

CITATION REPORT

List of articles citing

A statistical model for identifying proteins by tandem mass spectrometry

DOI: 10.1021/ac0341261

Analytical Chemistry, 2003, 75, 4646-58.

Source: <https://exaly.com/paper-pdf/35598657/citation-report.pdf>

Version: 2024-04-28

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

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

#	Paper	IF	Citations
2251	Practical and Efficient Searching in Proteomics: A Cross Engine Comparison. 2013 , 4,		13
2250	Decreased Gap Width in a Cylindrical High-Field Asymmetric Waveform Ion Mobility Spectrometry Device Improves Protein Discovery.		
2249	Kinetic Trapping of Folded Proteins Relative to Aggregates under Physiologically Relevant Conditions.		
2248	.		
2247	YTHDF2 Recognition of N1Methyladenosine (m1A)-Modified RNA Is Associated with Transcript Destabilization.		
2246	RNA Chemical Proteomics Reveals the N6Methyladenosine (m6A)-Regulated ProteinRNA Interactome.		
2245	Label-Free Neuroproteomics of the Hippocampal-Accumbal Circuit Reveals Deficits in Neurotransmitter and Neuropeptide Signaling in Mice Lacking Ethanol-Sensitive Adenosine Transporter.		
2244	Profiling Esterases in Mycobacterium tuberculosis Using Far-Red Fluorogenic Substrates.		
2243	Small-Molecule Probes Reveal Esterases with Persistent Activity in Dormant and Reactivating Mycobacterium tuberculosis.		
2242	Nucleation and Propagation of Heterochromatin by the Histone Methyltransferase PRC2: Geometric Constraints and Impact of the Regulatory Subunit JARID2.		
2241	.		
2240	A Rapid and Versatile Method for Generating Proteins with Defined Ubiquitin Chains.		
2239	A mass spectrometric journey into protein and proteome research. 2003 , 14, 685-95		91
2238	Automated statistical analysis of protein abundance ratios from data generated by stable-isotope dilution and tandem mass spectrometry. <i>Analytical Chemistry</i> , 2003 , 75, 6648-57	7.8	316
2237	Proteomic analysis of an extreme halophilic archaeon, Halobacterium sp. NRC-1. 2003 , 2, 506-24		50
2236	The application of new software tools to quantitative protein profiling via isotope-coded affinity tag (ICAT) and tandem mass spectrometry: II. Evaluation of tandem mass spectrometry methodologies for large-scale protein analysis, and the application of statistical tools for data analysis and interpretation. 2003 , 2, 123-42		83
2235	The application of new software tools to quantitative protein profiling via isotope-coded affinity tag (ICAT) and tandem mass spectrometry: I. Statistically annotated datasets for peptide sequences and proteins identified via the application of ICAT and tandem mass spectrometry to proteins copurifying with T cell lipid rafts. 2003 , 2, 125-7		45

2234 Challenges in the Overall Analysis of Microbial Proteomes. **2004**, 2, 79-86

2233 New approaches towards integrated proteomic databases and depositories. **2004**, 1, 267-74

7

2232 Proteomic informatics. **2004**, 61, 127-57

10

2231 Standard mixtures for proteome studies. **2004**, 8, 79-92

43

2230 Spectral quality assessment for high-throughput tandem mass spectrometry proteomics. **2004**, 8, 255-65

42

2229 Quantitative proteomic identification of six4 as the trex-binding factor in the muscle creatine kinase enhancer. **2004**, 24, 2132-43

68

2228 Quantitative proteomic analysis of metabolic regulation by copper ions in *Methylococcus capsulatus* (Bath). **2004**, 279, 51554-60

71

2227 Standardization and denoising algorithms for mass spectra to classify whole-organism bacterial specimens. **2004**, 20, 3128-36

64

2226 Improved peptide identification in proteomics by two consecutive stages of mass spectrometric fragmentation. **2004**, 101, 13417-22

288

2225 Experimental Peptide Identification Repository (EPIR): an integrated peptide-centric platform for validation and mining of tandem mass spectrometry data. **2004**, 3, 1023-38

37

2224 AMASS: software for automatically validating the quality of MS/MS spectrum from SEQUEST results. **2004**, 3, 1194-9

29

2223 A dataset of human liver proteins identified by protein profiling via isotope-coded affinity tag (ICAT) and tandem mass spectrometry. **2004**, 3, 1039-41

49

2222 Two-dimensional Blue native/SDS gel electrophoresis of multi-protein complexes from whole cellular lysates: a proteomics approach. **2004**, 3, 176-82

145

2221 The need for guidelines in publication of peptide and protein identification data: Working Group on Publication Guidelines for Peptide and Protein Identification Data. **2004**, 3, 531-3

408

2220 Protein identification by mass spectrometry: issues to be considered. **2004**, 3, 1-9

162

2219 Quantitative proteomic analysis of proteins released by neoplastic prostate epithelium. **2004**, 64, 347-55

108

2218 LIP index for peptide classification using MS/MS and SEQUEST search via logistic regression. **2004**, 8, 357-69

29

2217 Principles and applications of multidimensional protein identification technology. **2004**, 1, 275-82

28

2216	In Silico Metabolic Model and Protein Expression of Haemophilus influenzae Strain Rd KW20 in Rich Medium. 2004 , 8, 25-41		35
2215	A common open representation of mass spectrometry data and its application to proteomics research. 2004 , 22, 1459-66		632
2214	The ABC's (and XYZ's) of peptide sequencing. 2004 , 5, 699-711		829
2213	Dynamic changes in transcription factor complexes during erythroid differentiation revealed by quantitative proteomics. 2004 , 11, 73-80		188
2212	Proteomics in pathology research. 2004 , 84, 1227-44		55
2211	Analysis, statistical validation and dissemination of large-scale proteomics datasets generated by tandem MS. 2004 , 9, 173-81		155
2210	Identification and functional analysis of 'hypothetical' genes expressed in Haemophilus influenzae. 2004 , 32, 2353-61		64
2209	Strategies for automating top-down protein analysis with Q-FTICR MS. 2004 , 234, 175-184		19
2208	High-performance peptide identification by tandem mass spectrometry allows reliable automatic data processing in proteomics. 2004 , 4, 1977-84		64
2207	Database-independent, database-dependent, and extended interpretation of peptide mass spectra in VEMS V2.0. 2004 , 4, 2583-93		56
2206	In vitro and in silico processes to identify differentially expressed proteins. 2004 , 4, 2333-51		56
2205	A case study of de novo sequence analysis of N-sulfonated peptides by MALDI TOF/TOF mass spectrometry. 2004 , 15, 1838-52		45
2204	Untangling multi-gene families in plants by integrating proteomics into functional genomics. 2004 , 65, 1517-30		30
2203	Proteomics/genomics and signaling in lymphocytes. 2004 , 16, 337-44		11
2202	.		
2201	Increased identification of peptides by enhanced data processing of high-resolution MALDI TOF/TOF mass spectra prior to database searching. <i>Analytical Chemistry</i> , 2004 , 76, 6017-28	7.8	51
2200	High-throughput identification of proteins and unanticipated sequence modifications using a mass-based alignment algorithm for MS/MS de novo sequencing results. <i>Analytical Chemistry</i> , 2004 , 76, 2220-30	7.8	120
2199	DBParser: web-based software for shotgun proteomic data analyses. 2004 , 3, 1002-8		89

2198	Trypsin cleaves exclusively C-terminal to arginine and lysine residues. 2004 , 3, 608-14		804
2197	Application of peptide LC retention time information in a discriminant function for peptide identification by tandem mass spectrometry. 2004 , 3, 760-9		127
2196	Untangling multi-gene families in plants by integrating proteomics into functional genomics. 2004 , 65, 1517-1517		
2195	Bioinformatics in mass spectrometry data analysis for proteomics studies. 2004 , 1, 469-83		19
2194	Statistical models for protein validation using tandem mass spectral data and protein amino acid sequence databases. <i>Analytical Chemistry</i> , 2004 , 76, 1664-71	7.8	122
2193	Shotgun protein sequencing by tandem mass spectra assembly. <i>Analytical Chemistry</i> , 2004 , 76, 7221-33	7.8	44
2192	Proteomics. 2004 , 5, 267-93		159
2191	Towards a systems biology understanding of human health: interplay between genotype, environment and nutrition. 2004 , 10, 51-84		37
2190	Integration with the human genome of peptide sequences obtained by high-throughput mass spectrometry. 2005 , 6, R9		233
2189	System-based proteomic analysis of the interferon response in human liver cells. 2004 , 5, R54		55
2188	Systems biology, proteomics, and the future of health care: toward predictive, preventative, and personalized medicine. 2004 , 3, 179-96		587
2187	Analysis of large-scale MS data sets: the dramas and the delights. 2004 , 3, 43-49		0
2186	Mass spectrometry has married statistics: uncle is functionality, children are selectivity and sensitivity. 2004 , 3, 50-55		1
2185	Using proteomics and network analysis to elucidate the consequences of synaptic protein oxidation in a PS1 + AbetaPP mouse model of Alzheimer's disease. 2005 , 8, 227-41		23
2184	Poly(ADP-ribose) glycohydrolase is a component of the FMRP-associated messenger ribonucleoparticles. 2005 , 392, 499-509		18
2183	Protein identification using TurboSEQUENT. 2005 , Chapter 13, Unit 13.3		17
2182	LC-MS solvent composition monitoring and chromatography alignment using mobile phase tracer molecules. 2005 , 829, 107-14		6
2181	LC tandem MS in proteome characterization. 2005 , 24, 566-575		7

2180	Comparison of different search engines using validated MS/MS test datasets. 2005 , 534, 11-20	35
2179	Immunoaffinity profiling of tyrosine phosphorylation in cancer cells. 2005 , 23, 94-101	1056
2178	Identification of post-translational modifications by blind search of mass spectra. 2005 , 23, 1562-7	231
2177	Quantitative phosphoproteome analysis using a dendrimer conjugation chemistry and tandem mass spectrometry. 2005 , 2, 591-8	279
2176	Comparative evaluation of mass spectrometry platforms used in large-scale proteomics investigations. 2005 , 2, 667-75	612
2175	Identification of proteins from formalin-fixed paraffin-embedded cells by LC-MS/MS. 2005 , 85, 1405-15	130
2174	Analysing proteomic data. 2005 , 35, 543-53	61
2173	The continuing evolution of shotgun proteomics. 2005 , 10, 719-25	67
2172	Proteomics in developmental toxicology. 2005 , 19, 291-304	14
2171	CHASE, a charge-assisted sequencing algorithm for automated homology-based protein identifications with matrix-assisted laser desorption/ionization time-of-flight post-source decay fragmentation data. 2005 , 40, 475-88	5
2170	Mass spectrometry-based proteomics in the life sciences. 2005 , 62, 848-69	85
2169	Proteome profiling of human epithelial ovarian cancer cell line TOV-112D. 2005 , 275, 25-55	30
2168	Increased quantitative proteome coverage with (13)C/(12)C-based, acid-cleavable isotope-coded affinity tag reagent and modified data acquisition scheme. 2005 , 5, 380-7	105
2167	Large-scale evaluation of quantitative reproducibility and proteome coverage using acid cleavable isotope coded affinity tag mass spectrometry for proteomic profiling. 2005 , 5, 1204-8	51
2166	Analysis of phosphatase and tensin homolog tumor suppressor interacting proteins by in vitro and in silico proteomics. 2005 , 5, 1250-62	27
2165	A comparative evaluation of software for the analysis of liquid chromatography-tandem mass spectrometry data from isotope coded affinity tag experiments. 2005 , 5, 2748-60	24
2164	Proteomic analysis of synaptosomes using isotope-coded affinity tags and mass spectrometry. 2005 , 5, 2531-41	100
2163	Utility of electrophoretically derived protein mass estimates as additional constraints in proteome analysis of human serum based on MS/MS analysis. 2005 , 5, 3376-85	28

2162	Characterization of the human blood plasma proteome. 2005 , 5, 4034-45	164
2161	ProbiDtree: an automated software program capable of identifying multiple peptides from a single collision-induced dissociation spectrum collected by a tandem mass spectrometer. 2005 , 5, 4096-106	65
2160	A proteomic study of the HUPO Plasma Proteome Project's pilot samples using an accurate mass and time tag strategy. 2005 , 5, 3454-66	55
2159	Characterization of microsomal fraction proteome in human lymphoblasts reveals the down-regulation of galectin-1 by interleukin-12. 2005 , 5, 4719-32	14
2158	Protein and peptide identification algorithms using MS for use in high-throughput, automated pipelines. 2005 , 5, 4082-95	50
2157	An evaluation, comparison, and accurate benchmarking of several publicly available MS/MS search algorithms: sensitivity and specificity analysis. 2005 , 5, 3475-90	309
2156	Data management and preliminary data analysis in the pilot phase of the HUPO Plasma Proteome Project. 2005 , 5, 3246-61	51
2155	Overview of the HUPO Plasma Proteome Project: results from the pilot phase with 35 collaborating laboratories and multiple analytical groups, generating a core dataset of 3020 proteins and a publicly-available database. 2005 , 5, 3226-45	672
2154	Average peptide score: a useful parameter for identification of proteins derived from database searches of liquid chromatography/tandem mass spectrometry data. 2005 , 19, 9-14	16
2153	Confident protein identification using the average peptide score method coupled with search-specific, ab initio thresholds. 2005 , 19, 3363-8	23
2152	Tandem mass spectrometry database searching. 2005 ,	
2151	Mass spectrometric data mining for protein sequences. 2005 ,	
2150	Peptide Sequence Tags for Fast Database Search in Mass-Spectrometry. 2005 , 326-341	3
2149	A systematic characterization of mitochondrial proteome from human T leukemia cells. 2005 , 4, 169-81	98
2148	Comprehensive analysis of a multidimensional liquid chromatography mass spectrometry dataset acquired on a quadrupole selecting, quadrupole collision cell, time-of-flight mass spectrometer: II. New developments in Protein Prospector allow for reliable and comprehensive automatic analysis of large datasets. 2005 , 4, 1194-204	145
2147	A Heuristic method for assigning a false-discovery rate for protein identifications from Mascot database search results. 2005 , 4, 762-72	162
2146	Proteomic profiling of pancreatic cancer for biomarker discovery. 2005 , 4, 523-33	113
2145	A software suite for the generation and comparison of peptide arrays from sets of data collected by liquid chromatography-mass spectrometry. 2005 , 4, 1328-40	147

2144	Interpretation of shotgun proteomic data: the protein inference problem. 2005 , 4, 1419-40	756
2143	Complex proteome prefractionation using microscale solution isoelectrofocusing. 2005 , 2, 295-306	20
2142	Research in Computational Molecular Biology. 2005 ,	2
2141	New insights into viral structure and virus-cell interactions through proteomics. 2005 , 2, 577-88	13
2140	Proteomics: A new research area for the biomedical field. 2005 , 1, 83-94	4
2139	Bioinformatic methods to exploit mass spectrometric data for proteomic applications. 2005 , 402, 289-312	40
2138	Proteome analysis of liver cells expressing a full-length hepatitis C virus (HCV) replicon and biopsy specimens of posttransplantation liver from HCV-infected patients. 2005 , 79, 7558-69	74
2137	Elimination of redundant protein identifications in high throughput proteomics. 2005 , 2005, 4803-6	8
2136	Quantitative proteome analysis of human plasma following in vivo lipopolysaccharide administration using ¹⁶ O/ ¹⁸ O labeling and the accurate mass and time tag approach. 2005 , 4, 700-9	144
2135	A novel, evolutionarily conserved protein phosphatase complex involved in cisplatin sensitivity. 2005 , 4, 1725-40	148
2134	A uniform proteomics MS/MS analysis platform utilizing open XML file formats. 2005 , 1, 2005.0017	574
2133	Improving protein identification using complementary fragmentation techniques in fourier transform mass spectrometry. 2005 , 4, 835-45	123
2132	Robust accurate identification of peptides (RAId): deciphering MS2 data using a structured library search with de novo based statistics. 2005 , 21, 3726-32	20
2131	Analysis of BCL6-interacting proteins by tandem mass spectrometry. 2005 , 4, 1898-909	39
2130	Probability-based evaluation of peptide and protein identifications from tandem mass spectrometry and SEQUEST analysis: the human proteome. 2005 , 4, 53-62	293
2129	ICAT-MS-MS time course analysis of atrophying mouse skeletal muscle cytosolic subproteome. 2005 , 1, 229-41	17
2128	Development and evaluation of a micro- and nanoscale proteomic sample preparation method. 2005 , 4, 2397-403	141
2127	Randomized sequence databases for tandem mass spectrometry peptide and protein identification. 2005 , 9, 364-79	75

2126	Human plasma N-glycoproteome analysis by immunoaffinity subtraction, hydrazide chemistry, and mass spectrometry. 2005 , 4, 2070-80		365
2125	Improving mass and liquid chromatography based identification of proteins using bayesian scoring. 2005 , 4, 2174-84		14
2124	Proteomic identification of potential susceptibility factors in drug-induced liver disease. 2005 , 18, 924-33		67
2123	Proteomics strategies for protein identification. 2005 , 579, 885-9		73
2122	Informatics for protein identification by mass spectrometry. 2005 , 35, 223-36		84
2121	Identification of post-translational modifications via blind search of mass-spectra. 2005 , 157-66		13
2120	Pancreatic cancer proteome: the proteins that underlie invasion, metastasis, and immunologic escape. 2005 , 129, 1187-97		160
2119	Chapter 1 Emerging technologies the way forward on improving protein analysis. 2005 , 1-67		1
2118	Chapter 9 Mass spectrometry for protein identification. 2005 , 46, 429-447		
2117	Chapter 12 Bioinformatics standards and tools in proteomics. 2005 , 46, 501-521		
2116	Analysis of shotgun proteomics and RNA profiling data from Arabidopsis thaliana chloroplasts. 2005 , 4, 637-40		39
2115	Peptide sequence tags for fast database search in mass-spectrometry. 2005 , 4, 1287-95		103
2114	InsPecT: identification of posttranslationally modified peptides from tandem mass spectra. <i>Analytical Chemistry</i> , 2005 , 77, 4626-39	7.8	502
2113	Investigation of neutral loss during collision-induced dissociation of peptide ions. <i>Analytical Chemistry</i> , 2005 , 77, 4870-82	7.8	44
2112	VEMS 3.0: algorithms and computational tools for tandem mass spectrometry based identification of post-translational modifications in proteins. 2005 , 4, 2338-47		119
2111	Proteomics and the analysis of proteomic data: an overview of current protein-profiling technologies. 2005 , Chapter 13, Unit 13.1		23
2110	The Trypanosoma cruzi proteome. 2005 , 309, 473-6		322
2109	Integrated approach for manual evaluation of peptides identified by searching protein sequence databases with tandem mass spectra. 2005 , 4, 998-1005		156

2108	Multidimensional protein identification technology: current status and future prospects. 2005 , 2, 27-39	32
2107	Discovery of biomarker candidates within disease by protein profiling: principles and concepts. 2005 , 4, 1200-12	59
2106	Analysis of the <i>Saccharomyces cerevisiae</i> proteome with PeptideAtlas. 2006 , 7, R106	51
2105	Status of complete proteome analysis by mass spectrometry: SILAC labeled yeast as a model system. 2006 , 7, R50	224
2104	Plant Proteomics. 2006 ,	2
2103	Mass Spectrometry Data Analysis in Proteomics. 2006 ,	2
2102	Characterization of proteome of human cerebrospinal fluid. 2006 , 73, 29-98	27
2101	Analytical characteristics of cleavable isotope-coded affinity tag-LC-tandem mass spectrometry for quantitative proteomic studies. 2006 , 8, 513-20	19
2100	Characterization of the mouse brain proteome using global proteomic analysis complemented with cysteinyl-peptide enrichment. 2006 , 5, 361-9	122
2099	Quantification of membrane and membrane-bound proteins in normal and malignant breast cancer cells isolated from the same patient with primary breast carcinoma. 2006 , 5, 2632-41	57
2098	Experimental standards for high-throughput proteomics. 2006 , 10, 152-7	20
2097	Genome annotating proteomics pipelines: available tools. 2006 , 3, 621-9	4
2096	Alternative workflows for plant proteomic analysis. 2006 , 2, 621-6	21
2095	Mining the acute respiratory distress syndrome proteome: identification of the insulin-like growth factor (IGF)/IGF-binding protein-3 pathway in acute lung injury. 2006 , 169, 86-95	606
2094	Identification of glycoproteins in human cerebrospinal fluid with a complementary proteomic approach. 2006 , 5, 2769-79	85
2093	Evaluation of multiprotein immunoaffinity subtraction for plasma proteomics and candidate biomarker discovery using mass spectrometry. 2006 , 5, 2167-74	188
2092	Lumbar cerebrospinal fluid proteome in multiple sclerosis: characterization by ultrafiltration, liquid chromatography, and mass spectrometry. 2006 , 5, 1647-57	67
2091	Optimized peptide separation and identification for mass spectrometry based proteomics via free-flow electrophoresis. 2006 , 5, 2241-9	78

2090	Rapid validation of protein identifications with the borderline statistical confidence via de novo sequencing and MS BLAST searches. 2006 , 5, 2448-56		37
2089	Endogenously nitrated proteins in mouse brain: links to neurodegenerative disease. 2006 , 45, 8009-22		127
2088	Quantitative proteomic and genomic profiling reveals metastasis-related protein expression patterns in gastric cancer cells. 2006 , 5, 2727-42		68
2087	Identification of proteins from non-model organisms using mass spectrometry: application to a hibernating mammal. 2006 , 5, 829-39		29
2086	Characterization of the human pancreatic islet proteome by two-dimensional LC/MS/MS. 2006 , 5, 3345-54		54
2085	Quality control metrics for LC-MS feature detection tools demonstrated on <i>Saccharomyces cerevisiae</i> proteomic profiles. 2006 , 5, 1527-34		27
2084	New algorithm for 15N/14N quantitation with LC-ESI-MS using an LTQ-FT mass spectrometer. 2006 , 5, 2039-45		30
2083	Sequence-specific retention calculator. Algorithm for peptide retention prediction in ion-pair RP-HPLC: application to 300- and 100-A pore size C18 sorbents. <i>Analytical Chemistry</i> , 2006 , 78, 7785-95	7.8	177
2082	Proteins associated with Cisplatin resistance in ovarian cancer cells identified by quantitative proteomic technology and integrated with mRNA expression levels. 2006 , 5, 433-43		109
2081	Quantitative analysis of acrylamide labeled serum proteins by LC-MS/MS. 2006 , 5, 2009-18		106
2080	Multi-Q: a fully automated tool for multiplexed protein quantitation. 2006 , 5, 2328-38		98
2079	Analysis of complex protein mixtures with improved sequence coverage using (CE-MS/MS) _n . <i>Analytical Chemistry</i> , 2006 , 78, 7309-16	7.8	41
2078	PepHMM: a hidden Markov model based scoring function for mass spectrometry database search. <i>Analytical Chemistry</i> , 2006 , 78, 432-7	7.8	45
2077	Determination and comparison of the baseline proteomes of the versatile microbe <i>Rhodospseudomonas palustris</i> under its major metabolic states. 2006 , 5, 287-98		64
2076	Protein identification and expression analysis using mass spectrometry. 2006 , 14, 229-35		31
2075	Bioinformatics Tools for Proteomics. 2006 , 289-307		
2074	An evaluation, comparison, and accurate benchmarking of several publicly available MS/MS search algorithms: Sensitivity and specificity analysis. 2006 , 289-315		
2073	Overview of the HUPO Plasma Proteome Project: Results from the pilot phase with 35 collaborating laboratories and multiple analytical groups, generating a core dataset of 3020 proteins and a publicly-available database. 2006 , 1-35		3

2072	. 2006,	8
2071	. 2006,	6
2070	Validation of tandem mass spectrometry database search results using DTASelect. 2007 , Chapter 13, Unit 13.4	153
2069	Peptide Identification via Tandem Mass Spectrometry. 2006 , 253-278	1
2068	Proteomic biomarker discovery in cerebrospinal fluid for neurodegenerative diseases. 2005 , 8, 377-86	47
2067	RT-PSM, a real-time program for peptide-spectrum matching with statistical significance. 2006 , 20, 1199-208	16
2066	Human plasma proteome analysis by reversed sequence database search and molecular weight correlation based on a bacterial proteome analysis. 2006 , 6, 1121-32	23
2065	Identification of proteins released by follicular lymphoma-derived cells using a mass spectrometry-based approach. 2006 , 6, 3223-30	10
2064	Quantitative proteome analysis of breast cancer cell lines using 18O-labeling and an accurate mass and time tag strategy. 2006 , 6, 2903-15	33
2063	Shotgun identification of proteins from uredospores of the bean rust <i>Uromyces appendiculatus</i> . 2006 , 6, 2477-84	43
2062	Quantitative proteomic profiling of pancreatic cancer juice. 2006 , 6, 3871-9	105
2061	Guidelines for the next 10 years of proteomics. 2006 , 6, 4-8	297
2060	Protein probabilities in shotgun proteomics: evaluating different estimation methods using a semi-random sampling model. 2006 , 6, 6134-45	13
2059	Gel-free analysis of the human brain proteome: application of liquid chromatography and mass spectrometry on biopsy and autopsy samples. 2006 , 6, 4967-77	17
2058	Human body fluid proteome analysis. 2006 , 6, 6326-53	424
2057	Challenges in deriving high-confidence protein identifications from data gathered by a HUPO plasma proteome collaborative study. 2006 , 24, 333-8	288
2056	Quantitative proteomic analysis of B cell lipid rafts reveals that ezrin regulates antigen receptor-mediated lipid raft dynamics. 2006 , 7, 625-33	159
2055	Automated identification of SUMOylation sites using mass spectrometry and SUMmOn pattern recognition software. 2006 , 3, 533-9	106

2054	Quantitative proteome analysis using isotope-coded affinity tags and mass spectrometry. 2006 , 1, 139-45	158
2053	Quantitative proteomics and its applications for systems biology. 2006 , 71, 1060-72	7
2052	Organellar proteomics: turning inventories into insights. 2006 , 7, 874-9	175
2051	A biological approach to computational models of proteomic networks. 2006 , 10, 73-80	100
2050	Protein profiling of sickle cell versus control RBC core membrane skeletons by ICAT technology and tandem mass spectrometry. 2006 , 11, 326-37	17
2049	Protein identification by tandem mass spectrometry and sequence database searching. 2007 , 367, 87-119	129
2048	Developments in mass spectrometry for the analysis of complex protein mixtures. 2006 , 5, 98-111	12
2047	Informatics solutions for high-throughput proteomics. 2006 , 11, 509-16	9
2046	2DDB - a bioinformatics solution for analysis of quantitative proteomics data. 2006 , 7, 158	20
2045	Proteomic analysis of microglial contribution to mouse strain-dependent dopaminergic neurotoxicity. 2006 , 53, 567-82	55
2044	HepatoProteomics: applying proteomic technologies to the study of liver function and disease. 2006 , 44, 299-308	46
2043	Automated protein identification by tandem mass spectrometry: issues and strategies. 2006 , 25, 235-54	125
2042	MudPIT (Multidimensional Protein Identification Technology) for Identification of Post-Translational Protein Modifications in Complex Biological Mixtures. 2006 , 233-252	1
2041	The PeptideAtlas project. 2006 , 34, D655-8	590
2040	Two-dimensional nanoflow liquid chromatography-tandem mass spectrometry of proteins extracted from rice leaves and roots. 2007 , 355, 249-66	4
2039	An unconventional pathway for reduction of CO ₂ to methane in CO-grown Methanosarcina acetivorans revealed by proteomics. 2006 , 103, 17921-6	101
2038	A fast coarse filtering method for peptide identification by mass spectrometry. 2006 , 22, 1524-31	29
2037	Arabidopsis thaliana proteomics: from proteome to genome. 2006 , 57, 1485-91	43

2036	Proteome analysis of bell pepper (<i>Capsicum annuum</i> L.) chromoplasts. 2006 , 47, 1663-73	86
2035	Advances and challenges in liquid chromatography-mass spectrometry-based proteomics profiling for clinical applications. 2006 , 5, 1727-44	281
2034	Label-free semiquantitative peptide feature profiling of human breast cancer and breast disease sera via two-dimensional liquid chromatography-mass spectrometry. 2006 , 5, 1095-104	32
2033	Challenges and opportunities in proteomics data analysis. 2006 , 5, 1921-6	93
2032	Integrated molecular signature of disease: analysis of influenza virus-infected macaques through functional genomics and proteomics. 2006 , 80, 10813-28	110
2031	PEPPER, a platform for experimental proteomic pattern recognition. 2006 , 5, 1927-41	119
2030	Proteome analysis of <i>Halobacterium</i> sp. NRC-1 facilitated by the biomodule analysis tool BMSorter. 2006 , 5, 987-97	13
2029	Identification and characterization of SAP25, a novel component of the mSin3 corepressor complex. 2006 , 26, 1386-97	45
2028	Systematic characterization of nuclear proteome during apoptosis: a quantitative proteomic study by differential extraction and stable isotope labeling. 2006 , 5, 1131-45	54
2027	Dynamic spectrum quality assessment and iterative computational analysis of shotgun proteomic data: toward more efficient identification of post-translational modifications, sequence polymorphisms, and novel peptides. 2006 , 5, 652-70	143
2026	High dynamic range characterization of the trauma patient plasma proteome. 2006 , 5, 1899-913	131
2025	Modification of host lipid raft proteome upon hepatitis C virus replication. 2006 , 5, 2319-25	80
2024	The anti-HIV-1 editing enzyme APOBEC3G binds HIV-1 RNA and messenger RNAs that shuttle between polysomes and stress granules. 2006 , 281, 29105-19	147
2023	Biosynthesis of dermatan sulfate: chondroitin-glucuronate C5-epimerase is identical to SART2. 2006 , 281, 11560-8	101
2022	Global organization and function of mammalian cytosolic proteasome pools: Implications for PA28 and 19S regulatory complexes. 2006 , 17, 4962-71	65
2021	Improved classification of mass spectrometry database search results using newer machine learning approaches. 2006 , 5, 497-509	48
2020	Analyzing proteomes and protein function using graphical comparative analysis of tandem mass spectrometry results. 2006 , 5, 1497-513	29
2019	Bioinformatic Standards for Proteomics-Oriented Mass Spectrometry. 2006 , 3, 119-128	7

