303	Rie1 and Sgn1 form an RNA-binding complex that enforces the meiotic entry cell fate decision.	o
302	Accurate label-free quantification by directLFQ to compare unlimited numbers of proteomes.	o
301	Insights into the sulfur metabolism of <i>Chlorobaculum tepidum</i> by label-free quantitative proteomics. 2200138	o
300	A transformer architecture for retention time prediction in liquid chromatography mass spectrometry-based proteomics. <b>2023</b> , 23,	1
299	Evaluation of the use of different cell types as a substrate pool for in vitro kinase reaction.	o
298	The effect of G0S2 on insulin sensitivity: A proteomic analysis in a G0S2-overexpressed high-fat diet mouse model. 14,	o
297	Enhancing leaf photosynthesis from altered chlorophyll content requires optimal partitioning of nitrogen. <b>2023</b> , 2, 24-36	o
296	Machine learning predictions of MHC-II specificities reveal alternative binding mode of class II epitopes. <b>2023</b> ,	o
295	Proteomic Shotgun and Targeted Mass Spectrometric Datasets of Cerebrospinal Fluid (Liquor) Derived from Patients with Vestibular Schwannoma. <b>2023</b> , 8, 71	o
294	Endothelial FAT1 inhibits angiogenesis by controlling YAP/TAZ protein degradation via E3 ligase MIB2. <b>2023</b> , 14,	o
293	Activity-Guided Proteomic Profiling of Proteasomes Uncovers a Variety of Active (And Inactive) Proteasome species.	o
292	Prioritized mass spectrometry increases the depth, sensitivity and data completeness of single-cell proteomics.	o
291	NLR5-CIITA Fusion Protein as an Effective Inducer of MHC-I Expression and Antitumor Immunity. <b>2023</b> , 24, 7206	o

- 290 Zasp52 strengthens whole embryo tissue integrity through supracellular actomyosin networks. **2023**, 150, ○
- 289 Identification of pH-specific protein expression responses by *Campylobacter jejuni* strain NCTC 11168. **2023**, 104061 ○
- 288 Decrypting drug actions and protein modifications by dose- and time-resolved proteomics. **2023**, 380, 93-101 ○
- 287 High ploidy large cytoplasmic megakaryocytes are hematopoietic stem cells regulators and essential for platelet production. **2023**, 14, ○
- 286 Potential negative effect of long-term exposure to nitrofurans on bacteria isolated from wastewater. **2023**, 872, 162199 ○
- 285 Analysis of histomorphometric and proteome dynamics inside the silk gland lumen of *Bombyx mori* revealed the dynamic change of silk protein during the molt stage. **2023**, 236, 123926 ○
- 284 A proteomic overview of the major venom components from *Tityus championi* from Panama. **2023**, 227, 107082 ○
- 283 Mutation of *Arabidopsis* SME1 and Sm core assembly improves oxidative stress resilience. **2023**, 200, 117-129 ○
- 282 Proteomic and phosphoproteomic analyses of Jurkat T-cell treated with 2'3' cGAMP reveals various signaling axes impacted by cyclic dinucleotides. **2023**, 279, 104869 ○
- 281 Rat bronchoalveolar lavage proteome changes following e-cigarette aerosol exposures. **2023**, 324, L571-L583 ○
- 280 Residue selective crosslinking of proteins through photoactivatable or proximity-enabled reactivity. **2023**, 74, 102285 ○
- 279 Low level of antioxidant capacity biomarkers but not target overexpression predicts vulnerability to ROS-inducing drugs. **2023**, 62, 102639 ○
- 278 Donkey whey proteins ameliorate dextran sulfate sodium-induced ulcerative colitis in mice by downregulating the S100A8-TRAF6-NF- $\kappa$ B axis-mediated inflammatory response. **2023**, 12, 1809-1819 ○
- 277 Fitm2 is required for ER homeostasis and normal function of murine liver. **2023**, 299, 103022 ○
- 276 Integrative proteogenomic characterization of early esophageal cancer. **2023**, 14, ○
- 275 Protein structure prediction with in-cell photo-crosslinking mass spectrometry and deep learning. ○
- 274 Tumour mitochondrial DNA mutations drive aerobic glycolysis to enhance checkpoint blockade. ○
- 273 During heat stress in *Myxococcus xanthus*, the CdbS PilZ domain protein, along with two PilZ-DnaK chaperones, perturbs chromosome organization and accelerates cell death. ○