2018	Alzheimer disease-specific conformation of hyperphosphorylated paired helical filament-Tau is polyubiquitinated through Lys-48, Lys-11, and Lys-6 ubiquitin conjugation. 2006 , 281, 10825-38	201
2017	Distinctive repertoire of contingency genes conferring mutation-based phase variation and combinatorial expression of surface lipoproteins in <i>Mycoplasma capricolum</i> subsp. <i>capricolum</i> of the <i>Mycoplasma mycoides</i> phylogenetic cluster. 2006 , 188, 4926-41	24
2016	The disordered amino-terminus of SIMPL interacts with members of the 70-kDa heat-shock protein family. 2006 , 25, 704-14	9
2015	Quantitative proteomic analysis of myc-induced apoptosis: a direct role for Myc induction of the mitochondrial chloride ion channel, mtCLIC/CLIC4. 2006 , 281, 2750-6	63
2014	Discovery of regulatory molecular events and biomarkers using 2D capillary chromatography and mass spectrometry. 2006 , 3, 63-74	18
2013	Identification of a vacuolar sucrose transporter in barley and <i>Arabidopsis</i> mesophyll cells by a tonoplast proteomic approach. 2006 , 141, 196-207	257
2012	Optimization and use of peptide mass measurement accuracy in shotgun proteomics. 2006 , 5, 1326-37	241
2011	Proteomic Tools for Analysis of Cellular Dynamics. 63-166	
2010	Profiling signaling polarity in chemotactic cells. 2007 , 104, 8328-33	73
2009	Quantitative analysis of human immunodeficiency virus type 1-infected CD4+ cell proteome: dysregulated cell cycle progression and nuclear transport coincide with robust virus production. 2007 , 81, 7571-83	77
2008	Annexin-1 and peptide derivatives are released by apoptotic cells and stimulate phagocytosis of apoptotic neutrophils by macrophages. 2007 , 178, 4595-605	211
2007	MglA regulates <i>Francisella tularensis</i> subsp. <i>novicida</i> (<i>Francisella novicida</i>) response to starvation and oxidative stress. 2007 , 189, 6580-6	50
2006	The transcription elongation factor TFIIIS is a component of RNA polymerase II preinitiation complexes. 2007 , 104, 16068-73	82
2005	EBP, a program for protein identification using multiple tandem mass spectrometry datasets. 2007 , 6, 527-36	45
2004	General transcription factor specified global gene regulation in archaea. 2007 , 104, 4630-5	98
2003	Global survey of human T leukemic cells by integrating proteomics and transcriptomics profiling. 2007 , 6, 1343-53	29
2002	The Multi-Q web server for multiplexed protein quantitation. 2007 , 35, W707-12	13
2001	Intracellular trafficking of a polymorphism in the COOH terminus of the alpha-subunit of the human epithelial sodium channel is modulated by casein kinase 1. 2007 , 293, F868-76	12

2000	Characterization of immunisolated human gastric parietal cells tubulovesicles: identification of regulators of apical recycling. 2007 , 292, G1249-62	52
1999	Challenges and solutions in proteomics. 2007 , 8, 21-8	10
1998	From bytes to bedside: data integration and computational biology for translational cancer research. 2007 , 3, e12	48
1997	A predictive model for identifying proteins by a single peptide match. 2007 , 23, 277-80	50
1996	Current Status of Computational Approaches for Protein Identification Using Tandem Mass Spectra. 2007 , 4, 121-130	7
1995	Quantitative Proteomic Approaches to Investigate the Membrane Proteome in Neuropsychiatric Disorders. 2007 , 4, 131-140	
1994	Identification of putative androgen receptor interaction protein modules: cytoskeleton and endosomes modulate androgen receptor signaling in prostate cancer cells. 2007 , 6, 252-71	46
1993	Mass Spectrometry Data Analysis in the Proteomics Era. 2007 , 2, 63-93	27
1992	Computational methods for the comparative quantification of proteins in label-free LCn-MS experiments. 2008 , 9, 156-65	62
1991	Purification and characterization of cellular proteins associated with histone H4 tails. 2007 , 282, 21024-31	9
1990	Shotgun glycopeptide capture approach coupled with mass spectrometry for comprehensive glycoproteomics. 2007 , 6, 141-9	138
1989	Proteomics evaluation of chemically cleavable activity-based probes. 2007 , 6, 1761-70	72
1988	Proteomics analysis of conditioned media from three breast cancer cell lines: a mine for biomarkers and therapeutic targets. 2007 , 6, 1997-2011	164
1987	Current trends in computational inference from mass spectrometry-based proteomics. 2007 , 8, 304-17	27
1986	Identification of cellular interaction partners of the influenza virus ribonucleoprotein complex and polymerase complex using proteomic-based approaches. 2007 , 6, 672-82	179
1985	Plant Proteomics. 2007 ,	6
1984	The anatomy of microbial cell state transitions in response to oxygen. 2007 , 17, 1399-413	49
1983	High copper selectively alters lipid metabolism and cell cycle machinery in the mouse model of Wilson disease. 2007 , 282, 8343-55	160

1982	Systematic uncovering of multiple pathways underlying the pathology of Huntington disease by an acid-cleavable isotope-coded affinity tag approach. 2007 , 6, 781-97	27
1981	Identification of phosphorylation sites in betaPIX and PAK1. 2007 , 120, 3911-8	22
1980	Protection against beta-amyloid-induced apoptosis by peptides interacting with beta-amyloid. 2007 , 282, 31238-49	34
1979	Comparative proteomics analysis of Barrett metaplasia and esophageal adenocarcinoma using two-dimensional liquid mass mapping. 2007 , 6, 987-99	32
1978	Proteomics analysis of the interactome of N-myc downstream regulated gene 1 and its interactions with the androgen response program in prostate cancer cells. 2007 , 6, 575-88	72
1977	Endogenous phosphotyrosine signaling in zebrafish embryos. 2007 , 6, 2088-99	50
1976	Quantitative proteomics analysis reveals that proteins differentially expressed in chronic pancreatitis are also frequently involved in pancreatic cancer. 2007 , 6, 1331-42	117
1975	Mascot file parsing and quantification (MFPaQ), a new software to parse, validate, and quantify proteomics data generated by ICAT and SILAC mass spectrometric analyses: application to the proteomics study of membrane proteins from primary human endothelial cells. 2007 , 6, 1621-37	72
1974	Spatial mapping of protein abundances in the mouse brain by voxelation integrated with high-throughput liquid chromatography-mass spectrometry. 2007 , 17, 328-36	53
1973	.	
1972	Installation and use of the Computational Proteomics Analysis System (CPAS). 2007 , Chapter 13, Unit 13.5	2
1971	Moderation of the platelet releasate response by aspirin. 2007 , 109, 4786-92	99
1970	A role for the MLL fusion partner ENL in transcriptional elongation and chromatin modification. 2007 , 110, 4445-54	300
1969	Bibliography. 265-275	
1968	Comparison of pancreas juice proteins from cancer versus pancreatitis using quantitative proteomic analysis. 2007 , 34, 70-9	78
1967	Quantitative proteomic and microarray analysis of the archaeon Methanosarcina acetivorans grown with acetate versus methanol. 2007 , 6, 759-71	86
1966	Proteome analysis of chloroplast mRNA processing and degradation. 2007 , 6, 809-20	20
1965	An essential switch in subunit composition of a chromatin remodeling complex during neural development. 2007 , 55, 201-15	541

1964	Human saliva proteome analysis and disease biomarker discovery. 2007 , 4, 531-8		99
1963	Pfnek3 functions as an atypical MAPKK in Plasmodium falciparum. 2007 , 361, 439-44		12
1962	Activator-mediated recruitment of the MLL2 methyltransferase complex to the beta-globin locus. 2007 , 27, 573-84		111
1961	Estimating the statistical significance of peptide identifications from shotgun proteomics experiments. 2007 , 6, 1758-67		60
1960	A novel quantitative proteomics strategy to study phosphorylation-dependent peptide-protein interactions. 2007 , 6, 133-40		38
1959	Multidimensional separations-based shotgun proteomics. 2007 , 107, 3654-86		183
1958	Lookup peaks: a hybrid of de novo sequencing and database search for protein identification by tandem mass spectrometry. <i>Analytical Chemistry</i> , 2007 , 79, 1393-400	7.8	169
1957	Proteomics of Human Body Fluids. 2007 ,		17
1956	Plant Systems Biology. 2007 ,		1
1955	Proteomics for the analysis of environmental stress responses in organisms. 2007 , 41, 6891-900		70
1954	A novel approach to identify proteins modified by nitric oxide: the HIS-TAG switch method. 2007 , 6, 3224-31		79
1953	Proteomics data validation: why all must provide data. 2007 , 3, 518-22		39
1952	Advancing signaling networks through proteomics. 2007 , 4, 573-83		7
1951	Isolation and compositional analysis of trypanosomatid editosomes. 2007 , 424, 3-24		24
1950	Achieving in-depth proteomics profiling by mass spectrometry. 2007 , 2, 39-52		50
1949	Informatics strategies for large-scale novel cross-linking analysis. 2007 , 6, 3412-21		45
1948	Shotgun cross-linking analysis for studying quaternary and tertiary protein structures. 2007 , 6, 3908-17		55
1947	A new algorithm using cross-assignment for label-free quantitation with LC-LTQ-FT MS. 2007 , 6, 2186-94		45

1946	Contribution of protein fractionation to depth of analysis of the serum and plasma proteomes. 2007 , 6, 3558-65		144
1945	Personalized medicine and proteomics: lessons from non-small cell lung cancer. 2007 , 6, 2925-35		51
1944	Probing the membrane interface-interacting proteome using photoactivatable lipid cross-linkers. 2007 , 6, 1951-62		14
1943	Proteomic analysis of rat striatal synaptosomes during acrylamide intoxication at a low dose rate. 2007 , 100, 156-67		59
1942	Comprehensive analysis of proteins secreted by <i>Trichophyton rubrum</i> and <i>Trichophyton violaceum</i> under in vitro conditions. 2007 , 6, 3081-92		43
1941	Probability model for assessing proteins assembled from peptide sequences inferred from tandem mass spectrometry data. <i>Analytical Chemistry</i> , 2007 , 79, 3901-11	7.8	56
1940	YPED: a web-accessible database system for protein expression analysis. 2007 , 6, 4019-24		34
1939	Proteomic parsimony through bipartite graph analysis improves accuracy and transparency. 2007 , 6, 3549-57		266
1938	Use of quantitative mass spectrometry analysis in kidney research. 2007 , 27, 574-83		5
1937	Relative quantification of proteins across the species boundary through the use of shared peptides. 2007 , 6, 97-104		14
1936	MSNovo: a dynamic programming algorithm for de novo peptide sequencing via tandem mass spectrometry. <i>Analytical Chemistry</i> , 2007 , 79, 4870-8	7.8	73
1935	Research in Computational Molecular Biology. 2007 ,		1
1934	Cancer proteomics by quantitative shotgun proteomics. 2007 , 1, 144-59		59
1933	Overview of tandem mass spectrometry (MS/MS) database search algorithms. 2007 , Chapter 25, Unit25.2		41
1932	Identification of proteolytic cleavage sites by quantitative proteomics. 2007 , 6, 2850-8		76
1931	Accurate mass measurements in proteomics. 2007 , 107, 3621-53		92
1930	Sequence-specific retention calculator. A family of peptide retention time prediction algorithms in reversed-phase HPLC: applicability to various chromatographic conditions and columns. <i>Analytical Chemistry</i> , 2007 , 79, 8762-8	7.8	75
1929	. 2007 ,		27

1928	PARP-3 associates with polycomb group bodies and with components of the DNA damage repair machinery. 2007 , 100, 385-401	92
1927	Proteomic profiling of human liver biopsies: hepatitis C virus-induced fibrosis and mitochondrial dysfunction. 2007 , 46, 649-57	101
1926	Comprehensive analysis of proteins of pH fractionated samples using monolithic LC/MS/MS, intact MW measurement and MALDI-QIT-TOF MS. 2007 , 42, 312-34	8
1925	Rapid characterization of covalent modifications to rat brain mitochondrial proteins after ex vivo exposure to 4-hydroxy-2-nonenal by liquid chromatography-tandem mass spectrometry using data-dependent and neutral loss-driven MS3 acquisition. 2007 , 42, 1599-605	30
1924	Global metabolic changes following loss of a feedback loop reveal dynamic steady states of the yeast metabolome. 2007 , 9, 8-20	16
1923	Marine microgels: Optical and proteomic fingerprints. 2007 , 105, 229-239	33
1922	Validated MALDI-TOF/TOF mass spectra for protein standards. 2007 , 18, 850-5	46
1921	A Qit-q-ToF mass spectrometer for two-dimensional tandem mass spectrometry. 2007 , 21, 3223-6	4
1920	Analysis of membrane microdomain-associated proteins in the insular cortex of post-mortem human brain. 2007 , 1, 1324-31	8
1919	THE HUPO Human Plasma Proteome Project. 2007 , 1, 769-79	30
1918	Proteomics studies of pancreatic cancer. 2007 , 1, 1582-1591	27
1917	HSP27 and HSP70 interact with CD10 in C4-2 prostate cancer cells. 2007 , 67, 714-21	18
1916	A combined dataset of human cerebrospinal fluid proteins identified by multi-dimensional chromatography and tandem mass spectrometry. 2007 , 7, 469-73	100
1915	Implications of 15N-metabolic labeling for automated peptide identification in Arabidopsis thaliana. 2007 , 7, 1279-92	101
1914	SuperHirn - a novel tool for high resolution LC-MS-based peptide/protein profiling. 2007 , 7, 3470-80	269
1913	A la carte proteomics with an emphasis on gel-free techniques. 2007 , 7, 2698-718	79
1912	Methods, algorithms and tools in computational proteomics: a practical point of view. 2007 , 7, 2815-32	80
1911	Capture and analysis of quantitative proteomic data. 2007 , 7, 2787-99	51

1910	Two-dimensional separation of human plasma proteins using iterative free-flow electrophoresis. 2007 , 7, 4218-27	34
1909	Subcellular shotgun proteomics in plants: looking beyond the usual suspects. 2007 , 7, 2963-75	57
1908	A workflow to increase the detection rate of proteins from unsequenced organisms in high-throughput proteomics experiments. 2007 , 7, 4245-54	42
1907	Profiling of vitreous proteomes from proliferative diabetic retinopathy and nondiabetic patients. 2007 , 7, 4203-15	79
1906	Direct cancer tissue proteomics: a method to identify candidate cancer biomarkers from formalin-fixed paraffin-embedded archival tissues. 2007 , 26, 65-76	119
1905	Absolute protein expression profiling estimates the relative contributions of transcriptional and translational regulation. 2007 , 25, 117-24	921
1904	An integrated mass spectrometric and computational framework for the analysis of protein interaction networks. 2007 , 25, 345-52	147
1903	Analysis and validation of proteomic data generated by tandem mass spectrometry. 2007 , 4, 787-97	523
1902	Tandem affinity purification of functional TAP-tagged proteins from human cells. 2007 , 2, 1145-51	51
1901	Labeling, detection and identification of newly synthesized proteomes with bioorthogonal non-canonical amino-acid tagging. 2007 , 2, 532-40	230
1900	Comprehensive identification of proteins in Hodgkin lymphoma-derived Reed-Sternberg cells by LC-MS/MS. 2007 , 87, 1113-24	18
1899	Growth phenotypes of <i>Pseudomonas aeruginosa</i> lasR mutants adapted to the airways of cystic fibrosis patients. 2007 , 64, 512-33	263
1898	Optimization of filtering criterion for SEQUEST database searching to improve proteome coverage in shotgun proteomics. 2007 , 8, 323	23
1897	PARPs database: a LIMS systems for protein-protein interaction data mining or laboratory information management system. 2007 , 8, 483	16
1896	msmsEval: tandem mass spectral quality assignment for high-throughput proteomics. 2007 , 8, 51	33
1895	Characterization of the RNA polymerase II and III complexes in <i>Leishmania major</i> . 2007 , 37, 491-502	32
1894	TOPP--the OpenMS proteomics pipeline. 2007 , 23, e191-7	216
1893	The citrus fruit proteome: insights into citrus fruit metabolism. 2007 , 226, 989-1005	84

1892	The genome of the thermoacidophilic red microalga <i>Galdieria sulphuraria</i> encodes a small family of secreted class III peroxidases that might be involved in cell wall modification. 2008 , 227, 353-62	22
1891	Advances in proteomic workflows for systems biology. 2007 , 18, 378-84	86
1890	The neoplastically transformed (CD30hi) Marek's disease lymphoma cell phenotype most closely resembles T-regulatory cells. 2008 , 57, 1253-62	34
1889	Polygalacturonase causes lygus-like damage on plants: cloning and identification of western tarnished plant bug (<i>Lygus hesperus</i>) polygalacturonases secreted during feeding. 2008 , 2, 215-225	22
1888	Analysis of the experimental detection of central nervous system-related genes in human brain and cerebrospinal fluid datasets. 2008 , 8, 1138-48	18
1887	Comparative proteomic and transcriptional profiling of a bread wheat cultivar and its derived transgenic line overexpressing a low molecular weight glutenin subunit gene in the endosperm. 2008 , 8, 2948-66	62
1886	Protein expression profile of <i>Gluconacetobacter diazotrophicus</i> PAL5, a sugarcane endophytic plant growth-promoting bacterium. 2008 , 8, 1631-44	18
1885	Deciphering the proteomic profile of <i>Mycobacterium leprae</i> cell envelope. 2008 , 8, 2477-91	38
1884	Proteomic analysis of membrane rafts of melanoma cells identifies protein patterns characteristic of the tumor progression stage. 2008 , 8, 4733-47	30
1883	From complementarity to comprehensiveness--targeting the membrane proteome of growing <i>Bacillus subtilis</i> by divergent approaches. 2008 , 8, 4123-36	41
1882	Two-dimensional gel-based approaches for the assessment of N-Linked and O-GlcNAc glycosylation in human and simian immunodeficiency viruses. 2008 , 8, 4919-30	17
1881	Detergent-free biotin switch combined with liquid chromatography/tandem mass spectrometry in the analysis of S-nitrosylated proteins. 2008 , 22, 1137-45	40
1880	Exploration of the normal human bronchoalveolar lavage fluid proteome. 2008 , 2, 585-95	41
1879	Analysis of the human testis proteome by mass spectrometry and bioinformatics. 2008 , 2, 1651-7	26
1878	Characterization of the renal cyst fluid proteome in autosomal dominant polycystic kidney disease (ADPKD) patients. 2008 , 2, 1140-1152	42
1877	Proteomics cataloging analysis of human expressed prostatic secretions reveals rich source of biomarker candidates. 2008 , 2, 543-555	18
1876	Informatics development: challenges and solutions for MALDI mass spectrometry. 2008 , 27, 1-19	13
1875	Analysis of environmental stress response on the proteome level. 2008 , 27, 556-74	40

1874	A two step fractionation approach for plasma proteomics using immunodepletion of abundant proteins and multi-lectin affinity chromatography: Application to the analysis of obesity, diabetes, and hypertension diseases. 2008 , 31, 1156-66	65
1873	A comparison of 2-D chromatography separations using UV and (18)O quantification of proteins in similar proteomes. 2008 , 31, 314-20	1
1872	Focal adhesion targeting of v-Crk is essential for FAK phosphorylation and cell migration in mouse embryo fibroblasts deficient src family kinases or p130CAS. 2008 , 214, 604-13	7
1871	Comprehensive and quantitative proteome profiling of the mouse liver and plasma. 2008 , 47, 1043-51	56
1870	Electron capture/transfer versus collisionally activated/induced dissociations: solo or duet?. 2008 , 19, 753-61	127
1869	Low-coverage massively parallel pyrosequencing of cDNAs enables proteomics in non-model species: comparison of a species-specific database generated by pyrosequencing with databases from related species for proteome analysis of pea chloroplast envelopes. 2008 , 136, 44-53	59
1868	Experimental and computational approaches to quantitative proteomics: status quo and outlook. 2008 , 71, 19-33	99
1867	Quantitative proteomics as a new piece of the systems biology puzzle. 2008 , 71, 357-67	66
1866	Protein complexes in bacterial and yeast mitochondrial membranes differ in their sensitivity towards dissociation by SDS. 2008 , 1784, 2012-8	1
1865	Micro-proteome analysis using micro-chromatofocusing in intact protein separations. 2008 , 1194, 3-10	7
1864	Statistical validation of peptide identifications in large-scale proteomics using the target-decoy database search strategy and flexible mixture modeling. 2008 , 7, 286-92	98
1863	Semisupervised model-based validation of peptide identifications in mass spectrometry-based proteomics. 2008 , 7, 254-65	114
1862	PeptideAtlas: a resource for target selection for emerging targeted proteomics workflows. 2008 , 9, 429-34	457
1861	Building consensus spectral libraries for peptide identification in proteomics. 2008 , 5, 873-5	214
1860	Calculating absolute and relative protein abundance from mass spectrometry-based protein expression data. 2008 , 3, 1444-1451	65
1859	Proteomic identification of non-Gal antibody targets after pig-to-primate cardiac xenotransplantation. 2008 , 15, 268-76	75
1858	A systems biology investigation of the MEP/terpenoid and shikimate/phenylpropanoid pathways points to multiple levels of metabolic control in sweet basil glandular trichomes. 2008 , 54, 349-61	113
1857	Comprehensive proteomic analysis of bovine spermatozoa of varying fertility rates and identification of biomarkers associated with fertility. 2008 , 2, 19	183

1856	Structure and function of the native and recombinant mitochondrial MRP1/MRP2 complex from <i>Trypanosoma brucei</i> . 2008 , 38, 901-12	33
1855	Recent developments in microwave-assisted protein chemistries - can this be integrated into the drug discovery and validation process?. 2008 , 13, 1075-81	17
1854	Autophagosome and Phagosome. 2008 ,	9
1853	Endosperm and Amyloplast Proteomes of Wheat Grain. 207-222	2
1852	Correlating the transcriptome, proteome, and metabolome in the environmental adaptation of a hyperthermophile. 2008 , 7, 1027-35	60
1851	Characterization of the mouse pancreatic islet proteome and comparative analysis with other mouse tissues. 2008 , 7, 3114-26	41
1850	An assessment of software solutions for the analysis of mass spectrometry based quantitative proteomics data. 2008 , 7, 51-61	387
1849	Data analysis and bioinformatics tools for tandem mass spectrometry in proteomics. 2008 , 33, 18-25	122
1848	Spectral index for assessment of differential protein expression in shotgun proteomics. 2008 , 7, 845-54	92
1847	Proteomic analysis of mouse brain microsomes: identification and bioinformatic characterization of endoplasmic reticulum proteins in the mammalian central nervous system. 2008 , 7, 1046-54	23
1846	Improving sensitivity by probabilistically combining results from multiple MS/MS search methodologies. 2008 , 7, 245-53	138
1845	Statistical application and challenges in global gel-free proteomic analysis by mass spectrometry. 2008 , 28, 297-307	16
1844	The proteomic response of <i>Mycobacterium smegmatis</i> to anti-tuberculosis drugs suggests targeted pathways. 2008 , 7, 855-65	31
1843	Identification of CDK2 substrates in human cell lysates. 2008 , 9, R149	120
1842	A mouse plasma peptide atlas as a resource for disease proteomics. 2008 , 9, R93	20
1841	Assigning significance to peptides identified by tandem mass spectrometry using decoy databases. 2008 , 7, 29-34	449
1840	Organelle proteomics. Preface. 2008 , 432, v-viii	
1839	False discovery rates and related statistical concepts in mass spectrometry-based proteomics. 2008 , 7, 47-50	171

1838	The catalytic subunit of shiga-like toxin 1 interacts with ribosomal stalk proteins and is inhibited by their conserved C-terminal domain. 2008 , 378, 375-86	65
1837	Capsid size determination by Staphylococcus aureus pathogenicity island SaPI1 involves specific incorporation of SaPI1 proteins into procapsids. 2008 , 380, 465-75	43
1836	Genome-specific gas-phase fractionation strategy for improved shotgun proteomic profiling of proteotypic peptides. <i>Analytical Chemistry</i> , 2008 , 80, 1182-91	7.8 78
1835	Characterization of strategies for obtaining confident identifications in bottom-up proteomics measurements using hybrid FTMS instruments. <i>Analytical Chemistry</i> , 2008 , 80, 8514-25	7.8 23
1834	Spatially and temporally regulated alpha6 integrin cleavage during <i>Xenopus laevis</i> development. 2008 , 366, 779-85	7
1833	Identification of Fructose-1,6-bisphosphate aldolase cytosolic class I as an NMH7 MADS domain associated protein. 2008 , 376, 700-5	17
1832	What is the expectation maximization?. 2008 , 26, 897-9	298
1831	. 2008 ,	
1830	Profiling mitochondrial proteins in radiation-induced genome-unstable cell lines with persistent oxidative stress by mass spectrometry. 2008 , 169, 700-6	18
1829	Significance analysis of spectral count data in label-free shotgun proteomics. 2008 , 7, 2373-85	281
1828	The effects of shared peptides on protein quantitation in label-free proteomics by LC/MS/MS. 2008 , 7, 164-9	36
1827	Proteomics of multigenic families from species underrepresented in databases: the case of loquat (<i>Eriobotrya japonica</i> Lindl.) polyphenol oxidases. 2008 , 7, 4095-106	14
1826	Fractionation of complex protein mixture by virtual three-dimensional liquid chromatography based on combined pH and salt steps. 2008 , 7, 4525-37	19
1825	Online automated in vivo zebrafish phosphoproteomics: from large-scale analysis down to a single embryo. 2008 , 7, 1555-64	68
1824	Application of proteomics in the discovery of candidate protein biomarkers in a diabetes autoantibody standardization program sample subset. 2008 , 7, 698-707	47
1823	Heat-shock response in <i>Arabidopsis thaliana</i> explored by multiplexed quantitative proteomics using differential metabolic labeling. 2008 , 7, 780-5	66
1822	Comparative proteomics of human monkeypox and vaccinia intracellular mature and extracellular enveloped virions. 2008 , 7, 960-8	48
1821	Identification of differentially expressed proteins in the cervical mucosa of HIV-1-resistant sex workers. 2008 , 7, 4446-54	60

1820	Instance based algorithm for posterior probability calculation by target-decoy strategy to improve protein identifications. <i>Analytical Chemistry</i> , 2008 , 80, 9326-35	7.8	2
1819	Improved sequence tag generation method for peptide identification in tandem mass spectrometry. 2008 , 7, 4422-34		16
1818	Precursor-ion mass re-estimation improves peptide identification on hybrid instruments. 2008 , 7, 4031-9		49
1817	Isoform analysis of LC-MS/MS data from multidimensional fractionation of the serum proteome. 2008 , 7, 2546-52		5
1816	Proteomic analysis of conditioned media from the PC3, LNCaP, and 22Rv1 prostate cancer cell lines: discovery and validation of candidate prostate cancer biomarkers. 2008 , 7, 3329-38		127
1815	Peptide sequence confidence in accurate mass and time analysis and its use in complex proteomics experiments. 2008 , 7, 5148-56		14
1814	Spectral probabilities and generating functions of tandem mass spectra: a strike against decoy databases. 2008 , 7, 3354-63		341
1813	Highly efficient depletion strategy for the two most abundant erythrocyte soluble proteins improves proteome coverage dramatically. 2008 , 7, 3060-3		65
1812	The standard protein mix database: a diverse data set to assist in the production of improved Peptide and protein identification software tools. 2008 , 7, 96-103		134
1811	Mitochondrial dysfunction, oxidative stress, and apoptosis revealed by proteomic and transcriptomic analyses of the striata in two mouse models of Parkinson's disease. 2008 , 7, 666-77		79
1810	Proteomic characterization of mouse cytosolic and membrane prostate fractions: high levels of free SUMO peptides are androgen-regulated. 2008 , 7, 4492-9		8
1809	Global topology analysis of pancreatic zymogen granule membrane proteins. 2008 , 7, 2323-36		27
1808	Phosphoprotein profiling by PA-GeLC-MS/MS. 2008 , 7, 2812-24		17
1807	SALAMI (Spectrum ALignments using high Accuracy Mass and high sensitivity data): how to make the best out of hybrid MS/MS data. 2008 , 7, 1984-93		3
1806	Tandem immunoprecipitation of phosphotyrosine-mass spectrometry (TIPY-MS) indicates C19ORF19 becomes tyrosine-phosphorylated and associated with activated epidermal growth factor receptor. 2008 , 7, 1067-77		27
1805	The mammary epithelial cell secretome and its regulation by signal transduction pathways. 2008 , 7, 558-69		29
1804	The Future: Translation from Discovery to the Clinic [Roles of HUPO and Industry in Biomarker Discovery. 2008 , 593-613		
1803	Differential proteomic screen to evidence proteins ubiquitinated upon mitotic exit in cell-free extract of <i>Xenopus laevis</i> embryos. 2008 , 7, 4701-14		4

1802	ANIBAL, stable isotope-based quantitative proteomics by aniline and benzoic acid labeling of amino and carboxylic groups. 2008 , 7, 800-12	38
1801	Quantitative analysis of snake venoms using soluble polymer-based isotope labeling. 2008 , 7, 785-99	11
1800	Identification of paracrine neuroprotective candidate proteins by a functional assay-driven proteomics approach. 2008 , 7, 1349-61	33
1799	Targeted quantitative analysis of Streptococcus pyogenes virulence factors by multiple reaction monitoring. 2008 , 7, 1489-500	179
1798	Factors that contribute to the misidentification of tyrosine nitration by shotgun proteomics. 2008 , 7, 2442-51	50
1797	Peak bagging for peptide mass fingerprinting. 2008 , 24, 1293-9	5
1796	Host airway proteins interact with Staphylococcus aureus during early pneumonia. 2008 , 76, 888-98	15
1795	Comparison of proteins expressed on secretory vesicle membranes and plasma membranes of human neutrophils. 2008 , 180, 5575-81	80
1794	Structural and functional association of Trypanosoma brucei MIX protein with cytochrome c oxidase complex. 2008 , 7, 1994-2003	27
1793	Humoral response profiling reveals pathways to prostate cancer progression. 2008 , 7, 600-11	45
1792	TbRGG1, an essential protein involved in kinetoplastid RNA metabolism that is associated with a novel multiprotein complex. 2008 , 14, 970-80	75
1791	Analysis of human plasma proteins: a focus on sample collection and separation using free-flow electrophoresis. 2008 , 5, 571-87	30
1790	Research in Computational Molecular Biology. 2008 ,	0
1789	An integrated, directed mass spectrometric approach for in-depth characterization of complex peptide mixtures. 2008 , 7, 2138-50	119
1788	Quantitative proteomic identification of MAZ as a transcriptional regulator of muscle-specific genes in skeletal and cardiac myocytes. 2008 , 28, 6521-35	42
1787	Human cytomegalovirus secretome contains factors that induce angiogenesis and wound healing. 2008 , 82, 6524-35	89
1786	Trypanosoma brucei mitochondrial ribosomes: affinity purification and component identification by mass spectrometry. 2008 , 7, 1286-96	86
1785	Proteomic analysis of renal calculi indicates an important role for inflammatory processes in calcium stone formation. 2008 , 295, F1254-8	55

1784	De novo origination of a new protein-coding gene in <i>Saccharomyces cerevisiae</i> . 2008 , 179, 487-96	156
1783	Non-parametric estimation of posterior error probabilities associated with peptides identified by tandem mass spectrometry. 2008 , 24, i42-8	84
1782	A support vector machine model for the prediction of proteotypic peptides for accurate mass and time proteomics. 2008 , 24, 1503-9	40
1781	Mass spectrometry-based approaches toward absolute quantitative proteomics. 2008 , 9, 263-74	78
1780	Proteome-wide identification of poly(ADP-ribose) binding proteins and poly(ADP-ribose)-associated protein complexes. 2008 , 36, 6959-76	298
1779	Nitrosative stress with HIV dementia causes decreased L-prostaglandin D synthase activity. 2008 , 70, 1753-62	28
1778	Global liver proteomics of rats exposed for 5 days to phenobarbital identifies changes associated with cancer and with CYP metabolism. 2008 , 106, 556-69	14
1777	Combined statin and niacin therapy remodels the high-density lipoprotein proteome. 2008 , 118, 1259-67	109
1776	Mitochondrial complexes in <i>Trypanosoma brucei</i> : a novel complex and a unique oxidoreductase complex. 2008 , 7, 534-45	112
1775	A hierarchical statistical model to assess the confidence of peptides and proteins inferred from tandem mass spectrometry. 2008 , 24, 202-8	34
1774	Investigating MS2/MS3 matching statistics: a model for coupling consecutive stage mass spectrometry data for increased peptide identification confidence. 2008 , 7, 71-87	35
1773	Quantitative proteomics analysis of the effects of ionizing radiation in wild type and p53 K317R knock-in mouse thymocytes. 2008 , 7, 716-27	11
1772	Enhanced detection of low abundance human plasma proteins using a tandem IgY12-SuperMix immunoaffinity separation strategy. 2008 , 7, 1963-73	172
1771	Adaptive discriminant function analysis and reranking of MS/MS database search results for improved peptide identification in shotgun proteomics. 2008 , 7, 4878-89	35
1770	Improved ranking functions for protein and modification-site identifications. 2008 , 15, 705-19	25
1769	Proteomic analysis of polymeric salivary mucins: no evidence for MUC19 in human saliva. 2008 , 413, 545-52	22
1768	Metabolic pathways in <i>Anopheles stephensi</i> mitochondria. 2008 , 415, 309-16	32
1767	Optimizing Sensitivity and Specificity in Mass Spectrometric Proteome Analysis. 2008 , 211-221	

1766	A map of human protein interactions derived from co-expression of human mRNAs and their orthologs. 2008 , 4, 180	68
1765	Alterations in protein expression associated with the development of mealiness in peaches. 2008 , 83, 85-93	7
1764	. 2008 ,	8
1763	Comparison of a label-free quantitative proteomic method based on peptide ion current area to the isotope coded affinity tag method. 2008 , 6, 243-55	39
1762	From protein-disease associations to disease informatics. 2008 , 13, 3391-407	11
1761	C3b deposition on human erythrocytes induces the formation of a membrane skeleton-linked protein complex. 2009 , 119, 788-801	33
1760	Integrated proteomic analysis of human cancer cells and plasma from tumor bearing mice for ovarian cancer biomarker discovery. 2009 , 4, e7916	48
1759	Quantitative proteomics analysis integrated with microarray data reveals that extracellular matrix proteins, catenins, and p53 binding protein 1 are important for chemotherapy response in ovarian cancers. 2009 , 13, 345-54	65
1758	Protein identification using Sorcerer 2 and SEQUEST. 2009 , Chapter 13, Unit 13.3	36
1757	Epidermal growth factor receptor phosphorylation sites Ser991 and Tyr998 are implicated in the regulation of receptor endocytosis and phosphorylations at Ser1039 and Thr1041. 2009 , 8, 2131-44	59
1756	Shotgun protein identification and quantification by mass spectrometry. 2009 , 564, 261-88	22
1755	Mn(II) oxidation is catalyzed by heme peroxidases in "Aurantimonas manganoxydans" strain SI85-9A1 and Erythrobacter sp. strain SD-21. 2009 , 75, 4130-8	89
1754	A PP2A phosphatase high density interaction network identifies a novel striatin-interacting phosphatase and kinase complex linked to the cerebral cavernous malformation 3 (CCM3) protein. 2009 , 8, 157-71	257
1753	A "new" thematic series: mass spectrometry-based proteomics of lipid biology. 2009 , 50, 777-80	2
1752	In-depth proteome analysis of Arabidopsis leaf peroxisomes combined with in vivo subcellular targeting verification indicates novel metabolic and regulatory functions of peroxisomes. 2009 , 150, 125-43	222
1751	A bayesian approach to protein inference problem in shotgun proteomics. 2009 , 16, 1183-93	55
1750	Widespread reorganization of metabolic enzymes into reversible assemblies upon nutrient starvation. 2009 , 106, 10147-52	262
1749	Phosphorylation of the transcription elongation factor Spt5 by yeast Bur1 kinase stimulates recruitment of the PAF complex. 2009 , 29, 4852-63	135

1748	The oxazolidinone derivative locostatin induces cytokine appeasement. 2009 , 183, 7489-96	16
1747	An interaction network of the mammalian COP9 signalosome identifies Dda1 as a core subunit of multiple Cul4-based E3 ligases. 2009 , 122, 1035-44	59
1746	Analysis of the pumpkin phloem proteome provides insights into angiosperm sieve tube function. 2009 , 8, 343-56	174
1745	Grade-dependent proteomics characterization of kidney cancer. 2009 , 8, 971-85	82
1744	Reinterpretation of the protein identification process for proteomics data. 2009 , 1, 9.1-9.6	
1743	Proteomics analysis of nucleolar SUMO-1 target proteins upon proteasome inhibition. 2009 , 8, 2243-55	78
1742	Dynamic host energetics and cytoskeletal proteomes in human immunodeficiency virus type 1-infected human primary CD4 cells: analysis by multiplexed label-free mass spectrometry. 2009 , 83, 9283-95	54
1741	Deterministic protein inference for shotgun proteomics data provides new insights into Arabidopsis pollen development and function. 2009 , 19, 1786-800	135
1740	Genomic analyses of musashi1 downstream targets show a strong association with cancer-related processes. 2009 , 284, 12125-35	67
1739	Mining the ovarian cancer ascites proteome for potential ovarian cancer biomarkers. 2009 , 8, 661-9	88
1738	Proteomics: challenges, techniques and possibilities to overcome biological sample complexity. 2009 , 2009,	207
1737	Qupe--a Rich Internet Application to take a step forward in the analysis of mass spectrometry-based quantitative proteomics experiments. 2009 , 25, 3128-34	24
1736	Proteomics, metabolomics, and immunomics on microparticles derived from human atherosclerotic plaques. 2009 , 2, 379-88	98
1735	Recent developments in proteome informatics for mass spectrometry analysis. 2009 , 12, 194-202	11
1734	Defining elastic fiber interactions by molecular fishing: an affinity purification and mass spectrometry approach. 2009 , 8, 2715-32	24
1733	Quantitative proteomics identifies oxidant-induced, AtMPK6-dependent changes in Arabidopsis thaliana protein profiles. 2009 , 4, 497-505	12
1732	Brain-specific proteins decline in the cerebrospinal fluid of humans with Huntington disease. 2009 , 8, 451-66	56
1731	Protein Inference by Assembling Peptides Identified from Tandem Mass Spectra. 2009 , 4, 226-233	9

1730	Glomeruli of Dense Deposit Disease contain components of the alternative and terminal complement pathway. 2009 , 75, 952-60	140
1729	Bruton's tyrosine kinase revealed as a negative regulator of Wnt-beta-catenin signaling. 2009 , 2, ra25	47
1728	The F(0)F(1)-ATP synthase complex contains novel subunits and is essential for procyclic <i>Trypanosoma brucei</i> . 2009 , 5, e1000436	91
1727	Stress-dependent coordination of transcriptome and translome in yeast. 2009 , 7, e1000105	100
1726	RIN4 functions with plasma membrane H ⁺ -ATPases to regulate stomatal apertures during pathogen attack. 2009 , 7, e1000139	189
1725	An insight into high-resolution mass-spectrometry data. 2009 , 10, 481-500	25
1724	Improving peptide identification with single-stage mass spectrum peaks. 2009 , 25, 2969-74	5
1723	Quantitative proteomics identifies a Dab2/integrin module regulating cell migration. 2009 , 186, 99-111	95
1722	Quantitative proteomics reveals GIMAP family proteins 1 and 4 to be differentially regulated during human T helper cell differentiation. 2009 , 8, 32-44	43
1721	p38- γ -dependent gene silencing restricts entry into the myogenic differentiation program. 2009 , 187, 991-1005	83
1720	MaXIC-Q Web: a fully automated web service using statistical and computational methods for protein quantitation based on stable isotope labeling and LC-MS. 2009 , 37, W661-9	9
1719	The yeast vacuolar membrane proteome. 2009 , 8, 380-92	66
1718	Comprehensive proteome analysis of an Apc mouse model uncovers proteins associated with intestinal tumorigenesis. 2009 , 2, 224-33	45
1717	MMP-9 sheds the beta2 integrin subunit (CD18) from macrophages. 2009 , 8, 1044-60	69
1716	Combining results from lectin affinity chromatography and glyco-capture approaches substantially improves the coverage of the glycoproteome. 2009 , 8, 287-301	103
1715	The Cul3-KLHL21 E3 ubiquitin ligase targets aurora B to midzone microtubules in anaphase and is required for cytokinesis. 2009 , 187, 791-800	89
1714	Kinase-dependent regulation of inositol 1,4,5-trisphosphate-dependent Ca ²⁺ release during oocyte maturation. 2009 , 284, 20184-96	28
1713	Identification of cardiac myosin-binding protein C as a candidate biomarker of myocardial infarction by proteomics analysis. 2009 , 8, 2687-99	60

1712	Exosomal secretion of cytoplasmic prostate cancer xenograft-derived proteins. 2009 , 8, 1192-205	86
1711	Proteomics at the center of nutrigenomics: comprehensive molecular understanding of dietary health effects. 2009 , 25, 1085-93	14
1710	Identification of proteins from tuberculin purified protein derivative (PPD) by LC-MS/MS. 2009 , 89, 423-30	43
1709	Adeno-associated virus capsid serotype identification: Analytical methods development and application. 2009 , 159, 167-77	20
1708	Improved results in proteomics by use of local and peptide-class specific false discovery rates. 2009 , 10, 179	37
1707	The <i>Drosophila melanogaster</i> PeptideAtlas facilitates the use of peptide data for improved fly proteomics and genome annotation. 2009 , 10, 59	32
1706	LC-MS/MS-based proteome profiling in <i>Daphnia pulex</i> and <i>Daphnia longicephala</i> : the <i>Daphnia pulex</i> genome database as a key for high throughput proteomics in <i>Daphnia</i> . 2009 , 10, 171	36
1705	Analyses of the spleen proteome of chickens infected with Marek's disease virus. 2009 , 390, 356-67	28
1704	Genome analysis of two virulent <i>Streptococcus thermophilus</i> phages isolated in Argentina. 2009 , 136, 101-9	33
1703	Capn4 overexpression underlies tumor invasion and metastasis after liver transplantation for hepatocellular carcinoma. 2009 , 49, 460-70	71
1702	The heat shock cognate protein 70 is associated with hepatitis C virus particles and modulates virus infectivity. 2009 , 49, 1798-809	66
1701	Quantitative proteomics investigation of pancreatic intraepithelial neoplasia. 2009 , 30, 1132-44	52
1700	A proteomic workflow for discovery of serum carrier protein-bound biomarker candidates of alcohol abuse using LC-MS/MS. 2009 , 30, 2207-14	26
1699	Plant proteomics: concepts, applications, and novel strategies for data interpretation. 2009 , 28, 93-120	74
1698	Distinct properties of murine alpha 5 gamma-aminobutyric acid type a receptors revealed by biochemical fractionation and mass spectroscopy. 2009 , 87, 1737-47	21
1697	Extensive fractionation and identification of proteins within nasal lavage fluids from allergic rhinitis and asthmatic chronic rhinosinusitis patients. 2009 , 32, 44-56	24
1696	Shotgun proteomic analysis of the microsomal fraction of eukaryotic cells using a two-dimensional reversed-phase x ion-pair reversed-phase HPLC setup. 2009 , 32, 1165-74	5
1695	Matching the proteome to the genome: the microbody of penicillin-producing <i>Penicillium chrysogenum</i> cells. 2009 , 9, 167-84	66

1694	Quantitative proteomic analysis of mitochondria in aging PS-1 transgenic mice. 2009 , 29, 649-64	30
1693	An Unsupervised, Model-Free, Machine-Learning Combiner for Peptide Identifications from Tandem Mass Spectra. 2009 , 5, 23-36	46
1692	Regulation of Plasmodium falciparum Pfnek3 relies on phosphorylation at its activation loop and at threonine 82. 2009 , 66, 3081-90	6
1691	On the estimation of false positives in peptide identifications using decoy search strategy. 2009 , 9, 194-204	9
1690	Protein composition of liver cyst fluid from the BALB/c-cpk/+ mouse model of autosomal recessive polycystic kidney disease. 2009 , 9, 3775-82	6
1689	Mass spectrometric and computational analysis of cytokine-induced alterations in the astrocyte secretome. 2009 , 9, 768-82	56
1688	Experimental annotation of channel catfish virus by probabilistic proteogenomic mapping. 2009 , 9, 2634-47	15
1687	Improving sensitivity in proteome studies by analysis of false discovery rates for multiple search engines. 2009 , 9, 1220-9	77
1686	A comprehensive analysis of Trypanosoma brucei mitochondrial proteome. 2009 , 9, 434-50	138
1685	Recent developments in public proteomic MS repositories and pipelines. 2009 , 9, 861-81	40
1684	BiomarkerDigger: a versatile disease proteome database and analysis platform for the identification of plasma cancer biomarkers. 2009 , 9, 3729-40	19
1683	Identification of proteins of Neisseria meningitidis induced under iron-limiting conditions using the isobaric tandem mass tag (TMT) labeling approach. 2009 , 9, 1771-81	39
1682	Proteome analysis of Edwardsiella ictaluri. 2009 , 9, 1353-63	14
1681	Proteomic profiling of the prechylomicron transport vesicle involved in the assembly and secretion of apoB-48-containing chylomicrons in the intestinal enterocytes. 2009 , 9, 3698-711	7
1680	Proteomic profiling of Cronobacter turicensis 3032, a food-borne opportunistic pathogen. 2009 , 9, 3564-79	15
1679	Detection and identification of 4-hydroxy-2-nonenal Schiff-base adducts along with products of Michael addition using data-dependent neutral loss-driven MS3 acquisition: method evaluation through an in vitro study on cytochrome c oxidase modifications. 2009 , 9, 5188-93	37
1678	Proteomics data repositories. 2009 , 9, 4653-63	33
1677	Protein composition of Trypanosoma brucei mitochondrial membranes. 2009 , 9, 5497-508	34

1676	Improving peptide identification using an empirical peptide retention time database. 2009 , 23, 109-18	4
1675	Precursor ion scans for the targeted detection of stable-isotope-labeled peptides. 2009 , 23, 3570-8	2
1674	Deep depletion of abundant serum proteins reveals low-abundant proteins as potential biomarkers for human ovarian cancer. 2009 , 3, 853-861	44
1673	Identification of CHI3L1 and MASP2 as a biomarker pair for liver cancer through integrative secretome and transcriptome analysis. 2009 , 3, 541-551	6
1672	Structural heterogeneity and protein composition of exosome-like vesicles (prostasomes) in human semen. 2009 , 69, 159-67	231
1671	Shotgun proteomics approach to characterizing the embryonic proteome of the silkworm, <i>Bombyx mori</i> , at labrum appearance stage. 2009 , 18, 649-60	17
1670	Distinguishing mouse strains by proteomic analysis of pelage hair. 2009 , 129, 2120-5	23
1669	Proteomic analysis of membrane microdomain-associated proteins in the dorsolateral prefrontal cortex in schizophrenia and bipolar disorder reveals alterations in LAMP, STXBP1 and BASP1 protein expression. 2009 , 14, 601-13	136
1668	Mass-spectrometric identification and relative quantification of N-linked cell surface glycoproteins. 2009 , 27, 378-86	422
1667	Proteomic analysis of seminal plasma from asthenozoospermia patients reveals proteins that affect oxidative stress responses and semen quality. 2009 , 11, 484-91	85
1666	The proteomic analysis of human neonatal umbilical cord serum by mass spectrometry. 2009 , 30, 1550-8	15
1665	A HUPO test sample study reveals common problems in mass spectrometry-based proteomics. 2009 , 6, 423-30	270
1664	Comparative analysis to guide quality improvements in proteomics. 2009 , 6, 717-19	56
1663	Differential stimulation of monocytic cells results in distinct populations of microparticles. 2009 , 7, 1019-28	110
1662	Proteomics of the TRAP-induced platelet releasate. 2009 , 72, 91-109	97
1661	pI-based fractionation of serum proteomes versus anion exchange after enhancement of low-abundance proteins by means of peptide libraries. 2009 , 72, 1061-70	19
1660	Photocrosslinking and click chemistry enable the specific detection of proteins interacting with phospholipids at the membrane interface. 2009 , 16, 3-14	76
1659	Chicken egg yolk cytoplasmic proteome, mined via combinatorial peptide ligand libraries. 2009 , 1216, 1241-52	100

1658	Pathway-based biomarker search by high-throughput proteomics profiling of secretomes. 2009 , 8, 1489-503	71
1657	An integrated workflow for charting the human interaction proteome: insights into the PP2A system. 2009 , 5, 237	218
1656	Dual role for the methyltransferase G9a in the maintenance of beta-globin gene transcription in adult erythroid cells. 2009 , 106, 18303-8	69
1655	Discovery of retinoblastoma-associated binding protein 46 as a novel prognostic marker for distant metastasis in nonsmall cell lung cancer by combined analysis of cancer cell secretome and pleural effusion proteome. 2009 , 8, 4428-40	57
1654	Software platform for rapidly creating computational tools for mass spectrometry-based proteomics. 2009 , 8, 3212-7	20
1653	PKC phosphorylation of titin's PEVK element: a novel and conserved pathway for modulating myocardial stiffness. 2009 , 105, 631-8, 17 p following 638	191
1652	Proteomic and bioinformatic analysis on endocrine organs of domesticated silkworm, <i>Bombyx mori</i> L. for a comprehensive understanding of their roles and relations. 2009 , 8, 2620-32	33
1651	Mapping the lung proteome in cystic fibrosis. 2009 , 8, 3020-8	38
1650	Comparative proteomic analysis of <i>Listeria monocytogenes</i> strains F2365 and EGD. 2009 , 75, 366-73	38
1649	N-linked glycoproteomic analysis of formalin-fixed and paraffin-embedded tissues. 2009 , 8, 1657-62	36
1648	Large-scale multiplexed quantitative discovery proteomics enabled by the use of an (18)O-labeled "universal" reference sample. 2009 , 8, 290-9	52
1647	Cell secretome analysis using hollow fiber culture system leads to the discovery of CLIC1 protein as a novel plasma marker for nasopharyngeal carcinoma. 2009 , 8, 5465-74	53
1646	Combining alkaline phosphatase treatment and hybrid linear ion trap/Orbitrap high mass accuracy liquid chromatography-mass spectrometry data for the efficient and confident identification of protein phosphorylation. <i>Analytical Chemistry</i> , 2009 , 81, 7778-87	7.8 17
1645	Automated 2D peptide separation on a 1D nano-LC-MS system. 2009 , 8, 1610-6	56
1644	Comparative interactomics: analysis of arabidopsis 14-3-3 complexes reveals highly conserved 14-3-3 interactions between humans and plants. 2009 , 8, 1913-24	35
1643	Proteomics of <i>Pyrococcus furiosus</i> , a hyperthermophilic archaeon refractory to traditional methods. 2009 , 8, 3844-51	19
1642	Proteomic study of human glioblastoma multiforme tissue employing complementary two-dimensional liquid chromatography- and mass spectrometry-based approaches. 2009 , 8, 4604-14	23
1641	Rapid label-free identification of estrogen-induced differential protein expression in vivo from mouse brain and uterine tissue. 2009 , 8, 3862-71	29

1640	Comparison of MS(2)-only, MSA, and MS(2)/MS(3) methodologies for phosphopeptide identification. 2009 , 8, 887-99	64
1639	'Two-stage double-technique hybrid (TSDTH)' identification strategy for the analysis of BMP2-induced transdifferentiation of premyoblast C2C12 cells to osteoblast. 2009 , 8, 4441-54	17
1638	Platelet proteome changes associated with diabetes and during platelet storage for transfusion. 2009 , 8, 2261-72	46
1637	Proteomic characteristics of ex vivo-enriched adult human bone marrow mononuclear cells in continuous perfusion cultures. 2009 , 8, 2079-89	10
1636	False discovery rates of protein identifications: a strike against the two-peptide rule. 2009 , 8, 4173-81	143
1635	Cell surface and secreted protein profiles of human thyroid cancer cell lines reveal distinct glycoprotein patterns. 2009 , 8, 3958-68	45
1634	Quantitative serum proteomics using dual stable isotope coding and nano LC-MS/MSMS. 2009 , 8, 5412-22	14
1633	An embryonic stem cell chromatin remodeling complex, esBAF, is essential for embryonic stem cell self-renewal and pluripotency. 2009 , 106, 5181-6	404
1632	Correlation of multiple peptide mass spectra for phosphoprotein identification. 2009 , 8, 5396-405	7
1631	An iterative strategy for precursor ion selection for LC-MS/MS based shotgun proteomics. 2009 , 8, 3239-51	16
1630	Analysis of RP-HPLC loading conditions for maximizing peptide identifications in shotgun proteomics. 2009 , 8, 4161-8	11
1629	Processing of the phalloidin proprotein by prolyl oligopeptidase from the mushroom <i>Conocybe albipes</i> . 2009 , 284, 18070-7	35
1628	Autoreactivity of serum immunoglobulin to periodontal tissue components: a pilot study. 2009 , 80, 625-33	27
1627	Identification and quantification of preterm birth biomarkers in human cervicovaginal fluid by liquid chromatography/tandem mass spectrometry. 2009 , 8, 2407-17	56
1626	Enrichment of glycoproteins using nanoscale chelating concanavalin A monolithic capillary chromatography. <i>Analytical Chemistry</i> , 2009 , 81, 3776-83	7.8 64
1625	Reduced genomic potential for secreted plant cell-wall-degrading enzymes in the ectomycorrhizal fungus <i>Amanita bisporigera</i> , based on the secretome of <i>Trichoderma reesei</i> . 2009 , 46, 427-35	112
1624	Discovery of naturally processed and HLA-presented class I peptides from vaccinia virus infection using mass spectrometry for vaccine development. 2009 , 28, 38-47	33
1623	Comprehensive proteomic analysis of <i>Schizosaccharomyces pombe</i> by two-dimensional HPLC-tandem mass spectrometry. 2009 , 48, 311-9	36

1622	Nucleotide oligomerization domain-2 interacts with 2'-5'-oligoadenylate synthetase type 2 and enhances RNase-L function in THP-1 cells. 2009 , 47, 560-6	39
1621	Proteomic study of the effects of microcystin-LR on organelle and membrane proteins in medaka fish liver. 2009 , 94, 153-61	41
1620	Integrating shotgun proteomics and mRNA expression data to improve protein identification. 2009 , 25, 1397-403	52
1619	Proteomic methodologies and their application in colorectal cancer research. 2009 , 46, 319-42	17
1618	The Identification of Protein S-Nitrosocysteine. 2009 , 1451-1465	1
1617	Comparative proteomics study of salt tolerance between a nonsequenced extremely halotolerant cyanobacterium and its mildly halotolerant relative using in vivo metabolic labeling and in vitro isobaric labeling. 2009 , 8, 818-28	43
1616	Proteomic identification of salivary biomarkers of type-2 diabetes. 2009 , 8, 239-45	201
1615	Network-assisted protein identification and data interpretation in shotgun proteomics. 2009 , 5, 303	45
1614	Orthogonal separation techniques for the characterization of the yeast nuclear proteome. 2009 , 8, 3451-63	15
1613	A dynamic range compression and three-dimensional peptide fractionation analysis platform expands proteome coverage and the diagnostic potential of whole saliva. 2009 , 8, 5590-600	141
1612	Neuroproteomics. 2009 ,	1
1611	Postmenopausal estrogen and progestin effects on the serum proteome. 2009 , 1, 121	29
1610	Application of serum proteomics to the Women's Health Initiative conjugated equine estrogens trial reveals a multitude of effects relevant to clinical findings. 2009 , 1, 47	34
1609	Proteomics. 2009 ,	3
1608	Utility of mass spectrometry for proteome analysis: part II. Ion-activation methods, statistics, bioinformatics and annotation. 2009 , 6, 171-97	13
1607	Mass spectrometry of proteins and peptides: methods and protocols. Preface. 2009 , 492, v	6
1606	Software tool for researching annotations of proteins: open-source protein annotation software with data visualization. <i>Analytical Chemistry</i> , 2009 , 81, 9819-23	7.8 183
1605	The mouse C2C12 myoblast cell surface N-linked glycoproteome: identification, glycosite occupancy, and membrane orientation. 2009 , 8, 2555-69	65

1604	Decoy methods for assessing false positives and false discovery rates in shotgun proteomics. <i>Analytical Chemistry</i> , 2009 , 81, 146-59	7.8	79
1603	Mining gene functional networks to improve mass-spectrometry-based protein identification. 2009 , 25, 2955-61		31
1602	Protein identification false discovery rates for very large proteomics data sets generated by tandem mass spectrometry. 2009 , 8, 2405-17		250
1601	Metabolic labeling and protein linearization technology allow the study of proteins secreted by cultured cells in serum-containing media. 2009 , 8, 4779-88		37
1600	Proteome analysis of Legionella vacuoles purified by magnetic immunoseparation reveals secretory and endosomal GTPases. 2009 , 10, 76-87		129
1599	Rational extension of the ribosome biogenesis pathway using network-guided genetics. 2009 , 7, e1000213		130
1598	Proteomic analysis reveals presence of platelet microparticles in endothelial progenitor cell cultures. 2009 , 114, 723-32		237
1597	Proteomics analysis of human dentin reveals distinct protein expression profiles. 2009 , 8, 1338-46		63
1596	Analysis of cell surface proteome changes via label-free, quantitative mass spectrometry. 2009 , 8, 624-38		78
1595	Mass spectrometry (LC-MS/MS) site-mapping of N-glycosylated membrane proteins for breast cancer biomarkers. 2009 , 8, 4151-60		73
1594	Ubiquitin-related modifier Urm1 acts as a sulphur carrier in thiolation of eukaryotic transfer RNA. 2009 , 458, 228-32		205
1593	An extensive survey of tyrosine phosphorylation revealing new sites in human mammary epithelial cells. 2009 , 8, 3852-61		45
1592	Barnacle cement: a polymerization model based on evolutionary concepts. 2009 , 212, 3499-510		105
1591	Identification of five candidate lung cancer biomarkers by proteomics analysis of conditioned media of four lung cancer cell lines. 2009 , 8, 2746-58		111
1590	Nitration of tyrosine residues 368 and 345 in the beta-subunit elicits FoF1-ATPase activity loss. 2009 , 423, 219-31		25
1589	The cAMP capture compound mass spectrometry as a novel tool for targeting cAMP-binding proteins: from protein kinase A to potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channels. 2009 , 8, 2843-56		36
1588	Proteomic analysis of biopsied human colonic mucosa. 2010 , 51, 46-54		8
1587	Proteomic Profiling From Paraffin-Embedded Tissue Sections by Mass-Spectrometry: A Novel Approach with Wide-Ranging Potential Applications in Pathology. 2010 , 33, 165-168		

1586	Quantitative proteomics analysis of the nuclear fraction of human CD4+ cells in the early phases of IL-4-induced Th2 differentiation. 2010 , 9, 1937-53	40
1585	Sequence signatures and mRNA concentration can explain two-thirds of protein abundance variation in a human cell line. 2010 , 6, 400	425
1584	Profiling of methyltransferases and other S-adenosyl-L-homocysteine-binding Proteins by Capture Compound Mass Spectrometry (CCMS). 2010 ,	10
1583	A nested mixture model for protein identification using mass spectrometry. 2010 , 4,	18
1582	Proteomic cell surface phenotyping of differentiating acute myeloid leukemia cells. 2010 , 116, e26-34	66
1581	Liquid Chromatography Mass Spectrometry-Based Proteomics: Biological and Technological Aspects. 2010 , 4, 1797-1823	85
1580	Rhizobial adaptation to hosts, a new facet in the legume root-nodule symbiosis. 2010 , 23, 784-90	55
1579	Quantitative changes in the mitochondrial proteome from subjects with mild cognitive impairment, early stage, and late stage Alzheimer's disease. 2010 , 19, 325-39	29
1578	Alternative methods for verifying the results of the mass spectrometric identification of peptides in shotgun proteomics. 2010 , 65, 1462-1468	1
1577	Role of spectral counting in quantitative proteomics. 2010 , 7, 39-53	302
1576	Understanding and exploiting Peptide fragment ion intensities using experimental and informatic approaches. 2010 , 604, 73-94	13
1575	Workflow comparison for label-free, quantitative secretome proteomics for cancer biomarker discovery: method evaluation, differential analysis, and verification in serum. 2010 , 9, 1913-22	119
1574	Evaluation of microwave-assisted enzymatic digestion and tandem mass spectrometry for the identification of protein residues from an inorganic solid matrix: implications in archaeological research. 2010 , 396, 1491-9	11
1573	Measuring the intra-individual variability of the plasma proteome in the chicken model of spontaneous ovarian adenocarcinoma. 2010 , 398, 737-49	24
1572	Optimization of parameters for coverage of low molecular weight proteins. 2010 , 398, 2867-81	36
1571	Advanced tool for characterization of microbial cultures by combining cytomics and proteomics. 2010 , 88, 575-84	41
1570	Application of displacement chromatography for the analysis of a lipid raft proteome. 2010 , 878, 309-14	5
1569	A new acid mix enhances phosphopeptide enrichment on titanium- and zirconium dioxide for mapping of phosphorylation sites on protein complexes. 2010 , 878, 515-24	26

1568	SUMOylation is required for normal development of linear elements and wild-type meiotic recombination in <i>Schizosaccharomyces pombe</i> . 2010 , 119, 59-72	23
1567	Differential proteomic analysis of a highly metastatic variant of human breast cancer cells using two-dimensional differential gel electrophoresis. 2010 , 136, 1545-56	54
1566	Shotgun proteomic analysis of the fat body during metamorphosis of domesticated silkworm (<i>Bombyx mori</i>). 2010 , 38, 1333-42	16
1565	Quantitative proteomic analysis of S-nitrosated proteins in diabetic mouse liver with ICAT switch method. 2010 , 1, 675-87	21
1564	Novel In Situ Collection of Tumor Interstitial Fluid from a Head and Neck Squamous Carcinoma Reveals a Unique Proteome with Diagnostic Potential. 2010 , 6, 75-82	16
1563	Hydrophobic Proteome Analysis of Triple Negative and Hormone-Receptor-Positive-Her2-Negative Breast Cancer by Mass Spectrometer. 2010 , 6, 93-103	10
1562	Membrane Protein Profiling of Human Islets of Langerhans Using Several Extraction Methods. 2010 , 6, 195-207	4
1561	Soybean Allergens Affecting North American Patients Identified by 2D Gels and Mass Spectrometry. 2010 , 3, 363-374	27
1560	Proteomics reveals novel components of the <i>Anopheles gambiae</i> eggshell. 2010 , 56, 1414-9	40
1559	An improved machine learning protocol for the identification of correct Sequest search results. 2010 , 11, 591	4
1558	A versatile palindromic amphipathic repeat coding sequence horizontally distributed among diverse bacterial and eucaryotic microbes. 2010 , 11, 430	9
1557	From an electrophoretic mobility shift assay to isolated transcription factors: a fast genomic-proteomic approach. 2010 , 11, 644	15
1556	Isolation of detergent resistant microdomains from cultured neurons: detergent dependent alterations in protein composition. 2010 , 11, 120	22
1555	Increasing the amylose content of durum wheat through silencing of the <i>SBEl1a</i> genes. 2010 , 10, 144	121
1554	Analysis of expressed sequence tags from a single wheat cultivar facilitates interpretation of tandem mass spectrometry data and discrimination of gamma gliadin proteins that may play different functional roles in flour. 2010 , 10, 7	31
1553	Proteomic analysis of prolactinoma cells by immuno-laser capture microdissection combined with online two-dimensional nano-scale liquid chromatography/mass spectrometry. 2010 , 8, 2	20
1552	Investigation of PARP-1, PARP-2, and PARG interactomes by affinity-purification mass spectrometry. 2010 , 8, 22	114
1551	Ser 524 is a phosphorylation site in MUTYH and Ser 524 mutations alter 8-oxoguanine (OG): a mismatch recognition. 2010 , 9, 1026-37	19