- 272 Lysosomal lipid peroxidation regulates tumor immunity. **2023**, 133, ○
- 271 Characterization of p38 $\beta$  Signaling Networks in Cancer Cells Using Quantitative Proteomics and Phosphoproteomics. **2023**, 22, 100527 ○
- 270 Trypsin  $\alpha$  regulation of joint lubrication and inflammation via proteoglycan-4 in osteoarthritis. **2023**, 14, ○
- 269 Sex-specific microglia state in the Neuroligin-4 knock-out mouse model of autism spectrum disorder. **2023**, 111, 61-75 ○
- 268 Ensembles of human myosin-19 bound to calmodulin and regulatory light chain RLC12B drive multimicron transport. **2023**, 299, 102906 ○
- 267 Denitrification by Bradyrhizobia under Feast and Famine and the Role of the bc1 Complex in Securing Electrons for N<sub>2</sub>O Reduction. **2023**, 89, ○
- 266 Glutathione transferase photoaffinity labeling demonstrates GST activation by safeners and NPR1-independent activation by BTH. ○
- 265 LPS-induced acute neuroinflammation, involving interleukin-1 beta signaling, leads to proteomic, cellular, and network-level changes in the prefrontal cortex of mice. **2023**, 28, 100594 1
- 264 Broadly neutralizing aptamers to SARS-CoV-2: A diverse panel of modified DNA antiviral agents. **2023**, 31, 370-382 ○
- 263 Pan-cancer Proteomics Analysis to Identify Tumor-Enriched and Highly Expressed Cell Surface Antigens as Potential Targets for Cancer Therapeutics. ○
- 262 Lung macrophages utilize unique cathepsin K-dependent phagosomal machinery to degrade intracellular collagen. **2023**, 6, e202201535 ○
- 261 The RALF Signaling Pathway Regulates Cell Wall Integrity during Pollen Tube Growth in Maize. ○
- 260 Elucidating colony bloom formation mechanism of a harmful alga *Phaeocystis globosa* (Prymnesiophyceae) using metaproteomics. **2023**, 869, 161846 ○
- 259 Surfaceome Profiling of Cell Lines and Patient-Derived Xenografts Confirm FGFR4, NCAM1, CD276, and Highlight AGRL2, JAM3, and L1CAM as Surface Targets for Rhabdomyosarcoma. **2023**, 24, 2601 ○
- 258 Influence of circadian clocks on adaptive immunity and vaccination responses. **2023**, 14, ○
- 257 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, ○
- 256 Persisting Effects in *Daphnia magna* Following an Acute Exposure to Flowback and Produced Waters from the Montney Formation. **2023**, 57, 2380-2392 ○
- 255 SUMO Proteomics Analyses Identify Protein Inhibitor of Activated STAT-Mediated Regulatory Networks Involved in Cell Cycle and Cell Proliferation. **2023**, 22, 812-825 ○

- 254 RNA-DNA hybrids prevent resection at dysfunctional telomeres. **2023**, 42, 112077 1
- 253 The role of pneumococcal extracellular vesicles on the pathophysiology of the kidney disease Hemolytic Uremic Syndrome. o
- 252 Common mouse models of tauopathy reflect early but not late human disease. **2023**, 18, o
- 251 eIF4A1-dependent mRNAs employ purine-rich 5'UTR sequences to activate localised eIF4A1-unwinding through eIF4A1-multimerisation to facilitate translation. **2023**, 51, 1859-1879 o
- 250 Shear Stress Markedly Alters the Proteomic Response to Hypoxia in Human Pulmonary Endothelial Cells. o
- 249 Deciphering the Kidney Matrisome: Identification and Quantification of Renal Extracellular Matrix Proteins in Healthy Mice. **2023**, 24, 2827 o
- 248 Getting Ready for Large-Scale Proteomics in Crop Plants. **2023**, 15, 783 o
- 247 Phenotypic effects of mutations observed in the neuraminidase of human origin H5N1 influenza A viruses. **2023**, 19, e1011135 o
- 246 The organizer of chromatin topology RIF1 ensures cellular resilience to DNA replication stress. **2023**, 6, e202101186 o
- 245 Muc2-dependent microbial colonization of the jejunal mucus layer is diet sensitive and confers local resistance to enteric pathogen infection. **2023**, 42, 112084 o
- 244 Small molecule inhibiting microglial nitric oxide release could become a potential treatment for neuroinflammation. **2023**, 18, e0278325 o
- 243 Ribosome Protein Composition Mediates Translation during the Escherichia coli Stationary Phase. **2023**, 24, 3128 o
- 242 Molecular characterization of the intact mouse muscle spindle using a multi-omics approach. 12, o
- 241 The Class IIA Histone Deacetylase (HDAC) Inhibitor TMP269 Downregulates Ribosomal Proteins and Has Anti-Proliferative and Pro-Apoptotic Effects on AML Cells. **2023**, 15, 1039 o
- 240 Identification of SARS-CoV-2 Main Protease (Mpro) Cleavage Sites Using Two-Dimensional Electrophoresis and In Silico Cleavage Site Prediction. **2023**, 24, 3236 o
- 239 Shift in vacuolar to cytosolic regime of infecting Salmonella from a dual proteome perspective. o
- 238 Omics analysis of Mycobacterium tuberculosis isolates uncovers Rv3094c, an ethionamide metabolism-associated gene. **2023**, 6, o
- 237 Snf1/AMPK fine-tunes TORC1 signaling in response to glucose starvation. 12, o