1550	Glypican 3 binds to GLUT1 and decreases glucose transport activity in hepatocellular carcinoma cells. 2010 , 111, 1252-9	10
1549	Identification of candidate biomarkers in ovarian cancer serum by depletion of highly abundant proteins and differential in-gel electrophoresis. 2010 , 31, 599-610	53
1548	High-level recombinant protein production in CHO cells using lentiviral vectors and the cumate gene-switch. 2010 , 106, 203-15	44
1547	Qualitative and quantitative profiling of the bovine milk fat globule membrane proteome. 2010 , 73, 1079-88	92
1546	Proteomic profiling of intestinal prechylomicron transport vesicle (PCTV)-associated proteins in an animal model of insulin resistance (94 char). 2010 , 73, 1291-305	9
1545	Meta sequence analysis of human blood peptides and their parent proteins. 2010 , 73, 1163-75	21
1544	The endogenous peptides of normal human serum extracted from the acetonitrile-insoluble precipitate using modified aqueous buffer with analysis by LC-ESI-Paul ion trap and Qq-TOF. 2010 , 73, 1254-69	25
1543	A worm rich in protein: Quantitative, differential, and global proteomics in <i>Caenorhabditis elegans</i> . 2010 , 73, 2186-97	13
1542	Proteome analysis of mouse model systems: A tool to model human disease and for the investigation of tissue-specific biology. 2010 , 73, 2205-18	10
1541	Implementation and evaluation of relative and absolute quantification in shotgun proteomics with label-free methods. 2010 , 73, 1740-6	120
1540	Chemical proteomic and bioinformatic strategies for the identification and quantification of vascular antigens in cancer. 2010 , 73, 1954-73	17
1539	Proteogenomics to discover the full coding content of genomes: a computational perspective. 2010 , 73, 2124-35	132
1538	A proteomic analysis of the mechanism of action of naphthoimidazoles in <i>Trypanosoma cruzi</i> epimastigotes in vitro. 2010 , 73, 2306-15	26
1537	A survey of computational methods and error rate estimation procedures for peptide and protein identification in shotgun proteomics. 2010 , 73, 2092-123	387
1536	The <i>Drosophila melanogaster</i> sperm proteome-II (DmSP-II). 2010 , 73, 2171-85	106
1535	Plasma proteomic analysis may identify new markers for radiation-induced lung toxicity in patients with non-small-cell lung cancer. 2010 , 77, 867-76	26
1534	Engineering of <i>N. benthamiana</i> L. plants for production of N-acetylgalactosamine-glycosylated proteins--towards development of a plant-based platform for production of protein therapeutics with mucin type O-glycosylation. 2010 , 10, 62	41
1533	The adsorption of biomolecules to multi-walled carbon nanotubes is influenced by both pulmonary surfactant lipids and surface chemistry. 2010 , 8, 31	76

1532	Microfiltration isolation of human urinary exosomes for characterization by MS. 2010 , 4, 84-96	139
1531	Shotgun proteomics identifies proteins specific for acute renal transplant rejection. 2010 , 4, 32-47	87
1530	Identification of diabetic nephropathy-selective proteins in human plasma by multi-lectin affinity chromatography and LC-MS/MS. 2010 , 4, 644-53	23
1529	HTAPP: high-throughput autonomous proteomic pipeline. 2010 , 10, 2113-22	32
1528	MassSieve: panning MS/MS peptide data for proteins. 2010 , 10, 3035-9	47
1527	Data management and functional annotation of the Korean reference plasma proteome. 2010 , 10, 1250-5	7
1526	A guided tour of the Trans-Proteomic Pipeline. 2010 , 10, 1150-9	590
1525	Using Laboratory Information Management Systems as central part of a proteomics data workflow. 2010 , 10, 1230-49	28
1524	Scaffold: a bioinformatic tool for validating MS/MS-based proteomic studies. 2010 , 10, 1265-9	390
1523	Environmental proteomics: analysis of structure and function of microbial communities. 2010 , 10, 785-98	120
1522	Computational analysis of unassigned high-quality MS/MS spectra in proteomic data sets. 2010 , 10, 2712-8	51
1521	Unrestricted identification of modified proteins using MS/MS. 2010 , 10, 671-86	77
1520	Immunoproteomic analyses of outer membrane proteins of <i>Mannheimia haemolytica</i> and identification of potential vaccine candidates. 2010 , 10, 2151-64	32
1519	Trans-Proteomic Pipeline supports and improves analysis of electron transfer dissociation data sets. 2010 , 10, 1190-5	35
1518	Estimating false discovery rates for peptide and protein identification using randomized databases. 2010 , 10, 2369-76	26
1517	Identification of candidate nasopharyngeal carcinoma serum biomarkers by cancer cell secretome and tissue transcriptome analysis: potential usage of cystatin A for predicting nodal stage and poor prognosis. 2010 , 10, 2644-60	42
1516	Proteome analysis of fungal and bacterial involvement in leaf litter decomposition. 2010 , 10, 1819-30	70
1515	Quantitative analysis of the secretome of TGF-beta signaling-deficient mammary fibroblasts. 2010 , 10, 2458-70	35

1514	An integrated proteomics and transcriptomics reference data set provides new insights into the Bradyrhizobium japonicum bacteroid metabolism in soybean root nodules. 2010 , 10, 1391-400	89
1513	Proteomic analysis identifies highly antigenic proteins in exosomes from M. tuberculosis-infected and culture filtrate protein-treated macrophages. 2010 , 10, 3190-202	119
1512	Expanding the mouse embryonic stem cell proteome: combining three proteomic approaches. 2010 , 10, 2728-32	16
1511	Time-resolved quantitative proteome profiling of host-pathogen interactions: the response of Staphylococcus aureus RN1HG to internalisation by human airway epithelial cells. 2010 , 10, 2801-11	43
1510	Comparative profiling of highly enriched 22L and Chandler mouse scrapie prion protein preparations. 2010 , 10, 2858-69	26
1509	Empirical approach to false discovery rate estimation in shotgun proteomics. 2010 , 24, 454-62	13
1508	Sequence assignment of ADP-ribosylated peptides is facilitated as peptide length increases. 2010 , 24, 2312-6	7
1507	Characterization of cellulose synthase complexes in Populus xylem differentiation. 2010 , 187, 777-90	80
1506	Evaluation of alkyne-modified isoprenoids as chemical reporters of protein prenylation. 2010 , 76, 460-71	66
1505	sigmaB-dependent protein induction in Listeria monocytogenes during vancomycin stress. 2010 , 308, 94-100	22
1504	Non-canonical inhibition of DNA damage-dependent ubiquitination by OTUB1. 2010 , 466, 941-6	256
1503	Prf immune complexes of tomato are oligomeric and contain multiple Pto-like kinases that diversify effector recognition. 2010 , 61, 507-18	89
1502	PeptideClassifier for protein inference and targeted quantitative proteomics. 2010 , 28, 647-50	61
1501	Generating and navigating proteome maps using mass spectrometry. 2010 , 11, 789-801	139
1500	Identification of enzymes involved in anaerobic benzene degradation by a strictly anaerobic iron-reducing enrichment culture. 2010 , 12, 2783-96	128
1499	Protein oxidation and aggregation in UVA-irradiated Escherichia coli cells as signs of accelerated cellular senescence. 2010 , 12, 2931-45	88
1498	Rapid pre-gel visualization of proteins with mass spectrometry compatibility. 2010 ,	
1497	Mass Spectrometry and its Applications to Functional Proteomics. 2010 , 307-323	

1496	Protein Bioinformatics Infrastructure for the Integration and Analysis of Multiple High-Throughput "omics" Data. 2010 , 423589	15
1495	Shewanella spp. genomic evolution for a cold marine lifestyle and in-situ explosive biodegradation. 2010 , 5, e9109	48
1494	Establishing the proteome of normal human cerebrospinal fluid. 2010 , 5, e10980	150
1493	Integrative proteomic analysis of serum and peritoneal fluids helps identify proteins that are up-regulated in serum of women with ovarian cancer. 2010 , 5, e11137	28
1492	HOIL-1L interacting protein (HOIP) as an NF-kappaB regulating component of the CD40 signaling complex. 2010 , 5, e11380	21
1491	Themis2/ICB1 is a signaling scaffold that selectively regulates macrophage Toll-like receptor signaling and cytokine production. 2010 , 5, e11465	23
1490	Aptamer-based multiplexed proteomic technology for biomarker discovery. 2010 , 5, e15004	876
1489	Oxidative stress and the regulation of complement activation in human glaucoma. 2010 , 51, 5071-82	138
1488	Comparative transcriptome and secretome analysis of wood decay fungi <i>Postia placenta</i> and <i>Phanerochaete chrysosporium</i> . 2010 , 76, 3599-610	213
1487	Integrated phosphoproteomics analysis of a signaling network governing nutrient response and peroxisome induction. 2010 , 9, 2076-88	31
1486	Protein and gene model inference based on statistical modeling in k-partite graphs. 2010 , 107, 12101-6	33
1485	Protein analysis of purified respiratory syncytial virus particles reveals an important role for heat shock protein 90 in virus particle assembly. 2010 , 9, 1829-48	77
1484	An SNP in an ultraconserved regulatory element affects <i>Dlx5/Dlx6</i> regulation in the forebrain. 2010 , 137, 3089-97	49
1483	The interaction of Epac1 and Ran promotes Rap1 activation at the nuclear envelope. 2010 , 30, 3956-69	41
1482	Glaucomatous tissue stress and the regulation of immune response through glial Toll-like receptor signaling. 2010 , 51, 5697-707	119
1481	Immunoproteomic identification of human T cell antigens of <i>Mycobacterium tuberculosis</i> that differentiate healthy contacts from tuberculosis patients. 2010 , 9, 538-49	25
1480	Myocardial ischemic preconditioning preserves postischemic function of the 26S proteasome through diminished oxidative damage to 19S regulatory particle subunits. 2010 , 106, 1829-38	72
1479	Role of Hsp90 in biogenesis of the beta-cell ATP-sensitive potassium channel complex. 2010 , 21, 1945-54	37

1478	Proteome analysis of human aqueous humor. 2010 , 51, 4921-31	126
1477	Activation of Rho GTPases in Smith-Lemli-Opitz syndrome: pathophysiological and clinical implications. 2010 , 19, 1347-57	34
1476	Detection of differentially expressed basal cell proteins by mass spectrometry. 2010 , 9, 351-61	18
1475	Deciphering the structure and function of Als2cr4 in the mouse retina. 2010 , 51, 4407-15	13
1474	Ephrin-B1 forward signaling regulates craniofacial morphogenesis by controlling cell proliferation across Eph-ephrin boundaries. 2010 , 24, 2068-80	74
1473	Elafin is a biomarker of graft-versus-host disease of the skin. 2010 , 2, 13ra2	177
1472	Regulation of the copper chaperone CCS by XIAP-mediated ubiquitination. 2010 , 30, 1923-36	55
1471	The RNA polymerase-associated factor 1 complex (Paf1C) directly increases the elongation rate of RNA polymerase I and is required for efficient regulation of rRNA synthesis. 2010 , 285, 14152-9	41
1470	Global proteomics reveal an atypical strategy for carbon/nitrogen assimilation by a cyanobacterium under diverse environmental perturbations. 2010 , 9, 2678-89	94
1469	Quantitative proteomics of caveolin-1-regulated proteins: characterization of polymerase i and transcript release factor/CAVIN-1 IN endothelial cells. 2010 , 9, 2109-24	33
1468	Dcp2 phosphorylation by Ste20 modulates stress granule assembly and mRNA decay in <i>Saccharomyces cerevisiae</i> . 2010 , 189, 813-27	71
1467	NF45 and NF90 regulate HS4-dependent interleukin-13 transcription in T cells. 2010 , 285, 8256-67	46
1466	Portrait of a pathogen: the <i>Mycobacterium tuberculosis</i> proteome in vivo. 2010 , 5, e13938	155
1465	Proteomic analysis of membrane preparations from developing <i>Pinus radiata</i> compression wood. 2010 , 30, 1456-68	28
1464	Functional proteomics of kallikrein-related peptidases in ovarian cancer ascites fluid. 2010 , 391, 381-90	21
1463	Comprehensive profiling of cartilage extracellular matrix formation and maturation using sequential extraction and label-free quantitative proteomics. 2010 , 9, 1296-313	58
1462	Of mice and men: comparative proteomics of bronchoalveolar fluid. 2010 , 35, 1388-95	37
1461	The phosphoproteome of the minimal bacterium <i>Mycoplasma pneumoniae</i> : analysis of the complete known Ser/Thr kinome suggests the existence of novel kinases. 2010 , 9, 1228-42	79

1460	Functional single-nucleotide polymorphism in acetyl-CoA carboxylase ACACB gene promoter. 2010 , 29, 703-12	3
1459	Statistical Analysis of Mascot Peptide Identification with Active Logistic Regression. 2010 ,	3
1458	Proteomic comparison of detergent-extracted sperm proteins from bulls with different fertility indexes. 2010 , 139, 545-56	111
1457	Proteomics characterization of extracellular space components in the human aorta. 2010 , 9, 2048-62	197
1456	Overview of Proteomic Tools and Their Links to Genomics. 2010 , 55-71	
1455	Studies of a biochemical factory: tomato trichome deep expressed sequence tag sequencing and proteomics. 2010 , 153, 1212-23	105
1454	NOS1AP associates with Scribble and regulates dendritic spine development. 2010 , 30, 4796-805	53
1453	Activity and cellular functions of the deubiquitinating enzyme and polyglutamine disease protein ataxin-3 are regulated by ubiquitination at lysine 117. 2010 , 285, 39303-13	71
1452	System-level analysis of neuroblastoma tumor-initiating cells implicates AURKB as a novel drug target for neuroblastoma. 2010 , 16, 4572-82	36
1451	mTORC1 directly phosphorylates and regulates human MAF1. 2010 , 30, 3749-57	123
1450	Quantitative proteomics analysis of inborn errors of cholesterol synthesis: identification of altered metabolic pathways in DHCR7 and SC5D deficiency. 2010 , 9, 1461-75	32
1449	Proteomics strategy for identifying candidate bioactive proteins in complex mixtures: application to the platelet releasate. 2010 , 2010, 107859	11
1448	Mass spectrometric analysis of multiple pertussis toxins and toxoids. 2010 , 2010, 942365	5
1447	Mass spectrometry-based proteomic diagnosis of renal immunoglobulin heavy chain amyloidosis. 2010 , 5, 2180-7	95
1446	Rational redesign of porcine pepsinogen containing an antimicrobial peptide. 2010 , 23, 711-9	3
1445	A proteomic investigation of ligand-dependent HSP90 complexes reveals CHORDC1 as a novel ADP-dependent HSP90-interacting protein. 2010 , 9, 255-70	63
1444	EspA acts as a critical mediator of ESX1-dependent virulence in Mycobacterium tuberculosis by affecting bacterial cell wall integrity. 2010 , 6, e1000957	67
1443	Temporal proteome and lipidome profiles reveal hepatitis C virus-associated reprogramming of hepatocellular metabolism and bioenergetics. 2010 , 6, e1000719	302

1442	Subnuclear proteomics in colorectal cancer: identification of proteins enriched in the nuclear matrix fraction and regulation in adenoma to carcinoma progression. 2010 , 9, 988-1005	55
1441	A statistics-based platform for quantitative N-terminome analysis and identification of protease cleavage products. 2010 , 9, 912-27	63
1440	Proteomics analysis of the cardiac myofilament subproteome reveals dynamic alterations in phosphatase subunit distribution. 2010 , 9, 497-509	66
1439	The significance of protein maturation by plastidic type I signal peptidase 1 for thylakoid development in <i>Arabidopsis</i> chloroplasts. 2010 , 152, 1297-308	42
1438	De novo proteomics of neuronal ischemic tolerance. 2010 ,	
1437	CLIMP-63 is a gentamicin-binding protein that is involved in drug-induced cytotoxicity. 2010 , 1, e102	31
1436	De novo sequencing methods in proteomics. 2010 , 604, 105-21	51
1435	Computational approaches to peptide identification via tandem MS. 2010 , 604, 23-42	4
1434	The DMM complex prevents spreading of DNA methylation from transposons to nearby genes in <i>Neurospora crassa</i> . 2010 , 24, 443-54	42
1433	Liverbase: a comprehensive view of human liver biology. 2010 , 9, 50-8	36
1432	Systematic identification of yeast proteins extracted into model wine during aging on the yeast lees. 2010 , 58, 2337-46	34
1431	Peek a peak: a glance at statistics for quantitative label-free proteomics. 2010 , 7, 249-61	35
1430	An overview of label-free quantitation methods in proteomics by mass spectrometry. 2010 , 604, 273-83	82
1429	Elevated level of anterior gradient-2 in pancreatic juice from patients with pre-malignant pancreatic neoplasia. 2010 , 9, 149	51
1428	A label-free differential quantitative mass spectrometry method for the characterization and identification of protein changes during citrus fruit development. 2010 , 8, 68	42
1427	Seminal plasma proteins as potential markers of relative fertility in boars. 2010 , 31, 188-200	66
1426	Statistical methods for proteomics. 2010 , 620, 497-507	3
1425	High-Throughput Biological Data Analysis. 2010 , 30, 81-100	2

1424	Efficient marginalization to compute protein posterior probabilities from shotgun mass spectrometry data. 2010 , 9, 5346-57		84
1423	Proteomic analysis of human nail plate. 2010 , 9, 6752-8		43
1422	Plasma proteome response to severe burn injury revealed by 18O-labeled "universal" reference-based quantitative proteomics. 2010 , 9, 4779-89		46
1421	Proteomic analysis of protein-protein interactions within the Cysteine Sulfinate Desulfinate Fe-S cluster biogenesis system. 2010 , 9, 5358-69		19
1420	An in vivo method for characterization of protein interactions within sulfur trafficking systems of E. coli. 2010 , 9, 6740-51		9
1419	Candidate serological biomarkers for cancer identified from the secretomes of 23 cancer cell lines and the human protein atlas. 2010 , 9, 1100-17		153
1418	Deconvolution of mixture spectra from ion-trap data-independent-acquisition tandem mass spectrometry. <i>Analytical Chemistry</i> , 2010 , 82, 833-41	7.8	102
1417	Identification of cell surface glycoprotein markers for glioblastoma-derived stem-like cells using a lectin microarray and LC-MS/MS approach. 2010 , 9, 2565-72		64
1416	First insight into the human liver proteome from PROTEOME(SKY)-LIVER(Hu) 1.0, a publicly available database. 2010 , 9, 79-94		35
1415	Unbiased statistical analysis for multi-stage proteomic search strategies. 2010 , 9, 700-7		39
1414	Proteomic profiling of lipopolysaccharide-activated macrophages by isotope coded affinity tagging. 2010 , 9, 2412-21		18
1413	Comparative protein profiling reveals minichromosome maintenance (MCM) proteins as novel potential tumor markers for meningiomas. 2010 , 9, 485-94		47
1412	Proteomics, genomics, and pathway analyses of Escherichia coli and Staphylococcus aureus infected milk whey reveal molecular pathways and networks involved in mastitis. 2010 , 9, 4604-19		62
1411	Analyzing the hydrophobic proteome of the antarctic archaeon Methanococcoides burtonii using differential solubility fractionation. 2010 , 9, 664-76		14
1410	Combined statistical analyses of peptide intensities and peptide occurrences improves identification of significant peptides from MS-based proteomics data. 2010 , 9, 5748-56		69
1409	MUDE: a new approach for optimizing sensitivity in the target-decoy search strategy for large-scale peptide/protein identification. 2010 , 9, 2265-77		15
1408	Proteomic analyses of the developing chicken cardiovascular system. 2010 , 9, 268-74		8
1407	Serum autoantibody profiling using a natural glycoprotein microarray for the prognosis of early melanoma. 2010 , 9, 6044-51		21

1406	Proteomic profile of uterine luminal fluid from early pregnant ewes. 2010 , 9, 3878-85	48
1405	Glycoprotein expression in human milk during lactation. 2010 , 58, 6440-8	73
1404	Phospholipid transfer protein in human plasma associates with proteins linked to immunity and inflammation. 2010 , 49, 7314-22	45
1403	Strategy for studying the liver secretome on the organ level. 2010 , 9, 1894-901	5
1402	Proteomic analysis of Src family kinases signaling complexes in Golgi/endosomal fractions using a site-selective anti-phosphotyrosine antibody: identification of LRP1-insulin receptor complexes. 2010 , 9, 708-17	12
1401	Aspergillus protein degradation pathways with different secreted protease sets at neutral and acidic pH. 2010 , 9, 3511-9	42
1400	Comparison of a protein-level and peptide-level labeling strategy for quantitative proteomics of synaptosomes using isobaric tags. 2010 , 9, 2725-33	23
1399	Global analysis of TDP-43 interacting proteins reveals strong association with RNA splicing and translation machinery. 2010 , 9, 1104-20	328
1398	Proteomic analysis of proteins involved in spermiogenesis in mouse. 2010 , 9, 1246-56	59
1397	Secretome analysis of human BMSCs and identification of SMOC1 as an important ECM protein in osteoblast differentiation. 2010 , 9, 2946-56	87
1396	Pig preovulatory oocytes modulate cumulus cell protein and gene expression in vitro. 2010 , 320, 87-96	11
1395	Macrophage migration inhibitory factor anti-thrombin III complexes are decreased in bladder cancer patient serum: Complex formation as a mechanism of inactivation. 2010 , 290, 49-57	10
1394	Phosphorylation at serine 318 is not required for inhibition of T cell activation by ALX. 2010 , 396, 994-8	1
1393	In vivo assessment and potential diagnosis of xenobiotics that perturb the thyroid pathway: Proteomic analysis of <i>Xenopus laevis</i> brain tissue following exposure to model T4 inhibitors. 2010 , 5, 138-50	9
1392	A differential proteomic approach to assess the effects of chemotherapeutics and production management strategy on giant tiger shrimp <i>Penaeus monodon</i> . 2010 , 5, 227-33	12
1391	A macrophage sterol-responsive network linked to atherogenesis. 2010 , 11, 125-35	59
1390	Mapping protein abundance patterns in the brain using voxelation combined with liquid chromatography and mass spectrometry. 2010 , 50, 77-84	28
1389	Purification and characterization of the ouabain-sensitive H ⁺ /K ⁺ -ATPase from guinea-pig distal colon. 2010 , 496, 21-32	6

1388	RNA interference silencing of a major lipid droplet protein affects lipid droplet size in <i>Chlamydomonas reinhardtii</i> . 2010 , 9, 97-106	324
1387	High-yield extraction of periplasmic asparaginase produced by recombinant <i>Pichia pastoris</i> harbouring the <i>Saccharomyces cerevisiae</i> ASP3 gene. 2010 , 47, 71-76	18
1386	Analysis of stage-specific expression of basic proteins in <i>Leishmania infantum</i> . 2010 , 9, 3842-53	36
1385	The profile of mitochondrial proteins and their phosphorylation signaling network in INS-1 beta cells. 2010 , 9, 2898-908	19
1384	A support vector machine model for the prediction of proteotypic peptides for accurate mass and time proteomics. 2010 , 26, 1677-83	37
1383	Proteomic changes in the photoreceptor outer segment upon intense light exposure. 2010 , 9, 1173-81	17
1382	Target-decoy search strategy for mass spectrometry-based proteomics. 2010 , 604, 55-71	399
1381	Quantitative organelle proteomics of MCF-7 breast cancer cells reveals multiple subcellular locations for proteins in cellular functional processes. 2010 , 9, 495-508	28
1380	Comprehensive identification of staurosporine-binding kinases in the hepatocyte cell line HepG2 using Capture Compound Mass Spectrometry (CCMS). 2010 , 9, 806-17	53
1379	Molecular analysis of tumor margins by MALDI mass spectrometry in renal carcinoma. 2010 , 9, 2182-90	133
1378	Proteomic characterization of human plasma high density lipoprotein fractionated by gel filtration chromatography. 2010 , 9, 5239-49	177
1377	Discovery of novel bladder cancer biomarkers by comparative urine proteomics using iTRAQ technology. 2010 , 9, 5803-15	115
1376	Proteome Bioinformatics. 2010 ,	7
1375	Improvement of proteolytic efficiency towards low-level proteins by an antifouling surface of alumina gel in a microchannel. 2010 , 10, 2887-93	22
1374	Novel proteins associated with risk for coronary heart disease or stroke among postmenopausal women identified by in-depth plasma proteome profiling. 2010 , 2, 48	52
1373	Shotgun proteomic analysis of yeast-elicited California poppy (<i>Eschscholzia californica</i>) suspension cultures producing enhanced levels of benzophenanthridine alkaloids. 2010 , 9, 4337-45	12
1372	alpha-Lipoic acid alters post-translational modifications and protects the chaperone activity of lens alpha-crystallin in naphthalene-induced cataract. 2010 , 35, 620-30	6
1371	Identification and confirmation of biomarkers using an integrated platform for quantitative analysis of glycoproteins and their glycosylations. 2010 , 9, 798-805	59

1370	Region-specific protein abundance changes in the brain of MPTP-induced Parkinson's disease mouse model. 2010 , 9, 1496-509	55
1369	Transcription profiling in human platelets reveals LRRFIP1 as a novel protein regulating platelet function. 2010 , 116, 4646-56	77
1368	Isobaric labeling and tandem mass spectrometry: a novel approach for profiling and quantifying proteins differentially expressed in amniotic fluid in preterm labor with and without intra-amniotic infection/inflammation. 2010 , 23, 261-80	69
1367	Metabolic capabilities and systems fluctuations in <i>Haloarcula marismortui</i> revealed by integrative genomics and proteomics analyses. 2011 , 10, 3261-73	8
1366	Improve Accuracy of Peptide Identification with Consistency between Peptides. 2011 ,	1
1365	pep2pro: a new tool for comprehensive proteome data analysis to reveal information about organ-specific proteomes in <i>Arabidopsis thaliana</i> . 2011 , 3, 225-37	60
1364	The Haptoglobin α chain as a supportive biomarker for human lung cancers. 2011 , 7, 1167-75	37
1363	<i>Trypanosoma brucei</i> mitochondrial respiratome: composition and organization in procyclic form. 2011 , 10, M110.006908	46
1362	iProphet: multi-level integrative analysis of shotgun proteomic data improves peptide and protein identification rates and error estimates. 2011 , 10, M111.007690	397
1361	Molecular mechanism of glyceraldehyde-3-phosphate dehydrogenase inactivation by α -unsaturated carbonyl derivatives. 2011 , 24, 2302-11	61
1360	Reproducibility of protein identification of selected cell types in Barrett's esophagus analyzed by combining laser-capture microdissection and mass spectrometry. 2011 , 10, 288-98	21
1359	Quantitative secretome analysis reveals that COL6A1 is a metastasis-associated protein using stacking gel-aided purification combined with iTRAQ labeling. 2011 , 10, 1110-25	60
1358	Using the Human Plasma PeptideAtlas to study human plasma proteins. 2011 , 728, 349-74	21
1357	Validation of the flush method as an alternative to basal or reflex tear collection. 2011 , 36, 198-207	57
1356	Exploration of bovine milk proteome in colostrum and mature whey using an ion-exchange approach. 2011 , 10, 692-704	68
1355	Proteome-wide identification of WRN-interacting proteins in untreated and nuclease-treated samples. 2011 , 10, 1216-27	34
1354	A statistical method for assessing peptide identification confidence in accurate mass and time tag proteomics. <i>Analytical Chemistry</i> , 2011 , 83, 6135-40	7.8 42
1353	Addressing trypsin bias in large scale (phospho)proteome analysis by size exclusion chromatography and secondary digestion of large post-trypsin peptides. 2011 , 10, 800-11	23

1352	On using samples of known protein content to assess the statistical calibration of scores assigned to peptide-spectrum matches in shotgun proteomics. 2011 , 10, 2671-8	38
1351	IsoformResolver: A peptide-centric algorithm for protein inference. 2011 , 10, 3060-75	30
1350	Subcellular tissue proteomics of hepatocellular carcinoma for molecular signature discovery. 2011 , 10, 5070-83	34
1349	T4-Like genome organization of the Escherichia coli O157:H7 lytic phage AR1. 2011 , 85, 6567-78	29
1348	Large-scale phosphoproteomics analysis of whole saliva reveals a distinct phosphorylation pattern. 2011 , 10, 1728-36	37
1347	Analysis of the soluble human tooth proteome and its ability to induce dentin/tooth regeneration. 2011 , 17, 181-91	55
1346	Identification of guanylate-binding protein 1 as a potential oral cancer marker involved in cell invasion using omics-based analysis. 2011 , 10, 3778-88	58
1345	In vivo termini amino acid labeling for quantitative proteomics. <i>Analytical Chemistry</i> , 2011 , 83, 6026-33	7.8 20
1344	Proteome of the Caenorhabditis elegans oocyte. 2011 , 10, 2300-5	12
1343	Proteomic response to sublethal cadmium exposure in a sentinel fish species, Cottus gobio. 2011 , 10, 470-8	35
1342	Systematic discovery of ectopic pregnancy serum biomarkers using 3-D protein profiling coupled with label-free quantitation. 2011 , 10, 1126-38	42
1341	A face in the crowd: recognizing peptides through database search. 2011 , 10, R111.009522	106
1340	Induced sputum proteome in healthy subjects and asthmatic patients. 2011 , 128, 1176-1184.e6	45
1339	Preview: a program for surveying shotgun proteomics tandem mass spectrometry data. <i>Analytical Chemistry</i> , 2011 , 83, 5259-67	7.8 29
1338	Gel-Based and Gel-Free Sample Preparation for LC-MS/MS Analysis. 2011 , 3-17	
1337	Characterization of the phosphoproteome in androgen-repressed human prostate cancer cells by Fourier transform ion cyclotron resonance mass spectrometry. 2011 , 10, 3920-8	10
1336	A novel alignment method and multiple filters for exclusion of unqualified peptides to enhance label-free quantification using peptide intensity in LC-MS/MS. 2011 , 10, 4799-812	54
1335	Mass Spectrometry of Amino Acids and Proteins. 2011 , 1-50	1