- 236 Role of the Mycobacterium tuberculosis ESX-4 Secretion System in Heme Iron Utilization and Pore Formation by PPE Proteins. **2023**, 8, ○
- 235 Data-Independent Acquisition Mass Spectrometry of EPS-Urine Coupled to Machine Learning: A Predictive Model for Prostate Cancer. **2023**, 8, 6244-6252 ○
- 234 Spontaneous onset of cellular markers of inflammation and genome instability during aging in the immune niche of the naturally short-lived turquoise killifish (*Nothobranchius furzeri*). ○
- 233 A subset of antibodies targeting citrullinated proteins confers protection from rheumatoid arthritis. **2023**, 14, ○
- 232 Heterogeneous effects of individual high-fat diet compositions on phenotype, metabolic outcome, and hepatic proteome signature in BL/6 male mice. **2023**, 20, ○
- 231 535. Detection of causative genes for resistance against cardiomyopathy syndrome in Atlantic salmon using omics data. **2022**, ○
- 230 Organ Protection by Caloric Restriction Depends on Activation of the De Novo NAD<sup>+</sup> Synthesis Pathway. **2023**, Publish Ahead of Print, ○
- 229 Microbial community succession patterns and drivers of Luxiang-flavor Jiupei during long fermentation. 14, ○
- 228 Enhanced Branched-Chain Amino Acid Metabolism Improves Age-related Reproductive Function. ○
- 227 Mass Spectrometry-Based Atlas of Extracellular Matrix Proteins across 25 Mouse Organs. **2023**, 22, 790-801 ○
- 226 Phosphoproteomics Profiling Defines a Target Landscape of the Basophilic Protein Kinases AKT, S6K, and RSK in Skeletal Myotubes. **2023**, 22, 768-789 ○
- 225 An integrated workflow for phosphopeptide identification in natural killer cells (NK-92MI) and their targets (MDA-MB-231) during immunological synapse formation. **2023**, 4, 102104 ○
- 224 Conservation, abundance, glycosylation profile, and localization of the TSP protein family in *Cryptosporidium parvum*. **2023**, 299, 103006 ○
- 223 Integrative proteomic characterization of adenocarcinoma of esophagogastric junction. **2023**, 14, 1
- 222 High cyclic electron transfer via the PGR5 pathway in the absence of photosynthetic control. ○
- 221 Deep Proteome Profiling of White Adipose Tissue Reveals Marked Conservation and Distinct Features Between Different Anatomical Depots. **2023**, 22, 100508 ○
- 220 Insight on physicochemical properties governing peptide MS1 response in HPLC-ESI-MS/MS proteomics: A deep learning approach. ○
- 219 Harnessing transcriptionally driven chromosomal instability adaptation to target therapy-refractory lethal prostate cancer. **2023**, 4, 100937 ○

- 218 Glycomics-Assisted Glycoproteomics Enables Deep and Unbiased N-Glycoproteome Profiling of Complex Biological Specimens. **2023**, 235-263 o
- 217 RNA polymerase II-associated proteins reveal pathways affected in VCP-related amyotrophic lateral sclerosis. o
- 216 MultiCell Line Analysis of Lysosomal Proteomes Reveals Unique Features and Novel Lysosomal Proteins. **2023**, 22, 100509 o
- 215 Discovery of DNA aptamers targeting SARS-CoV-2 nucleocapsid protein and protein-binding epitopes for label-free COVID-19 diagnostics. **2023**, 31, 731-743 o
- 214 The mechanism of *Pseudomonas aeruginosa* outer membrane vesicle biogenesis determines their protein composition. 2200464 o
- 213 A bench-top dark-root device built with LEGO® bricks enables a non-invasive plant root development analysis in soil conditions mirroring nature. o
- 212 The genetic background shapes the susceptibility to mitochondrial dysfunction and NASH progression. **2023**, 220, 1
- 211 Multilevel Omics-Readouts of in vitro Perturbation Studies are Determined by Memory Effects from Subculture. o
- 210 Red blood cells in proliferative kidney disease Rainbow trout (*Oncorhynchus mykiss*) infected by *Tetracapsuloides bryosalmonae* harbor IgM+ red blood cells. 14, o
- 209 Decoupling of mRNA and Protein Expression in Aging Brains Reveals the Age-Dependent Adaptation of Specific Gene Subsets. **2023**, 12, 615 o
- 208 Effects of Major Royal Jelly Proteins on the Immune Response and Gut Microbiota Composition in Cyclophosphamide-Treated Mice. **2023**, 15, 974 o
- 207 Effects of extremely low-frequency magnetic fields on human MDA-MB-231 breast cancer cells: proteomic characterization. **2023**, 253, 114650 o
- 206 Dual specificity and target gene selection by the MADS-domain protein FRUITFULL. **2023**, 9, 473-485 o
- 205 Spatial proteomics reveals secretory pathway disturbances caused by neuropathy-associated TECPR2. **2023**, 14, o
- 204 Proteome network analysis of skeletal muscle in lignan-enriched nutmeg extract-fed aged mice. **2023**, 14, o
- 203 Optimization of the Lead Compound NVP-BHG712 as a Colorectal Cancer Inhibitor. o
- 202 Evolutionary origins and interactomes of human, young microproteins and small peptides translated from short open reading frames. **2023**, 83, 994-1011.e18 o
- 201 UBR4 deficiency causes male sterility and developmental delay. o

200	The ABC transporter family efflux pump PvdRT-OpmQ of <i>Pseudomonas putida</i> KT2440: purification and initial characterization.	o
199	Phosphoproteomics reveals rewiring of the insulin signaling network and multi-nodal defects in insulin resistance. <b>2023</b> , 14,	o
198	Proximity-dependent biotinylation and identification of flagellar proteins in <i>Trypanosoma cruzi</i> .	o
197	Human Integrator provides a quality checkpoint during elongation to facilitate RNA polymerase II processivity.	o
196	Suppressing Mesenchymal Stromal Cell Ferroptosis Via Targeting a Metabolism-Epigenetics Axis Corrects their Poor Retention and Insufficient Healing Benefits in the Injured Liver Milieu. 2206439	o
195	Label-free single cell proteomics utilizing ultrafast LC and MS instrumentation: A valuable complementary technique to multiplexing. 2200162	o
194	To explore the regulatory effect of Buyang Huanwu Decoction on cerebral infarction based on quantitative proteomics. <b>2023</b> , 277, 104850	o
193	Space Omics and Tissue Response in Astronaut Skeletal Muscle after Short and Long Duration Missions. <b>2023</b> , 24, 4095	o
192	Tracheostomy in children is associated with neutrophilic airway inflammation. thorax-2022-219557	o
191	Targeting RBM10 deficiency in lung adenocarcinoma.	o
190	Apically-located P4-ATPase1-Lem1 complex internalizes phosphatidylserine and regulates motility-dependent invasion and egress in <i>Toxoplasma gondii</i> . <b>2023</b> , 21, 1893-1906	o
189	FLI1 and FRA1 transcription factors drive the transcriptional regulatory networks characterizing muscle invasive bladder cancer. <b>2023</b> , 6,	1
188	Mass spectrometry uncovers intermediates and off-pathway complexes for SNARE complex assembly. <b>2023</b> , 6,	o
187	A standardized and reproducible workflow for membrane glass slides in routine histology and spatial proteomics.	o
186	HLA-B*57:01/Carbamazepine-10,11-Epoxy Association Triggers Upregulation of the NF $\kappa$ B and JAK/STAT Pathways. <b>2023</b> , 12, 676	o
185	A molecular atlas reveals the tri-sectional spinning mechanism of spider dragline silk. <b>2023</b> , 14,	o
184	Short-chain fatty acids improve inflamm-aging and acute lung injury in old mice. <b>2023</b> , 324, L480-L492	o
183	Optimizing linear ion trap data independent acquisition towards single cell proteomics.	o

- 182 Specialized pathogenic cells release Tc toxins using a type 10 secretion system. o
- 181 TEFM variants impair mitochondrial transcription causing childhood-onset neurological disease. **2023**, 14, o
- 180 Large-Scale Immuno-peptidome Analysis Reveals Recurrent Posttranslational Splicing of Cancer- and Immune-Associated Genes. **2023**, 22, 100519 o
- 179 Challenges and Opportunities for Single-cell Computational Proteomics. **2023**, 22, 100518 o
- 178 Proteomic profiling of isolated immune synapses from primary mouse B cells. o
- 177 Biochemical characterisation of Mer3 helicase interactions and the protection of meiotic recombination intermediates. o
- 176 The Mba1 homologue of *Trypanosoma brucei* is involved in the biogenesis of oxidative phosphorylation complexes. o
- 175 Cyclin A and Cks1 promote kinase consensus switching to non-proline-directed CDK1 phosphorylation. **2023**, 42, 112139 o
- 174 The alphavirus nonstructural protein 2 NTPase induces a host translational shut-off through phosphorylation of eEF2 via cAMP-PKA-eEF2K signaling. **2023**, 19, e1011179 o
- 173 The language of posttranslational modifications and deciphering it from proteomics data. **2023**, 109-136 o
- 172 Analysis of proteomes **2023**, 111-138 o
- 171 Immediate targeting of host ribosomes by jumbo phage encoded proteins. o
- 170 Effect of spaceflight on the phenotype and proteome of *Escherichia coli*. **2023**, 18, o
- 169 cKMT1 is a New Lysine Methyltransferase That Methylates the Ferredoxin-NADP(+) Oxidoreductase and Regulates Energy Transfer in Cyanobacteria. **2023**, 22, 100521 o
- 168 Caveolae sense oxidative stress through membrane lipid peroxidation and cytosolic release of CAVIN1 to regulate NRF2. **2023**, 58, 376-397.e4 o
- 167 Human Mitochondrial Protein HSPD1 Binds to and Regulates the Repair of Deoxyinosine in DNA. **2023**, 22, 1339-1346 o
- 166 MRPS36 provides a structural link in the eukaryotic 2-oxoglutarate dehydrogenase complex. **2023**, 13, 1
- 165 A comprehensive proteomics analysis of the response of *Pseudomonas aeruginosa* to nanoceria cytotoxicity. **2023**, 17, 20-41 o