1334	Bioinformatics for qualitative and quantitative proteomics. 2011 , 719, 331-49	3
1333	Score regularization for peptide identification. 2011 , 12 Suppl 1, S2	8
1332	Data Mining in Proteomics. 2011 ,	5
1331	A proteomic approach to study parathyroid glands. 2011 , 7, 687-99	19
1330	Drug Safety Evaluation. 2011 ,	3
1329	Proteomic analysis of zebrafish brain tissue following exposure to the pesticide prochloraz. 2011 , 105, 618-28	24
1328	Protein alterations associated with pancreatic cancer and chronic pancreatitis found in human plasma using global quantitative proteomics profiling. 2011 , 10, 2359-76	82
1327	Analysis of secretome changes uncovers an autocrine/paracrine component in the modulation of cell proliferation and motility by c-Myc. 2011 , 10, 5326-37	27
1326	Comprehensive tissue processing strategy for quantitative proteomics of formalin-fixed multiple sclerosis lesions. 2011 , 10, 4855-68	23
1325	Mass spectrometry-driven proteomics: an introduction. 2011 , 753, 1-27	4
1324	Proteomic dissection of the von Hippel-Lindau (VHL) interactome. 2011 , 10, 5175-82	30
1323	SILAC compatible strain of <i>Pichia pastoris</i> for expression of isotopically labeled protein standards and quantitative proteomics. 2011 , 10, 5251-9	16
1322	Quantitative proteomic identification of the BRCA1 ubiquitination substrates. 2011 , 10, 5191-8	18
1321	Serum/Plasma Proteomics. 2011 ,	7
1320	Data-independent proteomic screen identifies novel tamoxifen agonist that mediates drug resistance. 2011 , 10, 4567-78	40
1319	Proteomic analysis of a model fish species exposed to individual pesticides and a binary mixture. 2011 , 101, 196-206	28
1318	Ecotoxicoproteomics in gills of the sentinel fish species, <i>Cottus gobio</i> , exposed to perfluorooctane sulfonate (PFOS). 2011 , 103, 1-8	38
1317	Differential epithelial and stromal protein profiles in keratoconus and normal human corneas. 2011 , 92, 282-98	72

1316	On the biomarkers and mechanisms of konzo, a distinct upper motor neuron disease associated with food (cassava) cyanogenic exposure. 2011 , 49, 571-8	29
1315	Elongin C is a mediator of Notch4 activity in human renal tubule cells. 2011 , 1814, 1748-57	9
1314	Differential phosphopeptide expression in a benign breast tissue, and triple-negative primary and metastatic breast cancer tissues from the same African-American woman by LC-LTQ/FT-ICR mass spectrometry. 2011 , 412, 127-31	9
1313	Sex-biased protein expression in threespine stickleback, <i>Gasterosteus aculeatus</i> . 2011 , 10, 4033-40	12
1312	Absolute quantification of microbial proteomes at different states by directed mass spectrometry. 2011 , 7, 510	80
1311	Label-free shotgun proteomics and metabolite analysis reveal a significant metabolic shift during citrus fruit development. 2011 , 62, 5367-84	72
1310	Recent developments in quantitative proteomics. 2011 , 722, 171-82	42
1309	Proteomic insights into the protective mechanisms of an in vitro oxidative stress model of early stage Parkinson's disease. 2011 , 488, 11-6	18
1308	Inhibition and covalent modification of tyrosine hydroxylase by 3,4-dihydroxyphenylacetaldehyde, a toxic dopamine metabolite. 2011 , 32, 471-7	34
1307	Identification of S-RNase and peroxidase in petunia nectar. 2011 , 168, 734-8	32
1306	Proteomic expression profiles of virulent and avirulent strains of <i>Listeria monocytogenes</i> isolated from macrophages. 2011 , 74, 1906-17	25
1305	Proteomic characterization of thymocyte-derived microvesicles and apoptotic bodies in BALB/c mice. 2011 , 74, 2025-33	103
1304	To tag or not to tag: a comparative evaluation of immunoaffinity-labeling and tandem mass spectrometry for the identification and localization of posttranslational protein carbonylation by 4-hydroxy-2-nonenal, an end-product of lipid peroxidation. 2011 , 74, 2360-9	28
1303	Fucosylated glycoproteomic approach to identify a complement component 9 associated with squamous cell lung cancer (SQLC). 2011 , 74, 2948-58	29
1302	The beginning of a beautiful friendship: cross-linking/mass spectrometry and modelling of proteins and multi-protein complexes. 2011 , 173, 530-40	314
1301	Elevated copper remodels hepatic RNA processing machinery in the mouse model of Wilson's disease. 2011 , 406, 44-58	29
1300	<i>Arabidopsis</i> plasmodesmal proteome. 2011 , 6, e18880	183
1299	Two-step protease digestion and glycopeptide capture approach for accurate glycosite identification and glycoprotein sequence coverage improvement. 2011 , 85, 70-5	13

1298	Hydrazide-functionalized magnetic microspheres for the selective enrichment of digested tryptophan-containing peptides in serum. 2011 , 85, 1001-6	11
1297	Nitrosative protein oxidation is modulated during early endotoxemia. 2011 , 25, 118-24	17
1296	Proteomic characterization of specific minor proteins in the human milk casein fraction. 2011 , 10, 5409-15	19
1295	Proteomic characterization of human milk whey proteins during a twelve-month lactation period. 2011 , 10, 1746-54	111
1294	Proteomic characterization of human milk fat globule membrane proteins during a 12 month lactation period. 2011 , 10, 3530-41	103
1293	Targeted proteomics by selected reaction monitoring mass spectrometry: applications to systems biology and biomarker discovery. 2011 , 7, 292-303	66
1292	Quantitative proteomics identify molecular targets that are crucial in larval settlement and metamorphosis of <i>Bugula neritina</i> . 2011 , 10, 349-60	20
1291	Modeling contaminants in AP-MS/MS experiments. 2011 , 10, 886-95	40
1290	Nutriproteomics: technologies and applications for identification and quantification of biomarkers and ingredients. 2011 , 70, 351-64	18
1289	Proteomic analysis of intra-arterial thrombus secretions reveals a negative association of clusterin and thrombospondin-1 with abdominal aortic aneurysm. 2011 , 219, 432-9	34
1288	Interaction of arrestin with enolase1 in photoreceptors. 2011 , 52, 1832-40	21
1287	Proteomic-based biosignatures in breast cancer classification and prediction of therapeutic response. 2011 , 2011, 896476	21
1286	Comprehensive proteomic profiling of aldehyde dehydrogenases in lung adenocarcinoma cell lines. 2011 , 2011, 145010	12
1285	RASSF1A and the rs2073498 Cancer Associated SNP. 2011 , 1, 54	11
1284	Identification of the <i>Lactobacillus</i> SLP domain that binds gastric mucin. 2011 , 16, 2128-43	4
1283	Radiation-induced signaling results in mitochondrial impairment in mouse heart at 4 weeks after exposure to X-rays. 2011 , 6, e27811	116
1282	REVEILLE8 and PSEUDO-RESPONSE REGULATOR5 form a negative feedback loop within the <i>Arabidopsis</i> circadian clock. 2011 , 7, e1001350	149
1281	Interactions between the Nse3 and Nse4 components of the SMC5-6 complex identify evolutionarily conserved interactions between MAGE and EID Families. 2011 , 6, e17270	36

1280	The serine 814 of TRPC6 is phosphorylated under unstimulated conditions. 2011 , 6, e18121	7
1279	Nanopods: a new bacterial structure and mechanism for deployment of outer membrane vesicles. 2011 , 6, e20725	54
1278	The 3-base periodicity and codon usage of coding sequences are correlated with gene expression at the level of transcription elongation. 2011 , 6, e21590	18
1277	MicroRNA-96 directly inhibits β globin expression in human erythropoiesis. 2011 , 6, e22838	51
1276	Impact of protein stability, cellular localization, and abundance on proteomic detection of tumor-derived proteins in plasma. 2011 , 6, e23090	14
1275	Characterizing the Escherichia coli O157:H7 proteome including protein associations with higher order assemblies. 2011 , 6, e26554	16
1274	Phosphorylation and activation of the plasma membrane Na^+/H^+ exchanger (NHE1) during osmotic cell shrinkage. 2011 , 6, e29210	13
1273	Physiological Adaptation of the Bacterium Lactococcus lactis in Response to the Production of Human CFTR. 2011 , 10, M000052-MCP200	11
1272	Labile disulfide bonds are common at the leucocyte cell surface. 2011 , 1, 110010	63
1271	Genomic insights into the metabolic potential of the polycyclic aromatic hydrocarbon degrading sulfate-reducing Deltaproteobacterium N47. 2011 , 13, 1125-37	59
1270	Analysis of in situ manganese(II) oxidation in the Columbia River and offshore plume: linking Aurantimonas and the associated microbial community to an active biogeochemical cycle. 2011 , 13, 1561-76	22
1269	Quantitative transcriptomic analysis of abscisic acid-induced and reactive oxygen species-dependent expression changes and proteomic profiling in Arabidopsis suspension cells. 2011 , 67, 105-18	63
1268	In vivo phosphorylation patterns of key stressosome proteins define a second feedback loop that limits activation of Bacillus subtilis B. 2011 , 80, 798-810	31
1267	Quantitative proteomics reveals metabolic and pathogenic properties of Chlamydia trachomatis developmental forms. 2011 , 82, 1185-203	121
1266	Derlin-dependent retrograde transport from endosomes to the Golgi apparatus. 2011 , 12, 1417-31	20
1265	Studies on botulinum neurotoxins type /C1 and mosaic/DC using Endopep-MS and proteomics. 2011 , 61, 288-300	22
1264	mProphet: automated data processing and statistical validation for large-scale SRM experiments. 2011 , 8, 430-5	357
1263	Integrated mass spectrometry-based analysis of plasma glycoproteins and their glycan modifications. 2011 , 6, 253-69	38

1262	The dynamic state of protein turnover: It's about time. 2011 , 21, 293-303	102
1261	Remodeling of protein and mRNA expression in <i>Leishmania mexicana</i> induced by deletion of glucose transporter genes. 2011 , 175, 39-48	7
1260	Immunoproteomic analysis of <i>Brucella melitensis</i> and identification of a new immunogenic candidate protein for the development of brucellosis subunit vaccine. 2011 , 49, 175-84	43
1259	Proteomic profiling of the human T-cell nucleolus. 2011 , 49, 441-52	35
1258	2'-Hydroxycinnamaldehyde targets low-density lipoprotein receptor-related protein-1 to inhibit lipopolysaccharide-induced microglial activation. 2011 , 230, 52-64	18
1257	IPM: An integrated protein model for false discovery rate estimation and identification in high-throughput proteomics. 2011 , 75, 116-21	12
1256	The host outer membrane proteins OmpA and OmpC are associated with the <i>Shigella</i> phage Sf6 virion. 2011 , 409, 319-27	10
1255	The proteome of the insoluble <i>Schistosoma mansoni</i> eggshell skeleton. 2011 , 41, 523-32	37
1254	Lung cancer signatures in plasma based on proteome profiling of mouse tumor models. 2011 , 20, 289-99	138
1253	In-depth proteomics of ovarian cancer ascites: combining shotgun proteomics and selected reaction monitoring mass spectrometry. 2011 , 10, 2286-99	63
1252	Co-compartmentalization of the astroglial glutamate transporter, GLT-1, with glycolytic enzymes and mitochondria. 2011 , 31, 18275-88	151
1251	A high-confidence human plasma proteome reference set with estimated concentrations in PeptideAtlas. 2011 , 10, M110.006353	341
1250	Model for membrane organization and protein sorting in the cyanobacterium <i>Synechocystis</i> sp. PCC 6803 inferred from proteomics and multivariate sequence analyses. 2011 , 10, 3617-31	63
1249	Proteomic analysis of integrin adhesion complexes. 2011 , 4, pt2	36
1248	Model-based discovery of circulating biomarkers. 2011 , 728, 87-107	2
1247	Comparative proteomics of colon cancer stem cells and differentiated tumor cells identifies BIRC6 as a potential therapeutic target. 2011 , 10, M111.011353	68
1246	Gel-Free Proteomics. 2011 ,	7
1245	Bioinformatics for Omics Data. 2011 ,	14

1244	Detection of <i>Staphylococcus aureus</i> using ¹⁵ N-labeled bacteriophage amplification coupled with matrix-assisted laser desorption/ionization-time-of-flight mass spectrometry. <i>Analytical Chemistry</i> , 2011 , 83, 2286-93	7.8	39
1243	A methodology for simultaneous fluorogenic derivatization and boronate affinity enrichment of 3-nitrotyrosine-containing peptides. 2011 , 418, 184-96		26
1242	Differential analysis of "protein corona" profile adsorbed onto different nonviral gene delivery systems. 2011 , 419, 180-9		35
1241	The insect repellent DEET (N,N-diethyl-3-methylbenzamide) increases the synthesis of glutathione S-transferase in cultured mosquito cells. 2011 , 27, 149-57		6
1240	AXR1-ECR1 and AXL1-ECR1 heterodimeric RUB-activating enzymes diverge in function in <i>Arabidopsis thaliana</i> . 2011 , 75, 515-26		15
1239	Characterization of the plasma membrane proteins and receptor-like kinases associated with secondary vascular differentiation in poplar. 2011 , 76, 97-115		30
1238	High-resolution mass spectrometric analysis of the secretome from mouse lung endothelial progenitor cells. 2011 , 14, 163-72		18
1237	Survivin is released from cancer cells via exosomes. 2011 , 16, 1-12		190
1236	Identification of new enzymes potentially involved in anaerobic naphthalene degradation by the sulfate-reducing enrichment culture N47. 2011 , 193, 241-50		59
1235	Shotgun proteomic analytical approach for studying proteins adsorbed onto liposome surface. 2011 , 401, 1195-202		27
1234	Utility of gel-free, label-free shotgun proteomics approaches to investigate microorganisms. 2011 , 90, 407-16		21
1233	Analysis of active ricin and castor bean proteins in a ricin preparation, castor bean extract, and surface swabs from a public health investigation. 2011 , 209, 70-9		44
1232	Automated analysis of mouse serum peptidome using restricted access media and nanoliquid chromatography-tandem mass spectrometry. 2011 , 879, 1112-20		6
1231	Microdialysis combined with proteomics for protein identification in breast tumor microenvironment in vivo. 2010 , 4, 61-71		11
1230	Improving proteome coverage on a LTQ-Orbitrap using design of experiments. 2011 , 22, 773-83		51
1229	Mitochondrial NAD ⁺ -dependent malic enzyme from <i>Anopheles stephensi</i> : a possible novel target for malaria mosquito control. 2011 , 10, 318		7
1228	NONO and RALY proteins are required for YB-1 oxaliplatin induced resistance in colon adenocarcinoma cell lines. 2011 , 10, 145		36
1227	A guide through the computational analysis of isotope-labeled mass spectrometry-based quantitative proteomics data: an application study. 2011 , 9, 30		18

1226	Identification of azurocidin as a potential periodontitis biomarker by a proteomic analysis of gingival crevicular fluid. 2011 , 9, 42	42
1225	Correspondence between salivary proteomic pattern and clinical course in primary Sjögren syndrome and non-Hodgkin's lymphoma: a case report. 2011 , 9, 188	16
1224	Impairment of adult hippocampal neural progenitor proliferation by methamphetamine: role for nitrotyrosination. 2011 , 4, 28	36
1223	Proteomic analysis of saliva: a unique tool to distinguish primary Sjögren's syndrome from secondary Sjögren's syndrome and other sicca syndromes. 2011 , 13, R194	78
1222	A honey bee (<i>Apis mellifera</i> L.) PeptideAtlas crossing castes and tissues. 2011 , 12, 290	13
1221	A combined approach for comparative exoproteome analysis of <i>Corynebacterium pseudotuberculosis</i> . 2011 , 11, 12	45
1220	In vivo versus in vitro protein abundance analysis of <i>Shigella dysenteriae</i> type 1 reveals changes in the expression of proteins involved in virulence, stress and energy metabolism. 2011 , 11, 147	37
1219	A historical and proteomic analysis of botulinum neurotoxin type/G. 2011 , 11, 232	14
1218	Proteome and transcriptome profiles of a Her2/Neu-driven mouse model of breast cancer. 2011 , 5, 179-88	12
1217	Identification of β -microglobulin as a urinary biomarker for chronic allograft nephropathy using proteomic methods. 2011 , 5, 422-31	21
1216	Recommendations for mass spectrometry data quality metrics for open access data (corollary to the Amsterdam principles). 2011 , 5, 580-9	8
1215	Proteomic analysis of male 4C germ cell proteins involved in mouse meiosis. 2011 , 11, 298-308	17
1214	Membrane proteomic signatures of karyotypically normal and abnormal human embryonic stem cell lines and derivatives. 2011 , 11, 2515-27	17
1213	Lights and shadows of proteomic technologies for the study of protein species including isoforms, splicing variants and protein post-translational modifications. 2011 , 11, 590-603	17
1212	Discussion on common data analysis strategies used in MS-based proteomics. 2011 , 11, 604-19	27
1211	Proteomic analysis of urinary exosomes from patients of early IgA nephropathy and thin basement membrane nephropathy. 2011 , 11, 2459-75	171
1210	Mining the soluble chloroplast proteome by affinity chromatography. 2011 , 11, 1287-99	38
1209	iTRAQ-based proteomic study of the effects of microcystin-LR on medaka fish liver. 2011 , 11, 2071-8	23

1208	Less label, more free: approaches in label-free quantitative mass spectrometry. 2011 , 11, 535-53	528
1207	A cost-benefit analysis of multidimensional fractionation of affinity purification-mass spectrometry samples. 2011 , 11, 2603-12	27
1206	Simulating and validating proteomics data and search results. 2011 , 11, 1189-211	32
1205	The endosomal proteome of macrophage and dendritic cells. 2011 , 11, 854-64	26
1204	Quality control in LC-MS/MS. 2011 , 11, 1026-30	30
1203	Constructing the metabolic and regulatory pathways in germinating rice seeds through proteomic approach. 2011 , 11, 2693-713	121
1202	COMPASS: a suite of pre- and post-search proteomics software tools for OMSSA. 2011 , 11, 1064-74	133
1201	Simplified enrichment of plasma membrane proteins for proteomic analyses in <i>Arabidopsis thaliana</i> . 2011 , 11, 1780-8	39
1200	Abacus: a computational tool for extracting and pre-processing spectral count data for label-free quantitative proteomic analysis. 2011 , 11, 1340-5	76
1199	Quantification of proteins using data-independent analysis (MSE) in simple and complex samples: a systematic evaluation. 2011 , 11, 3273-87	69
1198	Reversed-phase chromatography with multiple fraction concatenation strategy for proteome profiling of human MCF10A cells. 2011 , 11, 2019-26	387
1197	DNA affects the composition of lipoplex protein corona: a proteomics approach. 2011 , 11, 3349-58	26
1196	Current methodologies for proteomics of bacterial surface-exposed and cell envelope proteins. 2011 , 11, 3169-89	64
1195	Identification of glycoproteins associated with different histological subtypes of ovarian tumors using quantitative glycoproteomics. 2011 , 11, 4677-87	32
1194	Bacterial adaptation to life in association with plants - A proteomic perspective from culture to in situ conditions. 2011 , 11, 3086-105	42
1193	Quantitative proteomics analysis of adsorbed plasma proteins classifies nanoparticles with different surface properties and size. 2011 , 11, 4569-77	112
1192	Temporal proteomic profiling of embryonic stem cell secretome during cardiac and neural differentiation. 2011 , 11, 3972-82	27
1191	Identification of novel secreted proteases during extracellular proteolysis by dermatophytes at acidic pH. 2011 , 11, 4422-33	35

1190	Identification of tyrosine nitration in UCH-L1 and GAPDH. 2011 , 32, 1692-705	11
1189	Proteomic identification of novel targets regulated by the mammalian target of rapamycin pathway during oligodendrocyte differentiation. 2011 , 59, 1754-69	52
1188	Y-box protein-1 is a transcriptional regulator of BMP7. 2011 , 112, 1130-7	5
1187	Prefractionation enhances loading capacity and identification of basic proteins from human breast cancer tissues. 2011 , 411, 80-7	5
1186	Shotgun proteomic analysis of microdissected postmortem human pituitary using complementary two-dimensional liquid chromatography coupled with tandem mass spectrometer. 2011 , 688, 183-90	12
1185	A combination method of chemical with enzyme reactions for identification of membrane proteins. 2011 , 1814, 397-404	6
1184	Subtle proteome differences identified between post-dormant vegetative and floral peach buds. 2011 , 74, 607-19	25
1183	Proteomic characterisation of Echinococcus granulosus hydatid cyst fluid from sheep, cattle and humans. 2011 , 74, 1560-72	72
1182	Quantitative plasma proteome analysis reveals aberrant level of blood coagulation-related proteins in nasopharyngeal carcinoma. 2011 , 74, 744-57	13
1181	Unraveling tobacco BY-2 protein complexes with BN PAGE/LC-MS/MS and clustering methods. 2011 , 74, 1201-17	15
1180	Recent progress in liquid chromatography-based separation and label-free quantitative plant proteomics. 2011 , 72, 963-74	65
1179	AA amyloidosis associated with hepatitis B. 2011 , 26, 2407-12	13
1178	Extracellular matrix composition and remodeling in human abdominal aortic aneurysms: a proteomics approach. 2011 , 10, M111.008128	150
1177	Liquid chromatography-mass spectrometry-based proteomics of Nitrosomonas. 2011 , 486, 465-82	17
1176	Not4 E3 ligase contributes to proteasome assembly and functional integrity in part through Ecm29. 2011 , 31, 1610-23	54
1175	Mass spectrometric-based proteomic analysis of amyloid neuropathy type in nerve tissue. 2011 , 68, 195-9	92
1174	Significant alteration of gene expression in wood decay fungi Postia placenta and Phanerochaete chrysosporium by plant species. 2011 , 77, 4499-507	96
1173	A partial set covering model for protein mixture identification using mass spectrometry data. 2011 , 8, 368-80	12

1172	Bioinformatics for Comparative Proteomics. 2011 ,	2
1171	RNAcode: robust discrimination of coding and noncoding regions in comparative sequence data. 2011 , 17, 578-94	131
1170	Comprehensive proteomic analysis of influenza virus polymerase complex reveals a novel association with mitochondrial proteins and RNA polymerase accessory factors. 2011 , 85, 8569-81	77
1169	Inhibition of lens photodamage by UV-absorbing contact lenses. 2011 , 52, 8330-41	23
1168	Mitochondrion as a novel site of dichloroacetate biotransformation by glutathione transferase zeta 1. 2011 , 336, 87-94	33
1167	Neurodegenerative and inflammatory pathway components linked to TNF- α /TNFR1 signaling in the glaucomatous human retina. 2011 , 52, 8442-54	128
1166	Physiological adaptation of the bacterium <i>Lactococcus lactis</i> in response to the production of human CFTR. 2011 , 10, M000052MCP200	11
1165	The proteomic signature of <i>Aspergillus fumigatus</i> during early development. 2011 , 10, M111.010108	27
1164	Proteomic profiling of a layered tissue reveals unique glycolytic specializations of photoreceptor cells. 2011 , 10, M110.002469	66
1163	Selective chemoprecipitation and subsequent release of tagged species for the analysis of nitropeptides by liquid chromatography-tandem mass spectrometry. 2011 , 10, M110.002923	27
1162	Identification of phosphoproteins associated with human neutrophil granules following chemotactic peptide stimulation. 2011 , 10, M110.001552	15
1161	Transcriptional profiling of the iron starvation response in <i>Bordetella pertussis</i> provides new insights into siderophore utilization and virulence gene expression. 2011 , 193, 4798-812	48
1160	The ciliopathy-associated protein homologs RPGRIP1 and RPGRIP1L are linked to cilium integrity through interaction with Nek4 serine/threonine kinase. 2011 , 20, 3592-605	50
1159	Contribution of cathepsin L to secretome composition and cleavage pattern of mouse embryonic fibroblasts. 2011 , 392, 961-71	26
1158	Recommendations for mass spectrometry data quality metrics for open access data (corollary to the Amsterdam Principles). 2011 , 10, O111.015446	18
1157	Urinary glycoprotein biomarker discovery for bladder cancer detection using LC/MS-MS and label-free quantification. 2011 , 17, 3349-59	106
1156	Proteomic analysis yields an unexpected trans-acting point in control of the human sympathochromaffin phenotype. 2011 , 4, 437-45	1
1155	An FMN hydrolase of the haloacid dehalogenase superfamily is active in plant chloroplasts. 2011 , 286, 42091-42098	14

1154	Quantitative mass spectrometry reveals dynamics of factor-inhibiting hypoxia-inducible factor-catalyzed hydroxylation. 2011 , 286, 33784-94	19
1153	Site-mapping of in vitro S-nitrosation in cardiac mitochondria: implications for cardioprotection. 2011 , 10, M110.004721	49
1152	Proteome-wide dysregulation by PRA1 depletion delineates a role of PRA1 in lipid transport and cell migration. 2011 , 10, M900641MCP200	16
1151	Protein expression regulation under oxidative stress. 2011 , 10, M111.009217	93
1150	Installation and use of LabKey Server for proteomics. 2011 , Chapter 13, Unit 13.5.	2
1149	Quantification of mRNA and protein and integration with protein turnover in a bacterium. 2011 , 7, 511	207
1148	Modularity and hormone sensitivity of the <i>Drosophila melanogaster</i> insulin receptor/target of rapamycin interaction proteome. 2011 , 7, 547	53
1147	Androgen-sensitive microsomal signaling networks coupled to the proliferation and differentiation of human prostate cancer cells. 2011 , 2, 956-78	12
1146	Proteomic analysis of a sea-ice diatom: salinity acclimation provides new insight into the dimethylsulfoniopropionate production pathway. 2011 , 157, 1926-41	47
1145	Regulation of histone H2A and H2B deubiquitination and <i>Xenopus</i> development by USP12 and USP46. 2011 , 286, 7190-201	76
1144	Phosphorylation controls a dual-function polybasic nuclear localization sequence in the adapter protein SH2B1 to regulate its cellular function and distribution. 2011 , 124, 1542-52	13
1143	Association of ActA to peptidoglycan revealed by cell wall proteomics of intracellular <i>Listeria monocytogenes</i> . 2011 , 286, 34675-89	37
1142	Profiling the <i>Aspergillus fumigatus</i> proteome in response to caspofungin. 2011 , 55, 146-54	53
1141	Proliferative glomerulonephritis secondary to dysfunction of the alternative pathway of complement. 2011 , 6, 1009-17	114
1140	Proteome coverage prediction for integrated proteomics datasets. 2011 , 18, 283-93	8
1139	Assigning spectrum-specific P-values to protein identifications by mass spectrometry. 2011 , 27, 1128-34	27
1138	Highly reproducible label free quantitative proteomic analysis of RNA polymerase complexes. 2011 , 10, M110.000687	55
1137	Hierarchical clustering of shotgun proteomics data. 2011 , 10, M110.003822	40

1136	Protein composition and function of red and white skeletal muscle mitochondria. 2011 , 300, C1280-90	47
1135	Impairment of immunoproteasome function by β i/LMP7 subunit deficiency results in severe enterovirus myocarditis. 2011 , 7, e1002233	67
1134	Proteomics analyses of the opportunistic pathogen <i>Burkholderia vietnamiensis</i> using protein fractionations and mass spectrometry. 2011 , 2011, 701928	9
1133	SH3 domain-based phototrapping in living cells reveals Rho family GAP signaling complexes. 2011 , 4, rs13	25
1132	Extracellular matrix dynamics in hepatocarcinogenesis: a comparative proteomics study of PDGFC transgenic and Pten null mouse models. 2011 , 7, e1002147	70
1131	Novel structural components of the ventral disc and lateral crest in <i>Giardia intestinalis</i> . 2011 , 5, e1442	49
1130	Proteomic analysis of excretory-secretory products of <i>Heligmosomoides polygyrus</i> assessed with next-generation sequencing transcriptomic information. 2011 , 5, e1370	70
1129	Metaproteomic characterization of dissolved organic matter in the water column of the South China Sea. 2011 , 56, 1641-1652	18
1128	Human biomarker discovery and predictive models for disease progression for idiopathic pneumonia syndrome following allogeneic stem cell transplantation. 2012 , 11, M111.015479	27
1127	Nitroxyl-mediated disulfide bond formation between cardiac myofilament cysteines enhances contractile function. 2012 , 111, 1002-11	96
1126	Context-dependent dual role of SKI8 homologs in mRNA synthesis and turnover. 2012 , 8, e1002652	24
1125	A novel Th cell epitope of <i>Candida albicans</i> mediates protection from fungal infection. 2012 , 188, 5636-43	73
1124	Differentiating inbred mouse strains from each other and those with single gene mutations using hair proteomics. 2012 , 7, e51956	20
1123	Proteomic analysis of cell walls of two developmental stages of alfalfa stems. 2012 , 3, 279	30
1122	Effect of cold acclimation on troponin I isoform expression in striated muscle of rainbow trout. 2012 , 303, R168-76	18
1121	MOPED: Model Organism Protein Expression Database. 2012 , 40, D1093-9	93
1120	Mapping the phosphoproteome of influenza A and B viruses by mass spectrometry. 2012 , 8, e1002993	95
1119	Cross-talk between calcium signalling and protein phosphorylation at the thylakoid. 2012 , 63, 1725-33	36

1118	Monocyte-to-macrophage differentiation: synthesis and secretion of a complex extracellular matrix. 2012 , 287, 14122-35	71
1117	Looking deep inside: detection of low-abundance proteins in leaf extracts of Arabidopsis and phloem exudates of pumpkin. 2012 , 159, 902-14	47
1116	Direct maximization of protein identifications from tandem mass spectra. 2012 , 11, M111.012161	24
1115	The protein expression landscape of the Arabidopsis root. 2012 , 109, 6811-8	115
1114	Viable Staphylococcus aureus quantitation using ^{15}N metabolically labeled bacteriophage amplification coupled with a multiple reaction monitoring proteomic workflow. 2012 , 11, M111.012849	19
1113	Development of a pharmaceutical hepatotoxicity biomarker panel using a discovery to targeted proteomics approach. 2012 , 11, 394-410	32
1112	Quantitative proteomics and dynamic imaging reveal that G3BP-mediated stress granule assembly is poly(ADP-ribose)-dependent following exposure to MNNG-induced DNA alkylation. 2012 , 125, 4555-66	46
1111	File formats commonly used in mass spectrometry proteomics. 2012 , 11, 1612-21	66
1110	Evidence for pH-dependent protease activity in the adeno-associated virus capsid. 2012 , 86, 11877-85	46
1109	Proteomic characterization of phagosomal membrane microdomains during phagolysosome biogenesis and evolution. 2012 , 11, 1365-77	14
1108	Interactome-wide analysis identifies end-binding protein 1 as a crucial component for the speck-like particle formation of activated absence in melanoma 2 (AIM2) inflammasomes. 2012 , 11, 1230-44	23
1107	Nanospray FAIMS fractionation provides significant increases in proteome coverage of unfractionated complex protein digests. 2012 , 11, M111.014985	41
1106	Functional proteomics establishes the interaction of SIRT7 with chromatin remodeling complexes and expands its role in regulation of RNA polymerase I transcription. 2012 , 11, 60-76	130
1105	Architecture of the trypanosome RNA editing accessory complex, MRB1. 2012 , 40, 5637-50	55
1104	Enabling computational proteomics by public and local data management systems. 2012 , 5, 266	1
1103	Uterine smooth muscle S-nitrosylproteome in pregnancy. 2012 , 81, 143-53	19
1102	Cholesterol accumulation regulates expression of macrophage proteins implicated in proteolysis and complement activation. 2012 , 32, 2910-8	12
1101	Concordant release of glycolysis proteins into the plasma preceding a diagnosis of ER+ breast cancer. 2012 , 72, 1935-42	23