- 164 PGNNeo: A Proteogenomics-Based Neoantigen Prediction Pipeline in Noncoding Regions. **2023**, 12, 782 o
- 163 Multiomics reveals multilevel control of renal and systemic metabolism by the renal tubular circadian clock. **2023**, 133, o
- 162 Linking chromatin acylation mark-defined proteome and genome in living cells. **2023**, 186, 1066-1085.e36 2
- 161 Mice with renal-specific alterations of stem cell-associated signaling develop symptoms of chronic kidney disease but surprisingly no tumors. o
- 160 Integrative analysis of green ash phloem transcripts and proteins during an emerald ash borer infestation. **2023**, 23, o
- 159 RiccaB factors as mobile proteinaceous effectors of electrical signaling. **2023**, 186, 1337-1351.e20 o
- 158 GIPC3 couples to MYO6 and PDZ domain proteins and shapes the hair cell apical region. o
- 157 A Simplified and Effective Approach for the Isolation of Small Pluripotent Stem Cells Derived from Human Peripheral Blood. **2023**, 11, 787 o
- 156 Proteome Dynamics Analysis Reveals the Potential Mechanisms of Salinity and Drought Response during Seed Germination and Seedling Growth in *Tamarix hispida*. **2023**, 14, 656 o
- 155 An integrated workflow for quantitative analysis of the newly synthesized proteome. o
- 154 The double homeodomain protein DUX4c is associated with regenerating muscle fibers and RNA-binding proteins. **2023**, 13, o
- 153 A transcriptional activator effector of *Ustilago maydis* regulates hyperplasia in maize during pathogen-induced tumor formation. o
- 152 Discovery and characterization of non-canonical E2 conjugating enzymes. o
- 151 Morphine Re-arranges Chromatin Spatial Architecture of Primate Cortical Neurons. o
- 150 Choroid plexus-targeted NKCC1 overexpression to treat post-hemorrhagic hydrocephalus. **2023**, o
- 149 Tizoxanide Antiviral Activity on Dengue Virus Replication. **2023**, 15, 696 o
- 148 A Msp1-containing complex removes orphaned proteins in the mitochondrial outer membrane of trypanosomes. o
- 147 Comparison of Database Searching Programs for the Analysis of Single-Cell Proteomics Data. **2023**, 22, 1298-1308 o

- 146 Integrated Proteomics Unveils Nuclear PDE3A2 as a Regulator of Cardiac Myocyte Hypertrophy. **2023**, 132, 828-848 o
- 145 Analysis of context-specific KRAS-effector (sub)complexes in Caco-2 cells. **2023**, 6, e202201670 o
- 144 Removal and identification of external protein corona members from RBC-derived extracellular vesicles by surface manipulating antimicrobial peptides. **2023**, 2, o
- 143 CUDC-907, a dual PI3K/histone deacetylase inhibitor, increases meta-iodobenzylguanidine uptake (123/131I-mIBG) in vitro and in vivo: a promising candidate for advancing theranostics in neuroendocrine tumors. o
- 142 Neurofibromatosis type 1-dependent alterations in mouse microglia function are not cell-intrinsic. **2023**, 11, o
- 141 The human sperm proteome toward a panel for male fertility testing. o
- 140 Secretion of VGF relies on the interplay between LRRK2 and post-Golgi v-SNAREs. **2023**, 42, 112221 o
- 139 Phosphorylation-linked complex profiling identifies assemblies required for Hippo signal integration. **2023**, 19, o
- 138 Structures of wild-type and selected CMT1X mutant connexin 32 gap junction channels and hemichannels. o
- 137 Bottom-Up Proteomics: Advancements in Sample Preparation. **2023**, 24, 5350 o
- 136 Whitefly effector G4 interacts with tomato proteins of which MIPDB141 affects whitefly performance. o
- 135 DeepDetect: Deep Learning of Peptide Detectability Enhanced by Peptide Digestibility and Its Application to DIA Library Reduction. **2023**, 95, 6235-6243 o
- 134 Triap1 upregulation promotes escape from mitotic-slippage-induced G1 arrest. **2023**, 42, 112215 o
- 133 Progressive search in tandem mass spectrometry. **2023**, 24, o
- 132 GSE1 links the HDAC1/CoREST co-repressor complex to DNA damage. o
- 131 Advancing wide implementation of precision oncology: A liquid nitrogen-free snap freezer preserves molecular profiles of biological samples. o
- 130 Uptake-independent killing of macrophages by extracellular Mycobacterium tuberculosis aggregates. o
- 129 Estrogen receptor alpha deficiency in cardiomyocytes reprograms the heart-derived extracellular vesicle proteome and induces obesity in female mice. **2023**, 2, 268-289 o



- 128 Integration of pharmacoproteomic and computational approaches reveals the cellular signal transduction pathways affected by apatinib in gastric cancer cell lines. **2023**, 21, 2172-2187 ○
- 127 Phosphorylation barcodes direct biased chemokine signaling at CXCR3. ○
- 126 Proteomic and phosphoproteomic characteristics of the cortex, hippocampus, thalamus, lung, and kidney in COVID-19-infected female K18-hACE2 mice. **2023**, 90, 104518 ○
- 125 Detection and Isolation of Circulating Tumor Cells from Breast Cancer Patients Using CUB Domain-Containing Protein 1. **2023**, 22, 1213-1230 ○
- 124 B cell class switch recombination is regulated by DYRK1A through MSH6 phosphorylation. **2023**, 14, ○
- 123 An EOMES induced epigenetic deflection initiates lineage commitment at mammalian gastrulation. ○
- 122 lncRNA miR4458HG modulates hepatocellular carcinoma progression by activating m6A-dependent glycolysis and promoting the polarization of tumor-associated macrophages. **2023**, 80, ○
- 121 Integrative omics identifies conserved and pathogen-specific responses of sepsis-causing bacteria. **2023**, 14, ○
- 120 ADAM17 targeting by human cytomegalovirus remodels the cell surface proteome to simultaneously regulate multiple immune pathways. ○
- 119 HBV rewires liver cancer signaling by altering PP2A complexes. ○
- 118 Expanding the Characterization of Microbial Ecosystems using DIA-PASEF Metaproteomics. ○
- 117 CRISPR/Cas9-mediated knockout of the ubiquitin variant UbKEKS reveals a role in regulating nucleolar structures and composition. ○
- 116 Proximity interaction analysis of the *Plasmodium falciparum* putative ubiquitin ligase PFRNF1 reveals a role in RNA regulation. ○
- 115 PROTEOMAS: a workflow enabling harmonized proteomic meta-analysis and proteomic signature mapping. **2023**, 15, ○
- 114 prolfqua: A Comprehensive R-Package for Proteomics Differential Expression Analysis. **2023**, 22, 1092-1104 ○
- 113 Sexually dimorphic RNA helicases DDX3X and DDX3Y differentially regulate hollow condensates of DDX3X disease variants. ○
- 112 Impact of Bariatric Surgery on the Stability of the Genetic Material, Oxidation, and Repair of DNA and Telomere Lengths. **2023**, 12, 760 ○
- 111 Repertoire and abundance of secreted virulence factors shape the pathogenic capacity of *Pseudomonas syringae* pv. aptata. ○