1100	Linker for activation of T-cell family member2 (LAT2) a lipid raft adaptor protein for AKT signaling, is an early mediator of alkylphospholipid anti-leukemic activity. 2012 , 11, 1898-912	22
1099	Externalized glycolytic enzymes are novel, conserved, and early biomarkers of apoptosis. 2012 , 287, 10325-10343	39
1098	Changes in the chondrocyte and extracellular matrix proteome during post-natal mouse cartilage development. 2012 , 11, M111.014159	59
1097	Brainstem deficiency of the 14-3-3 regulator of serotonin synthesis: a proteomics analysis in the sudden infant death syndrome. 2012 , 11, M111.009530	26
1096	A cell surfaceome map for immunophenotyping and sorting pluripotent stem cells. 2012 , 11, 303-16	46
1095	Proteomic analysis of aneurysm healing mechanism after coil embolization: comparison of dense packing with loose packing. 2012 , 33, 1177-81	9
1094	Relationship between ATM and ribosomal protein S6 revealed by the chemical inhibition of Ser/Thr protein phosphatase type 1. 2012 , 76, 486-94	11
1093	DNA and chromatin modification networks distinguish stem cell pluripotent ground states. 2012 , 11, 1036-47	12
1092	Maintenance of gene silencing by the coordinate action of the H3K9 methyltransferase G9a/KMT1C and the H3K4 demethylase Jarid1a/KDM5A. 2012 , 109, 18845-50	72
1091	Laser microdissection and mass spectrometry-based proteomics aids the diagnosis and typing of renal amyloidosis. 2012 , 82, 226-34	137
1090	Urokinase-type plasminogen activator receptor (uPAR)-mediated regulation of WNT/ β -catenin signaling is enhanced in irradiated medulloblastoma cells. 2012 , 287, 20576-89	44
1089	Wilms tumor gene on X chromosome (WTX) inhibits degradation of NRF2 protein through competitive binding to KEAP1 protein. 2012 , 287, 6539-50	85
1088	PMCA2 via PSD-95 controls calcium signaling by α -containing nicotinic acetylcholine receptors on aspiny interneurons. 2012 , 32, 6894-905	29
1087	Disruption of proprotein convertase 1/3 (PC1/3) expression in mice causes innate immune defects and uncontrolled cytokine secretion. 2012 , 287, 14703-17	31
1086	Endoplasmic reticulum-quality control chaperones facilitate the biogenesis of Cf receptor-like proteins involved in pathogen resistance of tomato. 2012 , 159, 1819-33	52
1085	La autoantigen mediates oxidant induced de novo Nrf2 protein translation. 2012 , 11, M111.015032	31
1084	TGD1, -2, and -3 proteins involved in lipid trafficking form ATP-binding cassette (ABC) transporter with multiple substrate-binding proteins. 2012 , 287, 21406-15	69
1083	The Ph1 locus suppresses Cdk2-type activity during premeiosis and meiosis in wheat. 2012 , 24, 152-62	82

1082	Wnt antagonist SFRP1 functions as a secreted mediator of senescence. 2012 , 32, 4388-99	58
1081	Increased plasma levels of the APC-interacting protein MAPRE1, LRG1, and IGFBP2 preceding a diagnosis of colorectal cancer in women. 2012 , 5, 655-64	69
1080	Clinical proteomics: getting to the heart of the matter. 2012 , 5, 377	3
1079	Enigmatic presence of mitochondrial complex I in <i>Trypanosoma brucei</i> bloodstream forms. 2012 , 11, 183-93	38
1078	Characterization of two virulent phages of <i>Lactobacillus plantarum</i> . 2012 , 78, 8719-34	28
1077	Investigation of receptor interacting protein (RIP3)-dependent protein phosphorylation by quantitative phosphoproteomics. 2012 , 11, 1640-51	56
1076	Characterization of released polypeptides during an interferon- β -dependent antibacterial response in airway epithelial cells. 2012 , 32, 524-33	1
1075	Ubiquitination of neuronal nitric-oxide synthase in the calmodulin-binding site triggers proteasomal degradation of the protein. 2012 , 287, 42601-10	9
1074	A collapsin response mediator protein 2 isoform controls myosin II-mediated cell migration and matrix assembly by trapping ROCK II. 2012 , 32, 1788-804	19
1073	HSP90 and HSP70 proteins are essential for stabilization and activation of WASF3 metastasis-promoting protein. 2012 , 287, 10051-10059	64
1072	<i>Streptococcus pyogenes</i> in human plasma: adaptive mechanisms analyzed by mass spectrometry-based proteomics. 2012 , 287, 1415-25	33
1071	Identification and quantification of S-nitrosylation by cysteine reactive tandem mass tag switch assay. 2012 , 11, M111.013441	142
1070	Insights into the gene expression profile of uncultivable hemotrophic <i>Mycoplasma suis</i> during acute infection, obtained using proteome analysis. 2012 , 194, 1505-14	8
1069	Deep amino acid sequencing of native brain GABAA receptors using high-resolution mass spectrometry. 2012 , 11, M111.011445	49
1068	CLIPPER: an add-on to the Trans-Proteomic Pipeline for the automated analysis of TAILS N-terminomics data. 2012 , 393, 1477-83	32
1067	Quantitative proteomics profiling of the poly(ADP-ribose)-related response to genotoxic stress. 2012 , 40, 7788-805	118
1066	The mzIdentML data standard for mass spectrometry-based proteomics results. 2012 , 11, M111.014381	150
1065	The proteomic profile of circulating pentraxin 3 (PTX3) complex in sepsis demonstrates the interaction with azurocidin 1 and other components of neutrophil extracellular traps. 2012 , 11, M111.015073	44

1064	Database Searching in Mass Spectrometry Based Proteomics. 2012 , 7, 221-230	14
1063	Mining PeptideAtlas for biomarkers and therapeutics in human disease. 2012 , 18, 748-54	1
1062	Identification of proteins secreted into the medium by human lymphocytes irradiated in vitro with or without adaptive environments. 2012 , 102, 39-53	12
1061	Effects of stoichiometry and temperature perturbations on beech leaf litter decomposition, enzyme activities and protein expression. 2012 , 9, 4537-4551	43
1060	A likelihood-based scoring method for peptide identification using mass spectrometry. 2012 , 6,	3
1059	Cellular stress conditions are reflected in the protein and RNA content of endothelial cell-derived exosomes. 2012 , 1,	392
1058	Evaluation of electrophoretic protein extraction and database-driven protein identification from marine sediments. 2012 , 10, 353-366	9
1057	ECSASB2 mediates MLL degradation during hematopoietic differentiation. 2012 , 119, 1151-61	41
1056	Neurosteroid analog photolabeling of a site in the third transmembrane domain of the β subunit of the GABA(A) receptor. 2012 , 82, 408-19	63
1055	A linear programming model for protein inference problem in shotgun proteomics. 2012 , 28, 2956-62	19
1054	Proteomic profiling of the effect of metabolic acidosis on the apical membrane of the proximal convoluted tubule. 2012 , 302, F1465-77	13
1053	Naturally occurring variant of mouse apolipoprotein A-I alters the lipid and HDL association properties of the protein. 2012 , 53, 951-963	13
1052	A deep exploration of the transcriptome and "excretory/secretory" proteome of adult <i>Fascioloides magna</i> . 2012 , 11, 1340-53	26
1051	A method for large-scale identification of protein arginine methylation. 2012 , 11, 1489-99	99
1050	Integrated transcriptomic and proteomic analysis of the physiological response of <i>Escherichia coli</i> O157:H7 Sakai to steady-state conditions of cold and water activity stress. 2012 , 11, M111.009019	48
1049	Strain-level typing and identification of bacteria using mass spectrometry-based proteomics. 2012 , 11, 2710-20	39
1048	Proteomic and protein interaction network analysis of human T lymphocytes during cell-cycle entry. 2012 , 8, 573	16
1047	Proteomic characterization of the cellular response to nitrosative stress mediated by s-nitrosoglutathione reductase inhibition. 2012 , 11, 2480-91	25

1046	Yabi: An online research environment for grid, high performance and cloud computing. 2012 , 7, 1	75
1045	Proteomic approach reveals FKBP4 and S100A9 as potential prediction markers of therapeutic response to neoadjuvant chemotherapy in patients with breast cancer. 2012 , 11, 1078-88	40
1044	Inference and validation of protein identifications. 2012 , 11, 1097-104	26
1043	Developing a strong anion exchange/RP (SAX/RP) 2D LC system for high-abundance proteins depletion in human plasma. 2012 , 12, 3451-63	11
1042	A systematic analysis of a deep mouse epididymal sperm proteome. 2012 , 87, 141	31
1041	Identifying the CHO secretome using mucin-type O-linked glycosylation and click-chemistry. 2012 , 11, 6175-86	42
1040	Temporal changes in milk proteomes reveal developing milk functions. 2012 , 11, 3897-907	74
1039	Proteomic and transcriptomic profiling of Staphylococcus aureus surface LPXTG-proteins: correlation with agr genotypes and adherence phenotypes. 2012 , 11, 1123-39	32
1038	Protein inference: a review. 2012 , 13, 586-614	71
1037	Current methods for global proteome identification. 2012 , 9, 519-32	41
1036	Immunoproteomic analysis of potential serum biomarker candidates in human glaucoma. 2012 , 53, 8222-31	38
1035	In vitro MS-based proteomic analysis and absolute quantification of neuronal-glia injury biomarkers in cell culture system. 2012 , 33, 3786-97	24
1034	Proteomic analysis of ganglioside-associated membrane molecules: substantial basis for molecular clustering. 2012 , 12, 3154-63	38
1033	Autoimmunoreactive IgGs from patients with postural orthostatic tachycardia syndrome. 2012 , 6, 615-25	26
1032	An Optimized Approach for Protein Residue Extraction and Identification from Ceramics After Cooking. 2012 , 19, 407-439	13
1031	Lysine deacetylases Hda1 and Rpd3 regulate Hsp90 function thereby governing fungal drug resistance. 2012 , 2, 878-88	73
1030	Platelet proteome and clopidogrel response in patients with stable angina undergoing percutaneous coronary intervention. 2012 , 45, 758-65	18
1029	Physiological and proteomic responses to single and repeated hypoxia in juvenile Eurasian perch under domestication--clues to physiological acclimation and humoral immune modulations. 2012 , 33, 1112-22	46

1028	Proteomic profiles of soluble proteins from the esophageal gland in female <i>Meloidogyne incognita</i> . 2012 , 42, 1177-83	9
1027	Comparison and applications of label-free absolute proteome quantification methods on <i>Escherichia coli</i> . 2012 , 75, 5437-48	126
1026	Proteome signatures of inflammatory activated primary human peripheral blood mononuclear cells. 2012 , 76 Spec No., 150-62	39
1025	Antagonism of the protein kinase R pathway by the guinea pig cytomegalovirus US22-family gene gp145. 2012 , 433, 157-66	12
1024	Identification of FRAS1 as a human endometrial carcinoma-derived protein in serum of xenograft model. 2012 , 127, 406-11	4
1023	Mass spectrometry approaches to monitor protein-drug interactions. 2012 , 57, 430-40	19
1022	Proteomics reveals plastid- and periplastid-targeted proteins in the chlorarachniophyte alga <i>Bigeloviella natans</i> . 2012 , 4, 1391-406	28
1021	Diabetes-induced renal injury in rats is attenuated by suramin. 2012 , 343, 34-43	18
1020	Mass Spectrometry-Based (GeLC-MS/MS) Comparative Proteomic Analysis of Endoscopically (ePFT) Collected Pancreatic and Gastroduodenal Fluids. 2012 , 3, e14	11
1019	Method development for metaproteomic analyses of marine biofilms. <i>Analytical Chemistry</i> , 2012 , 84, 4006-13	7.8 27
1018	Spectral clustering in peptidomics studies allows homology searching and modification profiling: HomClus, a versatile tool. 2012 , 11, 2774-85	4
1017	Proteomic study of low-temperature responses in strawberry cultivars (<i>Fragaria x ananassa</i>) that differ in cold tolerance. 2012 , 159, 1787-805	75
1016	An integrated paradigm for cellulosic biorefineries: utilization of lignocellulosic biomass as self-sufficient feedstocks for fuel, food precursors and saccharolytic enzyme production. 2012 , 5, 7100	71
1015	Faster mass spectrometry-based protein inference: junction trees are more efficient than sampling and marginalization by enumeration. 2012 , 9, 809-17	13
1014	Discovery of novel glucose-regulated proteins in isolated human pancreatic islets using LC-MS/MS-based proteomics. 2012 , 11, 3520-32	48
1013	Proteomic analysis of extracellular matrix from the hepatic stellate cell line LX-2 identifies CYR61 and Wnt-5a as novel constituents of fibrotic liver. 2012 , 11, 4052-64	58
1012	Retinal proteome analysis in a mouse model of oxygen-induced retinopathy. 2012 , 11, 5186-203	21
1011	Identification of EFEMP2 as a serum biomarker for the early detection of colorectal cancer with lectin affinity capture assisted secretome analysis of cultured fresh tissues. 2012 , 11, 3281-94	44

1010	Chimeras taking shape: potential functions of proteins encoded by chimeric RNA transcripts. 2012 , 22, 1231-42	101
1009	Mass spectrometry-based identification of native cardiac Nav1.5 channel β subunit phosphorylation sites. 2012 , 11, 5994-6007	39
1008	Multidimensional identification of tissue biomarkers of gastric cancer. 2012 , 11, 3405-13	13
1007	Identification of potential mediators of retinotopic mapping: a comparative proteomic analysis of optic nerve from WT and Phr1 retinal knockout mice. 2012 , 11, 5515-26	1
1006	Re-fraction: a machine learning approach for deterministic identification of protein homologues and splice variants in large-scale MS-based proteomics. 2012 , 11, 3035-45	6
1005	Characterization of differential protein tethering at the plasma membrane in response to epidermal growth factor signaling. 2012 , 11, 3101-11	
1004	Changes in the striatal proteome of YAC128Q mice exhibit gene-environment interactions between mutant huntingtin and manganese. 2012 , 11, 1118-32	22
1003	Protein carbonylation in a murine model for early alcoholic liver disease. 2012 , 25, 1012-21	59
1002	Recommendations for mass spectrometry data quality metrics for open access data (corollary to the Amsterdam Principles). 2012 , 11, 1412-9	22
1001	Cell surface proteomics identifies glucose transporter type 1 and prion protein as candidate biomarkers for colorectal adenoma-to-carcinoma progression. 2012 , 61, 855-64	56
1000	BuildSummary: using a group-based approach to improve the sensitivity of peptide/protein identification in shotgun proteomics. 2012 , 11, 1494-502	42
999	Proteomic analysis of bronchoalveolar lavage fluid proteins from mice infected with <i>Francisella tularensis</i> ssp. <i>novicida</i> . 2012 , 11, 3690-703	7
998	Recognizing uncertainty increases robustness and reproducibility of mass spectrometry-based protein inferences. 2012 , 11, 5586-91	29
997	The problem with peptide presumption and the downfall of target-decoy false discovery rates. <i>Analytical Chemistry</i> , 2012 , 84, 9663-7	7.8 10
996	Integrated proteomic, transcriptomic, and biological network analysis of breast carcinoma reveals molecular features of tumorigenesis and clinical relapse. 2012 , 11, M111.014910	38
995	Role of cyclophilin A from brains of prion-infected mice in stimulation of cytokine release by microglia and astroglia in vitro. 2012 , 287, 4628-39	22
994	Acute sex steroid withdrawal increases cholesterol efflux capacity and HDL-associated clusterin in men. 2012 , 77, 454-60	18
993	Combined analysis of <i>Perca fluviatilis</i> reproductive performance and oocyte proteomic profile. 2012 , 78, 432-42, 442.e1-13	24

992	Proteome of melamine urinary bladder stones and implication for stone formation. 2012 , 212, 307-14	17
991	Bioinformatic challenges in targeted proteomics. 2012 , 11, 4393-402	15
990	Antibodies anti-CagA cross-react with trophoblast cells: a risk factor for pre-eclampsia?. 2012 , 17, 426-34	33
989	Comprehensive proteomic analysis of nonintegrin laminin receptor interacting proteins. 2012 , 11, 4863-72	14
988	Anti-NMDA receptor encephalitis antibody binding is dependent on amino acid identity of a small region within the GluN1 amino terminal domain. 2012 , 32, 11082-94	186
987	Structural probing of a protein phosphatase 2A network by chemical cross-linking and mass spectrometry. 2012 , 337, 1348-52	323
986	Protein expression changes in ovarian cancer during the transition from benign to malignant. 2012 , 11, 2876-89	36
985	Multiple myeloma-associated chromosomal translocation activates orphan snoRNA ACA11 to suppress oxidative stress. 2012 , 122, 2793-806	68
984	Analysis of oxygen/glucose-deprivation-induced changes in SUMO3 conjugation using SILAC-based quantitative proteomics. 2012 , 11, 1108-17	53
983	Charting the landscape of tandem BRCT domain-mediated protein interactions. 2012 , 5, rs6	74
982	Label-free protein quantitation using weighted spectral counting. 2012 , 893, 321-41	21
981	SAINT-MS1: protein-protein interaction scoring using label-free intensity data in affinity purification-mass spectrometry experiments. 2012 , 11, 2619-24	51
980	Functional proteomics establishes the interaction of SIRT7 with chromatin remodeling complexes and expands its role in regulation of RNA polymerase I transcription. 2012 , 11, M111.015156	29
979	Proteogenomic elucidation of the initial steps in the benzene degradation pathway of a novel halophile, <i>Arhodomonas</i> sp. strain Rozel, isolated from a hypersaline environment. 2012 , 78, 7309-16	30
978	Analysis of protein mixtures from whole-cell extracts by single-run nanoLC-MS/MS using ultralong gradients. 2012 , 7, 882-90	88
977	Important issues in planning a proteomics experiment: statistical considerations of quantitative proteomic data. 2012 , 893, 3-21	9
976	The interaction of the von Hippel-Lindau tumor suppressor and heterochromatin protein 1. 2012 , 518, 103-10	11
975	Comparison of three different enrichment strategies for serum low molecular weight protein identification using shotgun proteomics approach. 2012 , 740, 58-65	38

974	Malachite green toxicity assessed on Asian catfish primary cultures of peripheral blood mononuclear cells by a proteomic analysis. 2012 , 114-115, 142-52	30
973	A chemical proteomics approach to identify c-di-GMP binding proteins in <i>Pseudomonas aeruginosa</i> . 2012 , 88, 229-36	49
972	A gel-free proteomic-based method for the characterization of <i>Bordetella pertussis</i> clinical isolates. 2012 , 90, 119-33	11
971	A death effector domain chain DISC model reveals a crucial role for caspase-8 chain assembly in mediating apoptotic cell death. 2012 , 47, 291-305	237
970	A proteome reference map and virulence factors analysis of <i>Yersinia pestis</i> 91001. 2012 , 75, 894-907	17
969	The effect of selenium enrichment on baker's yeast proteome. 2012 , 75, 1018-30	14
968	Investigation of local primary structure effects on peroxynitrite-mediated tyrosine nitration using targeted mass spectrometry. 2012 , 75, 1691-700	12
967	Evidence for a new post-translational modification in <i>Staphylococcus aureus</i> : hydroxymethylation of asparagine and glutamine. 2012 , 75, 1742-51	6
966	Do plasma proteins distinguish between liposomes of varying charge density?. 2012 , 75, 1924-32	57
965	Proteomic analysis of secreted saliva from Russian wheat aphid (<i>Diuraphis noxia</i> Kurd.) biotypes that differ in virulence to wheat. 2012 , 75, 2252-68	114
964	MALDI imaging mass spectrometry reveals COX7A2, TAGLN2 and S100-A10 as novel prognostic markers in Barrett's adenocarcinoma. 2012 , 75, 4693-704	83
963	Targeted proteome investigation via selected reaction monitoring mass spectrometry. 2012 , 75, 3495-513	52
962	SIR: Deterministic protein inference from peptides assigned to MS data. 2012 , 75, 4176-83	19
961	The HDL proteome in acute coronary syndromes shifts to an inflammatory profile. 2012 , 1821, 405-15	135
960	Cloning, expression, and characterization of a cellobiose dehydrogenase from <i>Thielavia terrestris</i> induced under cellulose growth conditions. 2012 , 1824, 802-12	20
959	The sclerostin-bone protein interactome. 2012 , 417, 830-5	29
958	The ferroimmunomodulatory role of ectopic endometriotic stromal cells in ovarian endometriosis. 2012 , 98, 415-22.e1-12	23
957	Proteomics reveals a switch in CDK1-associated proteins upon M-phase exit during the <i>Xenopus laevis</i> oocyte to embryo transition. 2012 , 44, 53-64	10

956	Enhanced secretion of TIMP-1 by human hypertrophic scar keratinocytes could contribute to fibrosis. 2012 , 38, 421-7	47
955	A hydrophilic immobilized trypsin reactor with N-vinyl-2-pyrrolidinone modified polymer microparticles as matrix for highly efficient protein digestion with low peptide residue. 2012 , 1246, 111-6	21
954	Structure and characteristics of acid and pepsin-solubilized collagens from the skin of cobia (<i>Rachycentron canadum</i>). 2012 , 135, 1975-84	38
953	Identifying and tracking proteins through the marine water column: insights into the inputs and preservation mechanisms of protein in sediments. 2012 , 83, 324-359	33
952	Quantitative proteomic profiling identifies protein correlates to EGFR kinase inhibition. 2012 , 11, 1071-81	6
951	Identifying new therapeutic targets via modulation of protein corona formation by engineered nanoparticles. 2012 , 7, e33650	76
950	Human and rat brain lipofuscin proteome. 2012 , 12, 2445-54	33
949	A Bovine PeptideAtlas of milk and mammary gland proteomes. 2012 , 12, 2895-9	34
948	Protein profiling of epidermal bladder cells from the halophyte <i>Mesembryanthemum crystallinum</i> . 2012 , 12, 2862-5	32
947	Pairwise protein expression classifier for candidate biomarker discovery for early detection of human disease prognosis. 2012 , 13, 191	3
946	PAalyzer: a software tool for protein inference in shotgun proteomics. 2012 , 13, 288	25
945	Metaprotein expression modeling for label-free quantitative proteomics. 2012 , 13, 74	9
944	Development stage-specific proteomic profiling uncovers small, lineage specific proteins most abundant in the <i>Aspergillus Fumigatus</i> conidial proteome. 2012 , 10, 30	47
943	A comparison of E15.5 fetus and newborn rat serum proteomes. 2012 , 10, 64	2
942	The cerebrospinal fluid proteome in HIV infection: change associated with disease severity. 2012 , 9, 3	24
941	Plasma proteomics shows an elevation of the anti-inflammatory protein APOA-IV in chronic equine laminitis. 2012 , 8, 179	13
940	A systems biology approach reveals common metastatic pathways in osteosarcoma. 2012 , 6, 50	42
939	First analysis of the secretome of the canine heartworm, <i>Dirofilaria immitis</i> . 2012 , 5, 140	36

938	Experimental tools for the study of protein phosphorylation in Plasmodium. 2013 , 923, 241-57	4
937	Mass Spectrometry-Based Methods to Investigate Posttranslational Protein Modifications by Lipid Peroxidation Products. 2012 , 23-40	
936	UV-sensitive syndrome protein UVSSA recruits USP7 to regulate transcription-coupled repair. 2012 , 44, 598-602	165
935	Peptide reranking with protein-peptide correspondence and precursor peak intensity information. 2012 , 9, 1212-9	1
934	Identifying novel protein complexes in cancer cells using epitope-tagging of endogenous human genes and affinity-purification mass spectrometry. 2012 , 11, 5630-41	18
933	Coordinated regulation of transcription factor Bcl11b activity in thymocytes by the mitogen-activated protein kinase (MAPK) pathways and protein sumoylation. 2012 , 287, 26971-88	38
932	The proteomics of feather development in pied flycatchers (<i>Ficedula hypoleuca</i>) with different plumage coloration. 2012 , 21, 5762-77	11
931	Discrimination of differentially inhibited cysteine proteases by activity-based profiling using cystatin variants with tailored specificities. 2012 , 11, 5983-93	23
930	Analysis of membrane-enriched and high molecular weight proteins in <i>Leishmania infantum</i> promastigotes and axenic amastigotes. 2012 , 11, 3974-85	18
929	Proteomics of mouse BRCA1-deficient mammary tumors identifies DNA repair proteins with potential diagnostic and prognostic value in human breast cancer. 2012 , 11, M111.013334	21
928	The nucleotide synthesis enzyme CAD inhibits NOD2 antibacterial function in human intestinal epithelial cells. 2012 , 142, 1483-92.e6	24
927	Specific non-peroxide antibacterial effect of manuka honey on the <i>Staphylococcus aureus</i> proteome. 2012 , 40, 43-50	46
926	Pericellular proteins of the developing mouse tendon: a proteomic analysis. 2012 , 53, 2-13	24
925	Using ProHits to store, annotate, and analyze affinity purification-mass spectrometry (AP-MS) data. 2012 , Chapter 8, Unit8.16	17
924	Search and decoy: the automatic identification of mass spectra. 2012 , 893, 445-88	8
923	Cell surface capturing technologies for the surfaceome discovery of hepatocytes. 2012 , 909, 1-16	18
922	iTRAQ Proteomics Profiling of Regulatory Proteins During Oligodendrocyte Differentiation. 2012 , 119-138	
921	Current challenges in software solutions for mass spectrometry-based quantitative proteomics. 2012 , 43, 1087-108	87

920	Mass spectrometry (LC-MS/MS) identified proteomic biosignatures of breast cancer in proximal fluid. 2012 , 11, 5034-45	36
919	C3 glomerulonephritis: clinicopathological findings, complement abnormalities, glomerular proteomic profile, treatment, and follow-up. 2012 , 82, 465-73	215
918	Medullary amyloidosis associated with apolipoprotein A-IV deposition. 2012 , 81, 201-6	42
917	Psychiatric Disorders. 2012 ,	3
916	Quantitative Methods in Proteomics. 2012 ,	7
915	Key issues in the acquisition and analysis of qualitative and quantitative mass spectrometry data for peptide-centric proteomic experiments. 2012 , 43, 1075-85	12
914	Proximal fluid proteome profiling of mouse colon tumors reveals biomarkers for early diagnosis of human colorectal cancer. 2012 , 18, 2613-24	39
913	A critical appraisal of techniques, software packages, and standards for quantitative proteomic analysis. 2012 , 16, 431-42	46
912	Proteomic analysis of differences in ectoderm and mesoderm membranes by DiGE. 2012 , 11, 4575-93	4
911	Metaproteogenomic analysis of microbial communities in the phyllosphere and rhizosphere of rice. 2012 , 6, 1378-90	458
910	Proteomic characterization of histotroph during the preimplantation phase of the estrous cycle in cattle. 2012 , 11, 3004-18	41
909	Proteomic analysis of the aqueous humor in age-related macular degeneration (AMD) patients. 2012 , 11, 4034-43	45
908	Defining the boundaries and characterizing the landscape of functional genome expression in vascular tissues of Populus using shotgun proteomics. 2012 , 11, 449-60	31
907	Refining comparative proteomics by spectral counting to account for shared peptides and multiple search engines. 2012 , 404, 1115-25	6
906	Neisseria meningitidis. 2012 ,	
905	A cross-validation scheme for machine learning algorithms in shotgun proteomics. 2012 , 13 Suppl 16, S3	22
904	Computational approaches to protein inference in shotgun proteomics. 2012 , 13 Suppl 16, S4	36
903	A statistical model-building perspective to identification of MS/MS spectra with PeptideProphet. 2012 , 13 Suppl 16, S1	64

902	The protein interaction network of a taxis signal transduction system in a halophilic archaeon. 2012 , 12, 272	32
901	A feedback framework for protein inference with peptides identified from tandem mass spectra. 2012 , 10, 68	4
900	Glycoprotein profiles of human breast cells demonstrate a clear clustering of normal/benign versus malignant cell lines and basal versus luminal cell lines. 2012 , 11, 656-67	25
899	Proteomic approach used in the diagnosis of Riedel's thyroiditis: a case report. 2012 , 6, 103	1
898	Comprehensive assessment of milk composition in transgenic cloned cattle. 2012 , 7, e49697	14
897	Computational and statistical analysis of protein mass spectrometry data. 2012 , 8, e1002296	48
896	Accelerated identification of proteins by mass spectrometry by employing covalent pre-gel staining with Uniblue A. 2012 , 7, e31438	7
895	Unique proteomic signatures distinguish macrophages and dendritic cells. 2012 , 7, e33297	76
894	A fragment of the LG3 peptide of endorepellin is present in the urine of physically active mining workers: a potential marker of physical activity. 2012 , 7, e33714	14
893	Comparative proteomic analysis of <i>Aedes aegypti</i> larval midgut after intoxication with Cry11Aa toxin from <i>Bacillus thuringiensis</i> . 2012 , 7, e37034	42
892	Peptide array X-linking (PAX): a new peptide-protein identification approach. 2012 , 7, e37035	14
891	Extensive gene-specific translational reprogramming in a model of B cell differentiation and Abl-dependent transformation. 2012 , 7, e37108	6
890	Differences in immunoglobulin light chain species found in urinary exosomes in light chain amyloidosis (AL). 2012 , 7, e38061	29
889	Molecular characterization of podoviral bacteriophages virulent for <i>Clostridium perfringens</i> and their comparison with members of the Picovirinae. 2012 , 7, e38283	27
888	Warburg effect's manifestation in aggressive pheochromocytomas and paragangliomas: insights from a mouse cell model applied to human tumor tissue. 2012 , 7, e40949	27
887	Transcriptome and proteome dynamics of a light-dark synchronized bacterial cell cycle. 2012 , 7, e43432	105
886	Characterization of a distinct population of circulating human non-adherent endothelial forming cells and their recruitment via intercellular adhesion molecule-3. 2012 , 7, e46996	19
885	Quantitative proteomic analysis of Niemann-Pick disease, type C1 cerebellum identifies protein biomarkers and provides pathological insight. 2012 , 7, e47845	51

884	Improved flow cytometric assessment reveals distinct microvesicle (cell-derived microparticle) signatures in joint diseases. 2012 , 7, e49726	111
883	Integrative proteomics and tissue microarray profiling indicate the association between overexpressed serum proteins and non-small cell lung cancer. 2012 , 7, e51748	46
882	Cyclin-dependent kinase 6 phosphorylates NF- κ B P65 at serine 536 and contributes to the regulation of inflammatory gene expression. 2012 , 7, e51847	53
881	Effects of resource chemistry on the composition and function of stream hyporheic biofilms. 2012 , 3, 35	12
880	The phn Island: A New Genomic Island Encoding Catabolism of Polynuclear Aromatic Hydrocarbons. 2012 , 3, 125	36
879	An astrocyte-specific proteomic approach to inflammatory responses in experimental rat glaucoma. 2012 , 53, 4220-33	71
878	Proteomic Analysis of Wnt-Dependent Dishevelled-Based Supermolecular Complexes. 2012 ,	
877	Evolutionary Proteomics: Empowering Tandem Mass Spectrometry and Bioinformatics Tools for the Study of Evolution. 2012 ,	
876	Identification of Potential Glycoprotein Biomarkers in Estrogen Receptor Positive (ER+) and Negative (ER-) Human Breast Cancer Tissues by LC-LTQ/FT-ICR Mass Spectrometry. 2012 , 3, 269-84	14
875	Sulfur-36S stable isotope labeling of amino acids for quantification (SULAQ). 2012 , 12, 37-42	18
874	Proteomic analysis of the androgen receptor via MS-compatible purification of biotinylated protein on streptavidin resin. 2012 , 12, 43-53	5
873	Recommendations for mass spectrometry data quality metrics for open access data (corollary to the Amsterdam principles). 2012 , 12, 11-20	13
872	Mass spectrometry-based proteomics: qualitative identification to activity-based protein profiling. 2012 , 4, 141-62	10
871	Proteomic analysis of the microenvironment of developing oocytes. 2012 , 12, 1463-71	41
870	The current state of microbial proteomics: where we are and where we want to go. 2012 , 12, 638-50	16
869	Proteomic analysis of Taenia solium metacestode excretion-secretion proteins. 2012 , 12, 1860-9	37
868	Cell surface proteome of the marine planctomycete Rhodopirellula baltica. 2012 , 12, 1781-91	12
867	Search engine processor: Filtering and organizing peptide spectrum matches. 2012 , 12, 944-9	82

866	Deciphering the proteome of the in vivo diagnostic reagent "purified protein derivative" from <i>Mycobacterium tuberculosis</i> . 2012 , 12, 979-91	37
865	Generic comparison of protein inference engines. 2012 , 11, O110.007088	18
864	Substrate-controlled succession of marine bacterioplankton populations induced by a phytoplankton bloom. 2012 , 336, 608-11	846
863	Comprehensive description of the N-glycoproteome of mouse pancreatic β cells and human islets. 2012 , 11, 1598-608	27
862	TOPPAS: a graphical workflow editor for the analysis of high-throughput proteomics data. 2012 , 11, 3914-20	43
861	Analysis of the tau-associated proteome reveals that exchange of Hsp70 for Hsp90 is involved in tau degradation. 2012 , 7, 1677-86	53
860	Dynamin 2 mutations in Charcot-Marie-Tooth neuropathy highlight the importance of clathrin-mediated endocytosis in myelination. 2012 , 135, 1395-411	44
859	A neurosteroid analogue photolabeling reagent labels the colchicine-binding site on tubulin: a mass spectrometric analysis. 2012 , 33, 666-74	12
858	Comparative analysis of different label-free mass spectrometry based protein abundance estimates and their correlation with RNA-Seq gene expression data. 2012 , 11, 2261-71	108
857	Fibulin-5 binds urokinase-type plasminogen activator and mediates urokinase-stimulated α 5 β 1-integrin-dependent cell migration. 2012 , 443, 491-503	22
856	Computational framework for analysis of prey-prey associations in interaction proteomics identifies novel human protein-protein interactions and networks. 2012 , 11, 4476-87	3
855	Mitochondrial ROMK channel is a molecular component of mitoK(ATP). 2012 , 111, 446-54	152
854	Proteomic profiling following immunoaffinity capture of high-density lipoprotein: association of acute-phase proteins and complement factors with proinflammatory high-density lipoprotein in rheumatoid arthritis. 2012 , 64, 1828-37	112
853	Automated workflow for large-scale selected reaction monitoring experiments. 2012 , 11, 1644-53	20
852	Regulator of G-protein signaling 18 integrates activating and inhibitory signaling in platelets. 2012 , 119, 3799-807	48
851	Tissue proteomics by one-dimensional gel electrophoresis combined with label-free protein quantification. 2012 , 11, 3680-9	29
850	The small G protein Arl1 directs the trans-Golgi-specific targeting of the Arf1 exchange factors BIG1 and BIG2. 2012 , 196, 327-35	48
849	Phosphoproteomic analysis: an emerging role in deciphering cellular signaling in human embryonic stem cells and their differentiated derivatives. 2012 , 8, 16-31	9

848	Fish peripheral blood mononuclear cells preparation for future monitoring applications. 2012 , 426, 153-65	24
847	Proteomic analysis of rat skeletal muscle submitted to one bout of incremental exercise. 2012 , 22, 207-16	12
846	Displacement chromatography as first separating step in online two-dimensional liquid chromatography coupled to mass spectrometry analysis of a complex protein sample--the proteome of neutrophils. 2012 , 1232, 288-94	10
845	The proteome of the locus ceruleus in Parkinson's disease: relevance to pathogenesis. 2012 , 22, 485-98	37
844	Bovine milk exosome proteome. 2012 , 75, 1486-92	160
843	Optimized nLC-MS workflow for laser capture microdissected breast cancer tissue. 2012 , 75, 2844-54	39
842	Proteomic analysis of blood cells in fish exposed to chemotherapeutics: evidence for long term effects. 2012 , 75, 2454-67	9
841	Proteomic analysis provides new insight into the chicken eggshell cuticle. 2012 , 75, 2697-706	81
840	Soil metaproteomics - Comparative evaluation of protein extraction protocols. 2012 , 54, 14-24	126
839	Correspondence between two minor Glu-A3 genes of durum wheat and their encoded polypeptides by using a proteomic approach. 2012 , 55, 385-391	3
838	A quantitative proteomic approach for detecting protein profiles of activated human myeloid dendritic cells. 2012 , 375, 39-45	15
837	Role of a reducing environment in disassembly of the herpesvirus tegument. 2012 , 431, 71-9	16
836	Peptide fingerprinting of folate-responsive proteins in human B lymphoblasts and orofacial clefting. 2012 , 42, 738-50	
835	Assembly of the Yersinia injectisome: the missing pieces. 2012 , 85, 878-92	45
834	Involvement of Plasmodium falciparum protein kinase CK2 in the chromatin assembly pathway. 2012 , 10, 5	25
833	Post-transcriptional regulation of mu-opioid receptor: role of the RNA-binding proteins heterogeneous nuclear ribonucleoprotein H1 and F. 2012 , 69, 599-610	15
832	Myocardial infarction in mice alters sarcomeric function via post-translational protein modification. 2012 , 363, 203-15	59
831	Existing bioinformatics tools for the quantitation of post-translational modifications. 2012 , 42, 129-38	11

830	Whole gel processing procedure for GeLC-MS/MS based proteomics. 2013 , 11, 17	59
829	The BET protein FSH functionally interacts with ASH1 to orchestrate global gene activity in <i>Drosophila</i> . 2013 , 14, R18	22
828	Bovine milk proteome: quantitative changes in normal milk exosomes, milk fat globule membranes and whey proteomes resulting from <i>Staphylococcus aureus</i> mastitis. 2013 , 82, 141-54	129
827	Use of expressed sequence tags as an alternative approach for the identification of <i>Taenia solium</i> metacestode excretion/secretion proteins. 2013 , 6, 224	4
826	Purification of native HBHA from <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> . 2013 , 6, 55	8
825	Encyclopedia of Systems Biology. 2013 , 1621-1624	1
824	Honey protein extraction and determination by mass spectrometry. 2013 , 405, 3063-74	29
823	The CRAPome: a contaminant repository for affinity purification-mass spectrometry data. 2013 , 10, 730-6	894
822	Proteomic characterization of larval and adult developmental stages in <i>Echinococcus granulosus</i> reveals novel insight into host-parasite interactions. 2013 , 84, 158-75	68
821	Protein expression profiles of human lymph and plasma mapped by 2D-DIGE and 1D SDS-PAGE coupled with nanoLC-ESI-MS/MS bottom-up proteomics. 2013 , 78, 172-87	53
820	Proteomic analysis of nuclei dissected from fixed rat brain tissue using expression microdissection. <i>Analytical Chemistry</i> , 2013 , 85, 7139-45	7.8 9
819	Variant high-molecular-weight glutenin subunits arising from biolistic transformation of wheat. 2013 , 57, 496-503	8
818	Biochemical and biological characterization of exosomes containing prominin-1/CD133. 2013 , 12, 62	83
817	Vascular Proteomics. 2013 ,	
816	Proteomic profiling of the mitochondrial inner membrane of rat renal proximal convoluted tubules. 2013 , 13, 2495-9	4
815	Proteomics of <i>Pyrococcus furiosus</i> (Pfu): Identification of Extracted Proteins by Three Independent Methods. 2013 , 12, 763-70	16
814	Developmental analysis and influence of genetic background on the Lhx3 W227ter mouse model of combined pituitary hormone deficiency disease. 2013 , 154, 738-48	7
813	Proteomic characterization and cross species comparison of mammalian seminal plasma. 2013 , 91, 13-22	104

812	Surface charge of polymer coated SPIONs influences the serum protein adsorption, colloidal stability and subsequent cell interaction in vitro. 2013 , 5, 3723-32		113
811	Genomewide analysis of polysaccharides degrading enzymes in 11 white- and brown-rot Polyporales provides insight into mechanisms of wood decay. 2013 , 105, 1412-27		91
810	Optimal precursor ion selection for LC-MALDI MS/MS. 2013 , 14, 56		5
809	Comparative proteomics study on liver mitochondria of primary biliary cirrhosis mouse model. 2013 , 13, 64		5
808	Quantification-based mass spectrometry imaging of proteins by parafilm assisted microdissection. <i>Analytical Chemistry</i> , 2013 , 85, 8127-34	7.8	29
807	Proteomic analysis of the NOS2 interactome in human airway epithelial cells. 2013 , 34, 37-46		20
806	Differential protein expression in perfusates from metastasized rat livers. 2013 , 11, 37		6
805	Proteomics in Foods. 2013 ,		8
804	Gel-free proteomics reveal potential biomarkers of priming-induced salt tolerance in durum wheat. 2013 , 91, 486-99		51
803	Cytochrome P4502S1: a novel monocyte/macrophage fatty acid epoxygenase in human atherosclerotic plaques. 2013 , 108, 319		33
802	ANKS6 is a central component of a nephronophthisis module linking NEK8 to INVS and NPHP3. 2013 , 45, 951-6		144
801	Identification of differentially expressed proteins by treatment with PUGNAc in 3T3-L1 adipocytes through analysis of ATP-binding proteome. 2013 , 13, 2998-3012		11
800	Ribosome biogenesis requires a highly diverged XRN family 5'->3' exoribonuclease for rRNA processing in <i>Trypanosoma brucei</i> . 2013 , 19, 1419-31		15
799	Proteomic characterization of human platelet-derived microparticles. 2013 , 776, 57-63		37
798	Trauma-associated human neutrophil alterations revealed by comparative proteomics profiling. 2013 , 7, 571-83		16
797	Urine haptoglobin levels predict early renal functional decline in patients with type 2 diabetes. 2013 , 83, 1136-43		46
796	ProteinLasso: A Lasso regression approach to protein inference problem in shotgun proteomics. 2013 , 43, 46-54		18
795	Proteomics screen to reveal molecular changes mediated by C722G missense mutation in CHRM2 gene. 2013 , 89, 39-50		5

794	Cryptococcus neoformans promotes its transmigration into the central nervous system by inducing molecular and cellular changes in brain endothelial cells. 2013 , 81, 3139-47		45
793	Simple, miniaturized blood plasma extraction method. <i>Analytical Chemistry</i> , 2013 , 85, 11501-8	7.8	75
792	Reconstructing targetable pathways in lung cancer by integrating diverse omics data. 2013 , 4, 2617		54
791	Detection of the Wolbachia protein WPIP0282 in mosquito spermathecae: implications for cytoplasmic incompatibility. 2013 , 43, 867-78		77
790	Cytosolic proteins lose solubility as amyloid deposits in a transgenic mouse model of Alzheimer-type amyloidosis. 2013 , 22, 2765-74		34
789	Dimethyl fumarate regulates histone deacetylase expression in astrocytes. 2013 , 263, 13-9		31
788	Myosin 3A kinase activity is regulated by phosphorylation of the kinase domain activation loop. 2013 , 288, 37126-37		23
787	Filamentous fungal-specific septin AspE is phosphorylated in vivo and interacts with actin, tubulin and other septins in the human pathogen <i>Aspergillus fumigatus</i> . 2013 , 431, 547-53		17
786	Involvement of reactive oxygen species in a feed-forward mechanism of Na/K-ATPase-mediated signaling transduction. 2013 , 288, 34249-34258		65
785	Chicken corneocyte cross-linked proteome. 2013 , 12, 771-6		23
784	Analysis of mass spectrometry data from the secretome of an explant model of articular cartilage exposed to pro-inflammatory and anti-inflammatory stimuli using machine learning. 2013 , 14, 349		17
783	Proteomic analysis of Girdin-interacting proteins in migrating new neurons in the postnatal mouse brain. 2013 , 442, 16-21		3
782	Identification of potential bladder cancer markers in urine by abundant-protein depletion coupled with quantitative proteomics. 2013 , 85, 28-43		80
781	Insulin-like growth factor binding proteins 4 and 7 released by senescent cells promote premature senescence in mesenchymal stem cells. 2013 , 4, e911		114
780	Identification, prioritization, and evaluation of glycoproteins for aggressive prostate cancer using quantitative glycoproteomics and antibody-based assays on tissue specimens. 2013 , 13, 2268-77		36
779	Changes in male rat urinary protein profile during puberty: a pilot study. 2013 , 6, 232		10
778	HOXC9 directly regulates distinct sets of genes to coordinate diverse cellular processes during neuronal differentiation. 2013 , 14, 830		19
777	High-fat diet alters protein composition of detergent-resistant membrane microdomains. 2013 , 354, 771-81		12

776	Molecular cloning, overexpression, and an efficient one-step purification of $\beta 1$ integrin. 2013 , 92, 21-8	2
775	Maspin is a marker for early recurrence in primary stage III and IV colorectal cancer. 2013 , 109, 1636-47	29
774	A propofol binding site on mammalian GABAA receptors identified by photolabeling. 2013 , 9, 715-20	168
773	Glucocorticoids and histone deacetylase inhibitors cooperate to block the invasiveness of basal-like breast cancer cells through novel mechanisms. 2013 , 32, 1316-29	60
772	Plasticity in the proteome of <i>Emiliana huxleyi</i> CCMP 1516 to extremes of light is highly targeted. 2013 , 200, 61-73	33
771	Proteomic identification of <i>Listeria monocytogenes</i> surface-associated proteins. 2013 , 13, 3040-5	11
770	Proteome analysis of functionally differentiated bovine (<i>Bos indicus</i>) mammary epithelial cells isolated from milk. 2013 , 13, 3189-204	21
769	Myofibroblasts are important contributors to human hepatocellular carcinoma: evidence for tumor promotion by proteome profiling. 2013 , 34, 3315-25	17
768	O-linked protein glycosylation in <i>Mycoplasma</i> . 2013 , 90, 1046-53	9
767	A global <i>S. cerevisiae</i> small ubiquitin-related modifier (SUMO) system interactome. 2013 , 9, 668	35
766	Combining results of multiple search engines in proteomics. 2013 , 12, 2383-93	126
765	Cardiac myocyte exosomes: stability, HSP60, and proteomics. 2013 , 304, H954-65	158
764	Identification of the components of a glycolytic enzyme metabolon on the human red blood cell membrane. 2013 , 288, 848-58	76
763	Glycobioinformatics: current strategies and tools for data mining in MS-based glycoproteomics. 2013 , 13, 341-54	30
762	Label-free quantitative analysis for studying the interactions between nanoparticles and plasma proteins. 2013 , 405, 635-45	25
761	Proteomic analysis of <i>Trypanosoma cruzi</i> secretome: characterization of two populations of extracellular vesicles and soluble proteins. 2013 , 12, 883-97	167
760	Protein-protein interactions between the bilirubin-conjugating UDP-glucuronosyltransferase UGT1A1 and its shorter isoform 2 regulatory partner derived from alternative splicing. 2013 , 450, 107-14	5
759	In vivo effects of <i>Escherichia coli</i> lipopolysaccharide on regulation of immune response and protein expression in striped catfish (<i>Pangasianodon hypophthalmus</i>). 2013 , 34, 339-47	46

758	Autoantibody signatures involving glycolysis and spliceosome proteins precede a diagnosis of breast cancer among postmenopausal women. 2013 , 73, 1502-13	48
757	Hydrophilic strong anion exchange (hSAX) chromatography for highly orthogonal peptide separation of complex proteomes. 2013 , 12, 2449-57	53
756	Proteomic analysis of an unculturable bacterial endosymbiont (<i>Blochmannia</i>) reveals high abundance of chaperonins and biosynthetic enzymes. 2013 , 12, 704-18	28
755	Comparison of nanotube-protein corona composition in cell culture media. 2013 , 9, 2171-81	109
754	GenomewidePDB, a proteomic database exploring the comprehensive protein parts list and transcriptome landscape in human chromosomes. 2013 , 12, 106-11	20
753	Integrative proteomic and microRNA analysis of primary human coronary artery endothelial cells exposed to low-dose gamma radiation. 2013 , 52, 87-98	30
752	Proteomic analysis of the <i>Cyanophora paradoxa</i> muroplast provides clues on early events in plastid endosymbiosis. 2013 , 237, 637-51	30
751	CsrA-controlled proteins reveal new dimensions of <i>Acinetobacter baumannii</i> desiccation tolerance.	
750	The parasite-derived peptide FhHDM-1 activates the PI3K/Akt pathway to prevent cytokine-induced apoptosis of T cells. 2021 , 99, 1605-1621	3
749	Oleuropein Activates Neonatal Neocortical Proteasomes, but Proteasome Gene Targeting by AAV9 Is Variable in a Clinically Relevant Piglet Model of Brain Hypoxia-Ischemia and Hypothermia. 2021 , 10,	
748	CcrZ is a pneumococcal spatiotemporal cell cycle regulator that interacts with FtsZ and controls DNA replication by modulating the activity of DnaA. 2021 , 6, 1175-1187	9
747	Pancreatic ductal adenocarcinoma cells employ integrin $\alpha 4$ to form hemidesmosomes and regulate cell proliferation.	
746	Biopharmaceutical quality control with mass spectrometry. 2021 , 13, 1275-1291	2
745	Evidence for a "rap-and-flip" mechanism in a proton-dependent lipid transporter.	
744	ZNF768 links oncogenic RAS to cellular senescence. 2021 , 12, 4841	2
743	Soil Metaproteomics as a Tool for Environmental Monitoring of Minelands. 2021 , 12, 1158	1
742	Proteogenomic characterization of pancreatic ductal adenocarcinoma. 2021 , 184, 5031-5052.e26	26
741	Multi-modal profiling of the extracellular matrix of human fallopian tubes and serous tubal Intraepithelial carcinomas.	

740	A Streamlined Data Analysis Pipeline for the Identification of Sites of Citrullination. 2021 , 60, 2902-2914	2
739	Evidence for a nuclear role for Dlg as a regulator of the NURF complex. 2021 , 32, ar23	2
738	Proteomics-Based Retinal Target Engagement Analysis and Retina-Targeted Delivery of ¹⁷ Estradiol by the DHED Prodrug for Ocular Neurotherapy in Males. 2021 , 13,	0
737	Proteogenomics: an analysis of how and when it enhances proteomics.	
736	ATP-binding cassette transporters mediate differential biosynthesis of glycosphingolipid species. 2021 , 100128	3
735	Polycomb group protein CBX7 represses cardiomyocyte proliferation via modulation of the TARDBP/Rbm38 axis.	
734	DNA-PKcs kinase activity stabilizes the transcription factor Egr1 in activated immune cells. 2021 , 297, 101209	1
733	APOBEC3C, a nucleolar protein induced by genotoxins, is excluded from DNA damage sites. 2021 ,	0
732	Identification of Actin Filament-Associated Proteins in Giardia lamblia. 2021 , 9, e0055821	4
731	Defining the Tumor Microenvironment by Integration of Immunohistochemistry and Extracellular Matrix Targeted Imaging Mass Spectrometry. 2021 , 13,	2
730	IPMK physically binds to the SWI/SNF complex and modulates BRG1 occupancy.	
729	Properties of an acid-tolerant, persistent Cheddar cheese isolate, Lacticaseibacillus paracasei GCRL163. 2021 ,	
728	Surfaceome Profiling of Rhabdomyosarcoma Reveals B7-H3 as a Mediator of Immune Evasion. 2021 , 13,	3
727	Deep learning for peptide identification from metaproteomics datasets. 2021 , 247, 104316	1
726	Proteomics: Concepts and applications in human medicine. 2021 , 12, 57-69	4
725	Integrated transcriptomics and proteomics revealed the distinct toxicological effects of multi-metal contamination on oysters. 2021 , 284, 117533	1
724	Deletion of mFICD AMPylase alters cytokine secretion and affects visual short-term learning in vivo. 2021 , 297, 100991	0
723	A Sodium-Translocating Module Linking Succinate Production to Formation of Membrane Potential in Prevotella bryantii. 2021 , 87, e0121121	3

722	Elamipretide (SS-31) treatment attenuates age-associated post-translational modifications of heart proteins. 2021 , 43, 2395-2412	1
721	Ancient role of sulfakinin/cholecystokinin-type signalling in inhibitory regulation of feeding processes revealed in an echinoderm. 2021 , 10,	3
720	Small-molecule suppression of calpastatin degradation reduces neuropathology in models of Huntington's disease. 2021 , 12, 5305	5
719	Deciphering ploidal levels of <i>Lippia alba</i> by using proteomics. 2021 , 167, 385-389	0
718	Interaction of epigallocatechin-gallate and chlorhexidine with <i>Streptococcus mutans</i> stimulated odontoblast-like cells: Cytotoxicity, Interleukin-1 β and co-species proteomic analyses. 2021 , 131, 105268	2
717	Can we put Humpty Dumpty back together again? What does protein quantification mean in bottom-up proteomics?	
716	Qualitative and Quantitative Shotgun Proteomics Data Analysis from Data-Dependent Acquisition Mass Spectrometry. 2021 , 2259, 297-308	3
715	EBF1 drives hallmark B cell gene expression by enabling the interaction of PAX5 with the MLL H3K4 methyltransferase complex. 2021 , 11, 1537	1
714	. 2021 , 69, 1811-1827	1
713	Tandem Affinity Purification (TAP) of Low-Abundance Protein Complexes in Filamentous Fungi Demonstrated Using <i>Magnaporthe oryzae</i> . 2021 , 2356, 97-108	
712	Analysing the mechanism of mitochondrial oxidation-induced cell death using a multifunctional iridium(III) photosensitiser. 2021 , 12, 26	11
711	Atomic structures of respiratory complex III, complex IV, and supercomplex III-IV from vascular plants. 2021 , 10,	42
710	Ancient proteins provide evidence of dairy consumption in eastern Africa. 2021 , 12, 632	17
709	IonQuant Enables Accurate and Sensitive Label-Free Quantification With FDR-Controlled Match-Between-Runs. 2021 , 20, 100077	21
708	The Albuminome as a Tool for Biomarker Discovery. 263-278	1
707	Encyclopedia of Systems Biology. 2013 , 1775-1777	1
706	The secretome analysis by high-throughput proteomics and multiple reaction monitoring (MRM). 2014 , 1156, 323-35	4
705	Analysis of individual protein turnover in live animals on a proteome-wide scale. 2014 , 1156, 147-54	3

704	Protein Bioinformatics Databases and Resources. 2017 , 1558, 3-39	119
703	Retention Time Prediction and Protein Identification. 2020 , 2051, 115-132	3
702	Identifying bona fide components of an organelle by isotope-coded labeling of subcellular fractions : an example in peroxisomes. 2008 , 432, 357-71	4
701	Using stable isotope tagging and mass spectrometry to characterize protein complexes and to detect changes in their composition. 2007 , 359, 17-35	10
700	The use of a quantitative cysteinyl-peptide enrichment technology for high-throughput quantitative proteomics. 2007 , 359, 107-24	16
699	The Human Plasma and Serum Proteome. 2007 , 195-224	6
698	Proteomic global profiling for cancer biomarker discovery. 2009 , 492, 309-20	7
697	Quantitative peptide and protein profiling by mass spectrometry. 2009 , 492, 21-38	8
696	Shotgun protein identification and quantification by mass spectrometry in neuroproteomics. 2009 , 566, 229-59	6
695	Identification of glycoproteins in human cerebrospinal fluid. 2009 , 566, 263-76	13
694	Electrospray mass spectrometry for quantitative plasma proteome analysis. 2009 , 564, 227-42	4
693	Trans-proteomic pipeline: a pipeline for proteomic analysis. 2010 , 604, 213-38	107
692	The PeptideAtlas Project. 2010 , 604, 285-96	91
691	Identification of chemical-adducted proteins in urine by multi-dimensional protein identification technology (LC/LC-MS/MS). 2011 , 691, 339-47	1
690	Software pipeline and data analysis for MS/MS proteomics: the trans-proteomic pipeline. 2011 , 694, 169-89	35
689	Data management and data integration in the HUPO plasma proteome project. 2011 , 696, 247-57	15
688	Intact-protein analysis system for discovery of serum-based disease biomarkers. 2011 , 728, 69-85	11
687	Bioinformatics challenges in mass spectrometry-driven proteomics. 2011 , 753, 359-71	9

686	TMT labelling for the quantitative analysis of adaptive responses in the meningococcal proteome. 2012 , 799, 127-41	4
685	Investigation of age-specific behavioral and proteomic changes in an animal model of chronic ethanol exposure. 2012 , 829, 471-85	2
684	Global quantitative proteomics using spectral counting: an inexpensive experimental and bioinformatics workflow for deep proteome coverage. 2014 , 1072, 171-83	3
683	Measuring spatial restraints on native protein complexes using isotope-tagged chemical cross-linking and mass spectrometry. 2014 , 1091, 259-73	2
682	Statistical Methods in Proteomics. 2006 , 623-638	5
681	A Bayesian Approach to Protein Inference Problem in Shotgun Proteomics. 2008 , 167-180	10
680	Protein Identification from Tandem Mass Spectra with Probabilistic Language Modeling. 2009 , 554-569	2
679	Proteome Coverage Prediction for Integrated Proteomics Datasets. 2010 , 96-109	2
678	An Integration Architecture Designed to Deal with the Issues of Biological Scope, Scale and Complexity. 2010 , 179-191	1
677	Current challenges and approaches for the synergistic use of systems biology data in the scientific community. 2007 , 97, 277-307	6
676	Mass Spectrometry-Based Protein Sequencing Platforms. 2014 , 69-99	4
675	TRPM7 Mediates Neuronal Cell Death Upstream of Calcium/Calmodulin-Dependent Protein Kinase II and Calcineurin Mechanism in Neonatal Hypoxic-Ischemic Brain Injury. 2021 , 12, 164-184	15
674	Comparative protein profile analysis of wines made from <i>Botrytis cinerea</i> infected and healthy grapes reveals a novel biomarker for gushing in sparkling wine. 2017 , 99, 501-509	13
673	Identification of enzymatic activities involved in agave fructan consumption by <i>Bifidobacterium longum</i> subsp. <i>infantis</i> ATCC 15697. 2017 , 35, 267-278	4
672	Calculating absolute and relative protein abundance from mass spectrometry-based protein expression data. 2008 , 3, 1444-51	44
671	Comparative proteomic assessment of matrisome enrichment methodologies. 2016 , 473, 3979-3995	25
670	Bioinformatic and experimental evidence for suicidal and catalytic plant THI4s. 2020 , 477, 2055-2069	11
669	Analysis of the uterine flush fluid proteome of healthy mares and mares with endometritis or fibrotic endometrial degeneration. 2020 , 32, 572-581	5

668	Exotic foods reveal contact between South Asia and the Near East during the second millennium BCE. 2021 , 118,	11
667	The RNA-dependent RNA polymerase of enterovirus A71 associates with ribosomal proteins and positively regulates protein translation. 2020 , 17, 608-622	2
666	Interferon-stimulated gene 15 accelerates replication fork progression inducing chromosomal breakage. 2020 , 219,	17
665	Identification of a TeO32- reductase/mycothione reductase from Rhodococcus erythropolis PR4. 2020 , 97,	0
664	Qualitative proteomic analysis of Tipula oleracea nudivirus occlusion bodies. 2017 , 98, 284-295	5
663	Identification of antigenic proteins from Mycobacterium avium subspecies paratuberculosis cell envelope by comparative proteomic analysis. 2018 , 164, 322-337	5
662	Early urinary candidate biomarker discovery in a rat thioacetamide-induced liver fibrosis model.	3
661	Proteomic Architecture of Human Coronary and Aortic Atherosclerosis.	1
660	ERBB2 drives YAP activation and EMT-like processes during cardiac regeneration.	1
659	Heme Impairs Alveolar Epithelial Sodium Channels Post Toxic Gas Inhalation.	3
658	DNA-dependent macromolecular condensation drives self-assembly of the meiotic DNA break machinery.	5
657	Toxoplasma GRA15 limits parasite growth in IFN γ -activated fibroblasts through TRAF ubiquitin ligases.	2
656	A high-density human mitochondrial proximity interaction network.	4
655	Protein Interactomes Identify Distinct Pathways for Streptococcus mutans YidC1 and YidC2 Membrane Protein Insertases.	2
654	The 3.2 \AA resolution structure of human mTORC2.	4
653	A druggable oxidative folding pathway in the endoplasmic reticulum of human malaria parasites.	2
652	Fast and Comprehensive N- and O-glycoproteomics analysis with MSFragger-Glyco.	3
651	Proteomic pipeline to identify age-related compositional and structural changes of the human dentin extracellular matrix.	2