- 110 Integrative proteomics and transcriptomics of human T-cells reveals temporal metabolic reprogramming following TCR-induced activation. ○
- 109 Archaeal Kink-Turn Binding Protein Mediates Inhibition of Orthomyxovirus Splicing Biology. ○
- 108 Quantitation of small molecules from liquid chromatography-mass spectrometric accurate mass datasets using CycloBranch. **2023**, 29, 102-110 ○
- 107 Evidence for a Putative Isoprene Reductase in *Acetobacterium wieringae*. ○
- 106 Identification of novel smORFs and microprotein acting in response to rehydration of *Nostoc flagelliforme*. ○
- 105 RBFOX2 modulates a metastatic signature of alternative splicing in pancreatic cancer. ○
- 104 Directed growth and fusion of membrane-wall microdomains requires CASP-mediated inhibition and displacement of secretory foci. **2023**, 14, ○
- 103 Proteomic characterisation of polyethylene terephthalate and monomer degradation by *Ideonella sakaiensis*. **2023**, 279, 104888 ○
- 102 Global detection of human variants and isoforms by deep proteome sequencing. ○
- 101 Mena regulates nesprin-2 to control actin-nuclear lamina associations, trans-nuclear membrane signalling and gene expression. **2023**, 14, ○
- 100 Activity-based tyrosine phosphatomics using F2Pmp probes. ○
- 99 ARSK1 activates TORC1 signaling to adjust growth to phosphate availability in *Arabidopsis*. **2023**, ○
- 98 Proteome Dynamics of Persulfidation in Leaf Tissue under Light/Dark Conditions and Carbon Deprivation. **2023**, 12, 789 ○
- 97 Principles of phosphoproteomics and applications in cancer research. **2023**, 480, 403-420 ○
- 96 OpenCustomDB: Integration of Unannotated Open Reading Frames and Genetic Variants to Generate More Comprehensive Customized Protein Databases. ○
- 95 Structural basis of bacteriophage T5 infection trigger and *E. coli* cell wall perforation. **2023**, 9, ○
- 94 Proteome-wide lysine acetylation profiling to investigate the involvement of histone deacetylase HDA5 in the salt stress response of *Arabidopsis* leaves. ○
- 93 Serine peptidases and increased amounts of soluble proteins contribute to heat priming of the plant pathogenic fungus *Botrytis cinerea*. ○

92	Functional and structural diversification of incomplete phosphotransferase system in cellulose-degrading clostridia.	o
91	Investigation of targets and anticancer mechanisms of covalently acting natural products by functional proteomics.	o
90	Loss of H3K9 trimethylation alters chromosome compaction and transcription factor retention during mitosis. <b>2023</b> , 30, 489-501	o
89	Collagen constitutes about 12% in females and 17% in males of the total protein in mice. <b>2023</b> , 13,	o
88	Differentiated extracts from freshwater and terrestrial mollusks inhibit virulence factor production in <i>Cryptococcus neoformans</i> . <b>2023</b> , 13,	o
87	Changes in calpain-2 expression during glioblastoma progression predisposes tumor cells to temozolomide resistance by minimizing DNA damage and p53-dependent apoptosis. <b>2023</b> , 23,	o
86	SLAPSHOT reveals rapid dynamics of extracellularly exposed proteome in response to calcium-activated plasma membrane phospholipid scrambling.	o
85	Quantification of absolute transcription factor binding affinities in the native chromatin context using BANC-seq.	o
84	A comprehensive molecular profiling approach reveals metabolic alterations that steer bone tissue regeneration. <b>2023</b> , 6,	o
83	Targeting oncogenic KRasG13C with nucleotide-based covalent inhibitors. 12,	o
82	Interferon-inducible phospholipids govern IFITM3 -dependent endosomal antiviral immunity.	o
81	The root pathogen <i>Aphanomyces euteiches</i> secretes modular proteases in pea apoplast during host infection. 14,	o
80	Variation of wine preference amongst consumers is influenced by the composition of salivary proteins.	o
79	<i>Arabidopsis</i> TRB proteins function in H3K4me3 demethylation by recruiting JMJ14. <b>2023</b> , 14,	o
78	Comprehensive proteogenomic characterization of early duodenal cancer reveals the carcinogenesis tracks of different subtypes. <b>2023</b> , 14,	o
77	Inhibition of nonsense-mediated mRNA decay reduces the tumorigenicity of human fibrosarcoma cells.	o
76	Utilizing a nanobody recruitment approach for assessing serine palmitoyltransferase activity in ER sub-compartments of yeast.	o
75	Rab11A Depletion in Microglia-Derived Extracellular Vesicle Proteome upon Beta-Amyloid Treatment.	o

- 74 Systematic Analysis of Metabolic Bottlenecks in the Methylerythritol 4-Phosphate (MEP) Pathway of *Zymomonas mobilis*. ○
- 73 TIAR and FMRP shape pro-survival nascent proteome of leukemia cells in the bone marrow microenvironment. **2023**, 26, 106543 ○
- 72 *Staphylococcus aureus* induces tolerance in human monocytes accompanied with expression changes of cell surface markers. 14, ○
- 71 TopBP1 utilises a bipartite GINS binding mode to activate the replicative helicase. ○
- 70 Identification and Characterisation of Proteins Binding to a G-Quadruplex Origin G-rich Repeated Element in Mammalian Cells. ○
- 69 STAT5b is a key effector of NRG -1/ ERBB4 -mediated myocardial growth. ○
- 68 Cellular differentiation into hyphae and spores in halophilic archaea. **2023**, 14, ○
- 67 Skeletal muscle gene expression dysregulation in long-term spaceflights and aging is clock-dependent. **2023**, 9, ○
- 66 Cell-of-origin-specific proteomics of extracellular vesicles. **2023**, 2, ○
- 65 A high-throughput approach reveals distinct peptide charging behaviors in electrospray ionization mass spectrometry. ○
- 64 Quantitative proteomic analysis reveals apoE4-dependent phosphorylation of the actin-regulating protein VASP. **2023**, 100541 ○
- 63 Identification of levoglucosan degradation pathways in bacteria and sequence similarity network analysis. **2023**, 205, ○
- 62 Metataxonomic analysis and host proteome response in dairy cows with high and low somatic cell count: a quarter level investigation. **2023**, 54, ○
- 61 Integration of homeostatic and adaptive oxidative responses by a putative co-chaperone, Wos2, drives fungal virulence in cryptococcosis. ○
- 60 Shotgun Proteomics of Co-Cultured Leukemic and Bone Marrow Stromal Cells from Different Species as a Preliminary Approach to Detect Intercellular Protein Transfer. **2023**, 11, 15 ○
- 59 Proximity-Dependent Biotinylation and Identification of Flagellar Proteins in *Trypanosoma cruzi*. ○
- 58 Tracking chromatin state changes using nanoscale photo-proximity labelling. **2023**, 616, 574-580 ○
- 57 A lysosome membrane regeneration pathway depends on TBC1D15 and autophagic lysosomal reformation proteins. ○

- 56 Proteomic analysis of plasma to identify novel biomarkers for intra-amniotic infection and/or inflammation in preterm premature rupture of membranes. **2023**, 13, ○
- 55 Experimental characterization of de novo proteins and their unevolved random-sequence counterparts. **2023**, 7, 570-580 ○
- 54 Phosphorylation barcodes direct biased chemokine signaling at CXCR3. **2023**, 30, 362-382.e8 ○
- 53 PRC2.1- and PRC2.2-specific accessory proteins drive recruitment of different forms of canonical PRC1. **2023**, ○
- 52 Comprehensive proteomic analysis of autophagosomes derived from Leishmania-infected macrophages. **2023**, 18, e0284026 ○
- 51 Resolving the temporal splenic proteome during fungal infection for discovery of putative dual perspective biomarker signatures. ○
- 50 Evaluating proteomics imputation methods with improved criteria. ○
- 49 Archaeal self-activating GPN-loop GTPases involve a lock-switch-rock mechanism for GTP hydrolysis. ○
- 48 DT-109 ameliorates nonalcoholic steatohepatitis in nonhuman primates. **2023**, ○
- 47 Expression of a Siglec-Fc Protein and Its Characterization. **2023**, 12, 574 ○
- 46 Dissecting the Brain with Spatially Resolved Multi-Omics. **2023**, ○
- 45 Anaerobic thiosulfate oxidation by the Roseobacter group is prevalent in marine biofilms. **2023**, 14, ○
- 44 FXR1 regulates vascular smooth muscle cell cytoskeleton, VSMC contractility, and blood pressure by multiple mechanisms. **2023**, 42, 112381 ○
- 43 Cell division protein FtsK coordinates bacterial chromosome segregation and daughter cell separation in Staphylococcus aureus. ○
- 42 Proteomics reveals specific biological changes induced by the normothermic machine perfusion of donor kidneys with a significant up-regulation of Latexin. **2023**, 13, ○
- 41 Analyzing Iron and Oxygen-Regulated Protein Complex Formation Using Proteomic Mass Spectrometry. **2023**, 155-166 ○
- 40 A bacterial autotransporter impairs innate immune responses by targeting the transcription factor TFE3. **2023**, 14, ○
- 39 Interactome dynamics of RAF1-BRAF kinase monomers and dimers. **2023**, 10, ○

- 38 Interaction between poly-A binding protein PABPC4 and nuclear receptor corepressor NCoR1 modulates a metabolic stress response.. **2023**, 104702 ○
- 37 The RNA-binding protein landscapes differ between mammalian organs and cultured cells. **2023**, 14, ○
- 36 Astrocyte-neuron subproteomes and obsessive-compulsive disorder mechanisms. ○
- 35 Extracellular vesicles of the probiotic E. coli O83 activate innate immunity and prevent allergy in mice. ○
- 34 Immobility-associated thromboprotection is conserved across mammalian species from bear to human. **2023**, 380, 178-187 1
- 33 Histone 4 lysine 5/12 acetylation enables developmental plasticity of *Pristionchus* mouth form. **2023**, 14, ○
- 32 RNA cytosine methyltransferase NSUN5 promotes protein synthesis and tumorigenic phenotypes in glioblastoma. ○
- 31 Arg-tRNA synthetase links inflammatory metabolism to RNA splicing and nuclear trafficking via SRRM2. **2023**, 25, 592-603 ○
- 30 Specific pupylation as IDENTITY reporter (SPIDER) for the identification of protein-biomolecule interactions. ○
- 29 Complementary gene regulation by NRF1 and NRF2 protects against hepatic cholesterol overload. **2023**, 42, 112399 ○
- 28 Analysis of Nipah Virus Replication and Host Proteome Response Patterns in Differentiated Porcine Airway Epithelial Cells Cultured at the Air-Liquid Interface. **2023**, 15, 961 ○
- 27 Secretome Screening of BRAFV600E-Mutated Colon Cancer Cells Resistant to Vemurafenib. **2023**, 12, 608 ○
- 26 Neither random nor censored: estimating intensity-dependent probabilities for missing values in label-free proteomics. ○
- 25 Impact of inflammatory preconditioning on murine microglial proteome response induced by focal ischemic brain injury. ○
- 24 An algal-bacterial symbiotic system of carbon fixation using formate as a carbon source. **2023**, 103103 ○
- 23 PaxDB 5.0: curated protein quantification data suggests adaptive proteome changes. ○
- 22 Dosage sensitivity to Pumilio1 variants in the mouse brain reflects distinct molecular mechanisms. ○
- 21 Time-dependent regulation of cytokine production by RNA binding proteins defines T cell effector function. **2023**, 42, 112419 ○

- 20 Spatial and temporal dynamics of ATP synthase from mitochondria toward the cell surface. **2023**, 6, ○
- 19 Trypanosoma cruzi VDU deubiquitinase mediates surface protein trafficking and infectivity. ○
- 18 PepQuery2 democratizes public MS proteomics data for rapid peptide searching. **2023**, 14, ○
- 17 Orb weaver aggregate glue protein composition as a mechanism for rapid evolution of material properties. 11, ○
- 16 Proteomics analyses of herbicide-tolerant genetically modified, conventionally, and organically farmed soybean seeds. **2023**, 109795 ○
- 15 Proteomic Investigation of Neural Stem Cell to Oligodendrocyte Precursor Cell Differentiation Reveals Phosphorylation-Dependent Dclk1 Processing. ○
- 14 Yolk-deprived Caenorhabditis elegans secure brood size at the expense of competitive fitness. **2023**, 6, e202201675 ○
- 13 Identification of d-arabinan-degrading enzymes in mycobacteria. **2023**, 14, ○
- 12 DeepFLR facilitates false localization rate control in phosphoproteomics. **2023**, 14, ○
- 11 Blue Native PAGE Antibody Shift in Conjunction with Mass Spectrometry to Reveal Protein Subcomplexes: Detection of a Cerebellar  $\alpha/\beta$ -Subunits Containing  $\beta$ -Aminobutyric Acid Type A Receptor Subtype. **2023**, 24, 7632 ○
- 10 Thigh muscle metabolic response is linked to feed efficiency and meat characteristics in slow-growing chicken. **2023**, 102741 ○
- 9 A potential histone-chaperone activity for the MIER1 histone deacetylase complex. ○
- 8 MslImpute: Estimation of missing peptide intensity data in label-free quantitative mass spectrometry. **2023**, 100558 ○
- 7 Bacterial catabolism of membrane phospholipids links marine biogeochemical cycles. **2023**, 9, ○
- 6 Deficiency of the mitochondrial ribosomal subunit, MRPL50, causes autosomal recessive syndromic premature ovarian insufficiency. ○
- 5 Integrated multi-omics analysis reveals unique signatures of paclitaxel-loaded poly(lactide-co-glycolide) nanoparticles treatment of head and neck cancer cells. ○
- 4 A ParDE toxin-antitoxin system is responsible for the maintenance of the Yersinia virulence plasmid but not for type III secretion-associated growth inhibition. 13, ○
- 3 Cell-selective proteomics segregates pancreatic cancer subtypes by extracellular proteins in tumors and circulation. **2023**, 14, ○

- 2 Integrative analysis of cancer dependency data and comprehensive phosphoproteomics data revealed the EPHA2-PARD3 axis as a cancer vulnerability in KRAS-mutant colorectal cancer. ○
- 1 Integration of Metabolomic and Proteomic Data to Uncover Actionable Metabolic Pathways. **2023**, 137-148 ○