650	CCM signaling complex (CSC) is a master regulator governing homeostasis of progesterins and their mediated signaling cascades.	3
649	Conservation of the Toxoplasma conoid complex proteome reveals a cryptic conoid in Plasmodium that differentiates between blood- and vector-stage zoites.	1
648	Toxoplasma gondii secreted effectors co-opt host repressor complexes to inhibit necroptosis.	2
647	The new kid on the block: A dominant-negative mutation of phototropin1 enhances carotenoid content in tomato fruits.	0
646	DWV infection and replication at the early stage in vitro using honey bee pupal cells.	1
645	The Effects of Inter-Individual Biological Differences and Taphonomic Alteration on Human Bone Protein Profiles: Implications for the Development of PMI/AAD Estimation Methods.	2
644	Loss of MGA mediated Polycomb repression promotes tumor progression and invasiveness.	1
643	IonQuant enables accurate and sensitive label-free quantification with FDR-controlled match-between-runs.	3
642	Measuring proteomes with long strings: A new, unconstrained paradigm in mass spectrum interpretation.	1
641	Engineered Peptide Barcodes for In-Depth Analyses of Binding Protein Ensembles.	2
640	Molecular evolution of juvenile hormone esterase-like proteins in a socially exchanged fluid.	1
639	DART-ID increases single-cell proteome coverage.	2
638	Anoxygenic Photosynthesis and Dark Carbon Metabolism under micro-oxic conditions in the Purple Sulfur Bacterium Rhodospirillum rubrum strain Cad16T.	2
637	Microbial metabolism and adaptations in Atribacteria-dominated methane hydrate sediments.	4
636	Microvasculopathy, Luminal Calcification and Premature Aging in Fetuin-A Deficient Mice.	3
635	Extensive Transcriptional and Translational Regulation Occur During the Maturation of Malaria Parasite Sporozoites.	1
634	Aging Skeletal Muscle Proteomics Finds Changes in Spliceosome, Immune factors, Proteostasis and Mitochondria.	1
633	Ndc80/Nuf2-like protein KIP1 connects a stable kinetoplastid outer kinetochore complex to the inner kinetochore and responds to metaphase tension.	11

632	Spatio-temporal control of DNA replication by the pneumococcal cell cycle regulator CcrZ.	1
631	A proximity-dependent biotinylation map of a human cell: an interactive web resource.	28
630	Tailor: non-parametric and rapid score calibration method for database search-based peptide identification in shotgun proteomics.	1
629	Dietary restriction transforms the protein sulfhydrylome in a tissue-specific and cystathionine lyase-dependent manner.	1
628	Epigenetic Control of Protects Tumor-Infiltrating Lymphocytes from Metabolic Exhaustion. 2020 , 80, 4707-4719	9
627	Oxidative hotspots on actin promote skeletal muscle weakness in rheumatoid arthritis. 2019 , 5,	10
626	Plasminogen promotes cholesterol efflux by the ABCA1 pathway. 2017 , 2,	27
625	Synectin promotes fibrogenesis by regulating PDGFR isoforms through distinct mechanisms. 2017 , 2,	10
624	Interleukin-17 limits hypoxia-inducible factor 1 α and development of hypoxic granulomas during tuberculosis. 2017 , 2,	31
623	Antigen-mediated regulation in monoclonal gammopathies and myeloma. 2018 , 3,	28
622	Allele-specific RNA interference prevents neuropathy in Charcot-Marie-Tooth disease type 2D mouse models. 2019 , 129, 5568-5583	24
621	Epithelial-derived gasdermin D mediates nonlytic IL-1 β release during experimental colitis. 2020 , 130, 4218-4234	29
620	Shotgun proteomics implicates protease inhibition and complement activation in the antiinflammatory properties of HDL. 2007 , 117, 746-56	713
619	Peptidases released by necrotic cells control CD8+ T cell cross-priming. 2013 , 123, 4755-68	17
618	Computational methods for protein identification from mass spectrometry data. 2008 , 4, e12	68
617	DeepPep: Deep proteome inference from peptide profiles. 2017 , 13, e1005661	17
616	NINL and DZANK1 Co-function in Vesicle Transport and Are Essential for Photoreceptor Development in Zebrafish. 2015 , 11, e1005574	16
615	Tracking the Fragile X Mental Retardation Protein in a Highly Ordered Neuronal RiboNucleoParticles Population: A Link between Stalled Polyribosomes and RNA Granules. 2016 , 12, e1006192	41

614	A mouse to human search for plasma proteome changes associated with pancreatic tumor development. 2008 , 5, e123	209
613	Proteogenomic analysis of the total and surface-exposed proteomes of Plasmodium vivax salivary gland sporozoites. 2017 , 11, e0005791	48
612	Proteomic analysis of ovarian cancer cells reveals dynamic processes of protein secretion and shedding of extra-cellular domains. 2008 , 3, e2425	105
611	Media ion composition controls regulatory and virulence response of Salmonella in spaceflight. 2008 , 3, e3923	107
610	Barrier-to-autointegration factor proteome reveals chromatin-regulatory partners. 2009 , 4, e7050	77
609	Proteomic interrogation of androgen action in prostate cancer cells reveals roles of aminoacyl tRNA synthetases. 2009 , 4, e7075	39
608	Proteomics-based systems biology modeling of bovine germinal vesicle stage oocyte and cumulus cell interaction. 2010 , 5, e11240	33
607	Blood peptidome-degradome profile of breast cancer. 2010 , 5, e13133	50
606	Quantitative proteomics identifies the Myb-binding protein p160 as a novel target of the von Hippel-Lindau tumor suppressor. 2011 , 6, e16975	18
605	Distinct cerebrospinal fluid proteomes differentiate post-treatment lyme disease from chronic fatigue syndrome. 2011 , 6, e17287	80
604	Identification of contractile vacuole proteins in Trypanosoma cruzi. 2011 , 6, e18013	52
603	The Ccr4-Not complex interacts with the mRNA export machinery. 2011 , 6, e18302	39
602	Proteomic-based identification of CD4-interacting proteins in human primary macrophages. 2011 , 6, e18690	8
601	Proteomics portrait of archival lesions of chronic pancreatitis. 2011 , 6, e27574	40
600	Plasma biomarkers for detecting Hodgkin's lymphoma in HIV patients. 2011 , 6, e29263	8
599	Heterodimerization of glycosylated insulin-like growth factor-1 receptors and insulin receptors in cancer cells sensitive to anti-IGF1R antibody. 2012 , 7, e33322	37
598	Network analysis of epidermal growth factor signaling using integrated genomic, proteomic and phosphorylation data. 2012 , 7, e34515	32
597	Time-course proteome analysis reveals the dynamic response of Cryptococcus gattii cells to fluconazole. 2012 , 7, e42835	15

596	Venom proteome of the box jellyfish <i>Chironex fleckeri</i> . 2012 , 7, e47866	52
595	Identification of proteins sensitive to thermal stress in human neuroblastoma and glioma cell lines. 2012 , 7, e49021	25
594	Disruption of the S41 peptidase gene in <i>Mycoplasma mycoides capri</i> impacts proteome profile, H ₂ O ₂ production, and sensitivity to heat shock. 2012 , 7, e51345	10
593	New model of action for mood stabilizers: phosphoproteome from rat pre-frontal cortex synaptoneurosomal preparations. 2013 , 8, e52147	25
592	N-glycoproteome of E14.Tg2a mouse embryonic stem cells. 2013 , 8, e55722	13
591	Proteomic profiling of bronchoalveolar lavage fluid in critically ill patients with ventilator-associated pneumonia. 2013 , 8, e58782	26
590	Concerted action of sphingomyelinase and non-hemolytic enterotoxin in pathogenic <i>Bacillus cereus</i> . 2013 , 8, e61404	46
589	Identification of cisplatin-binding proteins using agarose conjugates of platinum compounds. 2013 , 8, e66220	39
588	Proteomic View of Interactions of Shiga Toxin-Producing <i>Escherichia coli</i> with the Intestinal Environment in Gnotobiotic Piglets. 2013 , 8, e66462	17
587	The cardiac acetyl-lysine proteome. 2013 , 8, e67513	68
586	Early insights into the function of KIAA1199, a markedly overexpressed protein in human colorectal tumors. 2013 , 8, e69473	39
585	Distinguishing ichthyoses by protein profiling. 2013 , 8, e75355	26
584	Analysis of the sperm head protein profiles in fertile men: consistency across time in the levels of expression of heat shock proteins and peroxiredoxins. 2013 , 8, e77471	11
583	Exposure to cobalt causes transcriptomic and proteomic changes in two rat liver derived cell lines. 2013 , 8, e83751	31
582	Human traumatic brain injury induces autoantibody response against glial fibrillary acidic protein and its breakdown products. 2014 , 9, e92698	118
581	Absence of metalloprotease GP63 alters the protein content of <i>Leishmania</i> exosomes. 2014 , 9, e95007	68
580	In vivo substrates of the lens molecular chaperones A-crystallin and B-crystallin. 2014 , 9, e95507	25
579	Insight into PreImplantation Factor (PIF*) mechanism for embryo protection and development: target oxidative stress and protein misfolding (PDI and HSP) through essential RIKP [corrected] binding site. 2014 , 9, e100263	28

578	The <i>Pseudomonas syringae</i> type III effector HopF2 suppresses <i>Arabidopsis</i> stomatal immunity. 2014 , 9, e114921	44
577	Proteomic analysis of mitochondrial-associated ER membranes (MAM) during RNA virus infection reveals dynamic changes in protein and organelle trafficking. 2015 , 10, e0117963	71
576	A draft map of rhesus monkey tissue proteome for biomedical research. 2015 , 10, e0126243	2
575	Resistance to Inhibitors of Cholinesterase 3 (Ric-3) Expression Promotes Selective Protein Associations with the Human α -Nicotinic Acetylcholine Receptor Interactome. 2015 , 10, e0134409	6
574	High Resolution Discovery Proteomics Reveals Candidate Disease Progression Markers of Alzheimer's Disease in Human Cerebrospinal Fluid. 2015 , 10, e0135365	44
573	Proteomic Analysis of Disease Stratified Human Pancreas Tissue Indicates Unique Signature of Type 1 Diabetes. 2015 , 10, e0135663	21
572	Differential Subcellular Localization of <i>Leishmania</i> Alba-Domain Proteins throughout the Parasite Development. 2015 , 10, e0137243	29
571	Metabolic Interplay between the Asian Citrus Psyllid and Its Proffftella Symbiont: An Achilles' Heel of the Citrus Greening Insect Vector. 2015 , 10, e0140826	50
570	MAS C-Terminal Tail Interacting Proteins Identified by Mass Spectrometry- Based Proteomic Approach. 2015 , 10, e0140872	8
569	Identification of Interactions in the NMD Complex Using Proximity-Dependent Biotinylation (BioID). 2016 , 11, e0150239	23
568	The dsRNA Virus Papaya Meleira Virus and an ssRNA Virus Are Associated with Papaya Sticky Disease. 2016 , 11, e0155240	24
567	A Large and Phylogenetically Diverse Class of Type 1 Opsins Lacking a Canonical Retinal Binding Site. 2016 , 11, e0156543	7
566	The Eukaryotic-Specific ISD11 Is a Complex-Orphan Protein with Ability to Bind the Prokaryotic IscS. 2016 , 11, e0157895	6
565	A Proteomic Approach to Lipo-Chitooligosaccharide and Thuricin 17 Effects on Soybean Germination Unstressed and Salt Stress. 2016 , 11, e0160660	30
564	The Specific α -Adrenergic Receptor Antagonist Prazosin Influences the Urine Proteome. 2016 , 11, e0164796	7
563	A High-Yield Two-Hour Protocol for Extraction of Human Hair Shaft Proteins. 2016 , 11, e0164993	18
562	Partial Purification of a Megadalton DNA Replication Complex by Free Flow Electrophoresis. 2016 , 11, e0169259	4
561	Lys48 ubiquitination during the intraerythrocytic cycle of the rodent malaria parasite, <i>Plasmodium chabaudi</i> . 2017 , 12, e0176533	3

560	PGCA: An algorithm to link protein groups created from MS/MS data. 2017 , 12, e0177569	1
559	A large scale Plasmodium vivax- Saimiri boliviensis trophozoite-schizont transition proteome. 2017 , 12, e0182561	13
558	Chemical crosslinking and mass spectrometry to elucidate the topology of integral membrane proteins. 2017 , 12, e0186840	7
557	Profiling of proteins secreted in the bovine oviduct reveals diverse functions of this luminal microenvironment. 2017 , 12, e0188105	30
556	Carcinogenic Parasite Secretes Growth Factor That Accelerates Wound Healing and Potentially Promotes Neoplasia. 2015 , 11, e1005209	62
555	Biological Chemistry. ---	1
554	Proteomic network analysis of human uterine smooth muscle in pregnancy, labor, and preterm labor. 2015 , 2, 261-269	4
553	Proteomic Profiling Reveals New Insights into the Allergomes of Anisakis simplex, Pseudoterranova decipiens, and Contracaecum osculatum. 2020 , 106, 572-588	8
552	Molecular basis of senescence transmitting in the population of human endometrial stromal cells. 2019 , 11, 9912-9931	8
551	FGF19 functions as autocrine growth factor for hepatoblastoma. 2016 , 7, 125-35	14
550	EWS-FLI-1 creates a cell surface microenvironment conducive to IGF signaling by inducing pappalysin-1. 2017 , 8, 762-770	7
549	Different non-synonymous polymorphisms modulate the interaction of the WRN protein to its protein partners and its enzymatic activities. 2016 , 7, 85680-85696	3
548	Autophagy is highly targeted among host comparative proteomes during infection with different virulent RABV strains. 2017 , 8, 21336-21350	6
547	Novel downstream molecular targets of SIRT1 in melanoma: a quantitative proteomics approach. 2014 , 5, 1987-99	22
546	Progesterone receptor isoforms, agonists and antagonists differentially reprogram estrogen signaling. 2018 , 9, 4282-4300	33
545	Quantitative mass spectrometry analysis reveals a panel of nine proteins as diagnostic markers for colon adenocarcinomas. 2018 , 9, 13530-13544	12
544	Exosomal survivin facilitates vesicle internalization. 2018 , 9, 34919-34934	11
543	Filamin C, a dysregulated protein in cancer revealed by label-free quantitative proteomic analyses of human gastric cancer cells. 2015 , 6, 1171-89	18

542	Analysis of the Skeletal Muscle Proteome Uncovers Alteration in Splicing, Mitochondria, and Immune Factors with Aging.	0
541	Bioinformatics Tools for Mass Spectrometry-Based High-Throughput Quantitative Proteomics Platforms. 2011 , 8, 125-137	5
540	Mass Spectrometry for Proteomics and Recent Developments in ESI, MALDI and other Ionization Methodologies. 2019 , 16, 267-276	2
539	Characterization of Carotenoid-protein Complexes and Gene Expression Analysis Associated with Carotenoid Sequestration in Pigmented Cassava (<i>Manihot Esculenta</i> Crantz) Storage Root. 2012 , 6, 116-30	23
538	In Silico Analysis Validates Proteomic Findings of Formalin-fixed Paraffin Embedded Cutaneous Squamous Cell Carcinoma Tissue. 2016 , 13, 453-465	12
537	Secretory granule protein chromogranin B (CHGB) forms an anion channel in membranes. 2018 , 1, e2018001395	
536	The effect of chronic, mild heat stress on metabolic changes of nutrition and adaptations in rumen papillae of lactating dairy cows. 2020 , 103, 8601-8614	9
535	Protein recycling in Bering Sea algal incubations. 2014 , 515, 45-59	8
534	A Novel Probe for Spliceosomal Proteins that Induces Autophagy and Death of Melanoma Cells Reveals New Targets for Melanoma Drug Discovery. 2019 , 53, 656-686	5
533	Progress of Protein Quality Control Methods in Shotgun Proteomics*. 2009 , 2009, 668-675	2
532	Up-regulation of mitochondrial chaperone TRAP1 in ulcerative colitis associated colorectal cancer. 2014 , 20, 17037-48	17
531	Proteomic analysis of energy metabolism and signal transduction in irradiated melanoma cells. 2013 , 6, 286-94	6
530	Current Omics Technologies in Biomarker Discovery. 2011 , 79-111	1
529	Spermatozoa protein alterations in infertile men with bilateral varicocele. 2016 , 18, 43-53	32
528	Proteomic analysis of mature and immature ejaculated spermatozoa from fertile men. 2016 , 18, 735-46	24
527	Optimization of the Use of Consensus Methods for the Detection and Putative Identification of Peptides via Mass Spectrometry Using Protein Standard Mixtures. 2009 , 2, 262-273	14
526	Hydrophobic Fractionation Enhances Novel Protein Detection by Mass Spectrometry in Triple Negative Breast Cancer. 2010 , 3, 1-10	3
525	Evaluation of the Consensus of Four Peptide Identification Algorithms for Tandem Mass Spectrometry Based Proteomics. 2010 , 3, 39-47	28

524	Comparative Proteomics Reveals Set of Oxidative Stress and Thaumatin-Like Proteins Associated with Resistance to Late Blight of Tomato. 2018 , 09, 789-816	1
523	The Structural Proteins of Bdellovibrio bacteriovorus Bacteriophage MAC-1. 2016 , 04, 7-13	1
522	Serum Carbonic Anhydrase 1 is a Biomarker for Diagnosis of Human Infection. 2017 , 96, 842-849	4
521	A review of statistical methods for protein identification using tandem mass spectrometry. 2012 , 5, 3-20	47
520	Protein identification problem from a Bayesian point of view. 2012 , 5, 21-37	8
519	Protein quantitation using iTRAQ: Review on the sources of variations and analysis of nonrandom missingness. 2012 , 5, 99-107	20
518	Comprehensive Proteome Analysis of the Excretory/Secretory Proteins of Toxoplasma gondii. 2014 , 35, 3071-3076	4
517	Analytical methods for proteome data obtained from SDS-PAGE multi-dimensional separation and mass spectrometry. 2010 , 1, 1-14	5
516	From proteomics toward systems biology: integration of different types of proteomics data into network models. 2008 , 41, 184-93	24
515	Affinity chromatography and capillary electrophoresis for analysis of the yeast ribosomal proteins. 2012 , 45, 233-8	3
514	Network-Based Protein Biomarker Discovery Platforms. 2016 , 14, 2-11	8
513	Business intelligence strategies enables rapid analysis of quantitative proteomics data. 2012 , 1, 5	3
512	Coordination of peptidoglycan synthesis and outer membrane constriction during Escherichia coli cell division. 2015 , 4,	127
511	PCH1 integrates circadian and light-signaling pathways to control photoperiod-responsive growth in Arabidopsis. 2016 , 5, e13292	53
510	Oral transfer of chemical cues, growth proteins and hormones in social insects. 2016 , 5,	61
509	TAPBPR bridges UDP-glucose:glycoprotein glucosyltransferase 1 onto MHC class I to provide quality control in the antigen presentation pathway. 2017 , 6,	43
508	AIRE is a critical spindle-associated protein in embryonic stem cells. 2017 , 6,	14
507	An ESCRT-LEM protein surveillance system is poised to directly monitor the nuclear envelope and nuclear transport system. 2019 , 8,	60

506	Discovery proteomics in aging human skeletal muscle finds change in spliceosome, immunity, proteostasis and mitochondria. 2019 , 8,	60
505	arginine-rich dipeptide repeat proteins disrupt karyopherin-mediated nuclear import. 2020 , 9,	46
504	ATR expands embryonic stem cell fate potential in response to replication stress. 2020 , 9,	15
503	CB-receptor-mediated inhibitory LTD triggers presynaptic remodeling via protein synthesis and ubiquitination. 2020 , 9,	13
502	Proteomic analysis of the dorsal spinal cord in the mouse model of spared nerve injury-induced neuropathic pain. 2017 ,	3
501	An evolving computational platform for biological mass spectrometry: workflows, statistics and data mining with MASSyPup64. 2015 , 3, e1401	16
500	Sequence/structural analysis of xylem proteome emphasizes pathogenesis-related proteins, chitinases and E1, 3-glucanases as key players in grapevine defense against Xylella fastidiosa. 2016 , 4, e2007	12
499	Potential urinary aging markers of 20-month-old rats. 2016 , 4, e2058	6
498	Human hair shaft proteomic profiling: individual differences, site specificity and cuticle analysis. 2014 , 2, e506	35
497	Identification of a native strain from Sri Lanka active against Dipel-resistant. 2019 , 7, e7535	7
496	Effects of anesthetics pentobarbital sodium and chloral hydrate on urine proteome. 2015 , 3, e813	6
495	Therapeutic potential of garlic chive-derived vesicle-like nanoparticles in NLRP3 inflammasome-mediated inflammatory diseases. 2021 , 11, 9311-9330	0
494	Alveolar-like Macrophages Attenuate Respiratory Syncytial Virus Infection. 2021 , 13,	0
493	TRAIP regulates DNA double-strand break-induced ATM activation.	
492	Hallstatt miners consumed blue cheese and beer during the Iron Age and retained a non-Westernized gut microbiome until the Baroque period. 2021 , 31, 5149-5162.e6	3
491	Palmitoylation targets the calcineurin phosphatase to the phosphatidylinositol 4-kinase complex at the plasma membrane. 2021 , 12, 6064	4
490	Enzymes degraded under high light maintain proteostasis by transcriptional regulation in Arabidopsis.	0
489	The Chorion Proteome of , the Vector of Huanglongbing Disease in Citrus. 2021 , 12,	

- 488 Revisiting the Role of *Toxoplasma gondii* ERK7 in the Maintenance and Stability of the Apical Complex. **2021**, 12, e0205721 3
- 487 Plant Proteomic Data Acquisition and Data Analyses: Lessons from Spaceflight. **2022**, 2368, 199-214
- 486 Mechanistic insights into COVID-19 by global analysis of the SARS-CoV-2 3CL substrate degradome. **2021**, 37, 109892 11
- 485 Nutritional dependence of sperm mitochondrial metabolism and small RNA biogenesis.
- 484 Identification of the Park Grass Experiment soil metaproteome.
- 483 Deep representation features from DreamDIA improve the analysis of data-independent acquisition proteomics. **2021**, 4, 1190 1
- 482 Proteomics Data Analysis using Representative Database. **2007**, 1, 46-51
- 481 Large-scale purification of latex bead phagosomes from mouse macrophage cell lines and subsequent preparation for high-throughput quantitative proteomics. **2008**, 445, 339-51 2
- 480 Invited Keynote Talk: Computing P-Values for Peptide Identifications in Mass Spectrometry. **2008**, 100-109
- 479 Applications of Stable Isotope Tagging Based Quantitative Proteomics in Cancer Research. 121-143
- 478 High-Throughput Data Analysis of Proteomic Mass Spectra on the SwissBioGrid. **2009**, 228-244
- 477 Automated generic analysis tools for protein quantitation using stable isotope labeling. **2010**, 604, 257-72
- 476 Assigning probabilities to Mascot peptide identification using logistic regression. **2010**, 680, 229-36
- 475 Quantitative Plant Proteomics Using Hydroponic Isotope Labeling of Entire Plants (HILEP). **2011**, 363-380
- 474 Modules in Biological Networks. **2011**, 248-274
- 473 Bioinformatics challenges in the proteomic analysis of human plasma. **2011**, 728, 333-47
- 472 Data management in mass spectrometry-based proteomics. **2011**, 728, 321-32 1
- 471 Effects of stoichiometry and temperature perturbations on beech litter decomposition, enzyme activities and protein expression.

470 References. **2013**, 239-262

469 Proteomics in the Systems-Level Study of the Metabolic Syndrome. **2014**, 185-212

468 Mass Spectrometry for Biomarker Development. **2014**, 1-25

467 Chapter 4:PSM Scoring and Validation. **2016**, 69-92

1

466 Chapter 5:Protein Inference and Grouping. **2016**, 93-115

465 Identification of a novel putative interaction partner of the nucleoporin ALADIN.

464 Proteomic Analysis Reveals GLUT1 to be a Novel Discriminating Marker of Human Arterial Endothelium In vivo and loss of Venous Identity in Cell Culture. **2016**, 1, 001-007

463 Differential protein expression marks the transition from infection with *Opisthorchis viverrini* to cholangiocarcinoma.

462 Identification of Fungal T Cell Epitopes by Mass Spectrometry-Based Proteomics. **2017**, 1625, 65-74

461 Analysis of GAPDH by Mass Spectrometry. **2017**, 95-98

460 The microprotein Minion controls cell fusion and muscle formation.

1

459 A dry method for preserving tear protein samples.

1

458 Cross-species complementation reveals conserved functions for EARLY FLOWERING 3 between monocots and dicots.

457 Contrasting patterns of evolutionary constraint and novelty revealed by comparative sperm proteomic analysis.

456 Native KCC2 interactome reveals PACSIN1 as a critical regulator of synaptic inhibition.

455 Diagnosis of respiratory diseases using the proteomic analysis of exhaled breath condensate. **2017**, 27, 187-197

454 Blazing Signature Filter: a library for fast pairwise similarity comparisons.

1

453 Microwave & magnetic proteomics of macrophages from patients with HIV-associated cognitive impairment. **2017**, 12, e0181779

1

- 452 Differential protein expression profile in the hypothalamic GT1-7 cell line after exposure to anabolic androgenic steroids. **2017**, 12, e0180409
- 451 C-BERST: Defining subnuclear proteomic landscapes at genomic elements with dCas9-APEX2.
- 450 Magnetoresistive biosensors for quantitative proteomics. **2017**,
- 449 Neurochondrin interacts with the SMN protein suggesting a novel mechanism for Spinal Muscular Atrophy pathology.
- 448 EWS-FLI-1 creates a cell surface microenvironment conducive to IGF signaling by inducing pappalysin-1.
- 447 NuMA is a negative regulator of 53BP1 in DNA double-strand break repair.
- 446 Chemoproteomic Profiling Uncovers CDK4-Mediated Phosphorylation of the Translational Suppressor 4E-BP1.
- 445 Distinct Plastids Trigger Local Signaling for Systemic Stress Response in Plants.
- 444 Gas chromatographic-mass spectrometric investigation of n-alkanes and carboxylic acids in bottom sediments of the northern Caspian Sea. **2018**, 24, 69-78 ○
- 443 Human and Rodent Temporal Lobe Epilepsy is Characterized by Changes in O-GLCNAC Homeostasis that can be Reversed to Dampen Epileptiform Activity.
- 442 Development of reduced gluten wheat enabled by determination of the genetic basis of thely3alow hordein barley mutant. 2
- 441 The foliar endophyte *Phialocephala scopiformis* DAOMC 229536 secretes enzymes supporting growth on wood as sole carbon source.
- 440 A comparative analysis of label-free liquid chromatography-mass spectrometry liver proteomic profiles highlights metabolic differences between pig breeds. ○
- 439 Corticospinal neuroplasticity and sensorimotor recovery in rats treated by infusion of neurotrophin-3 into disabled forelimb muscles started 24 h after stroke.
- 438 Genetic control of the HDL proteome.
- 437 Sexual selection rewires reproductive protein networks.
- 436 Expression of TorsinA in a heterologous yeast system reveals interactions with conserved luminal domains of LINC and nuclear pore complexes.
- 435 Proteomic Profile of TGF- β treated Lung Fibroblasts identifies Novel Markers of Activated Fibroblasts in the Silica Exposed Rat Lung.

- 434 Reconstitution of eukaryotic chromosomes and manipulation of DNA N6-methyladenine alters chromatin and gene expression.
- 433 Identification of proteins involved in *Trypanosoma brucei* DNA replication fork dynamics using nascent DNA proteomics. 2
- 432 An ESCRT-LEM domain inner nuclear membrane protein surveillance system is poised to directly monitor the integrity of the nuclear envelope barrier and nuclear transport system.
- 431 A Proteomic Analysis of Mitochondrial Complex III Inhibition in SH-SY5Y Human Neuroblastoma Cell Line. **2019**, 16, 136-147
- 430 H2A.Z-dependent and -independent recruitment of metabolic enzymes to chromatin required for histone modifications.
- 429 HCF-2 inhibits cell proliferation and activates differentiation-gene expression programs.
- 428 Proteomics analysis of extracellular matrix remodeling during zebrafish heart regeneration. 1
- 427 Dynamic response in the larval geoduck clam proteome to elevated pCO₂. 0
- 426 Long non-coding RNA GRASLND enhances chondrogenesis via suppression of interferon type II signaling pathway.
- 425 PTMProphet: Fast and Accurate Mass Modification Localization for the Trans-Proteomic Pipeline. 1
- 424 A robust metaproteomics pipeline for a holistic taxonomic and functional characterization of microbial communities from marine particles.
- 423 EPIFANY [A] method for efficient high-confidence protein inference.
- 422 Mutation of CFAP57 causes primary ciliary dyskinesia by disrupting the asymmetric targeting of a subset of ciliary inner dynein arms.
- 421 C9orf72 arginine-rich dipeptide repeat proteins disrupt importin [mediated nuclear import]. 0
- 420 N6-methyladenine DNA glycosylase associates with transcription elongation to coordinate DNA repair with gene expression [].
- 419 Absolute quantification of transcription factors reveals principles of gene regulation in erythropoiesis. 0
- 418 Coessential Genetic Networks Reveal the Organization and Constituents of a Dynamic Cellular Stress Response. 1
- 417 Annexin A2 depletion exacerbates the intracerebral microhemorrhage induced by acute rickettsia and Ebola virus infections. 0

- 416 ARP-T1 is a ciliogenesis protein associated with a novel ciliopathy in inherited basal cell cancer, Bazex-Duprè-Christol Syndrome.
- 415 A receptor-like kinase mediated phosphorylation of G β protein affects signaling during nodulation.
- 414 ATR expands embryonic stem cell fate potential in response to replication stress.
- 413 CHAPTER 3:Proteomics in Precision Medicine. **2020**, 58-72
- 412 Necrosignaling: Cell death triggers antibiotic survival pathways in bacterial swarms. 1
- 411 MealTime-MS: A Machine Learning-Guided Real-Time Mass Spectrometry Analysis for Protein Identification and Efficient Dynamic Exclusion.
- 410 Inhibition of tryptophan 2,3-dioxygenase impairs DNA damage tolerance and repair in glioma cells.
- 409 Atomic structures of respiratory complex III₂, complex IV and supercomplex III₂-IV from vascular plants.
- 408 Methionine stress induces a ferroptotic gene signature in methionine dependent cancer cells.
- 407 The Impact of N-Acetyl Cysteine and Coenzyme Q10 Supplementation on Skeletal Muscle Antioxidants and Proteome in Fit Thoroughbred Horses. **2021**, 10, 2
- 406 The genomic origins of the Bronze Age Tarim Basin mummies. **2021**, 599, 256-261 14
- 405 BtuB-Dependent Infection of the T5-like Phage ϕ R2-01. **2021**, 13, 0
- 404 Protein Palmitoylation in Bovine Ovarian Follicle. **2021**, 22, 0
- 403 Mouse Organ Specific Proteins and Functions.
- 402 Studies of Glyoxalase 1-Linked Multidrug Resistance Reveal Glycolysis-Derived Reactive Metabolite, Methylglyoxal, Is a Common Contributor in Cancer Chemotherapy Targeting the Spliceosome. **2021**, 11, 748698 1
- 401 Multi-attribute Glycan Identification and FDR Control for Glycoproteomics.
- 400 Ycs4 Subunit of Condensin Binds DNA and Modulates the Enzyme Turnover. **2021**, 60, 3385-3397
- 399 Proteome analysis of an aggressive and a hypoaggressive isolates of *Fusarium oxysporum* f. sp *albendinis* showing several differently expressed-proteins related to the aggressiveness. **2021**, 116, 101738 0

- 398 Evolutionarily ancient role of cholecystokinin-type neuropeptide signalling as an inhibitory regulator of feeding-related processes revealed in an echinoderm.
- 397 High levels of glucose alter *Physcomitrella patens* metabolism and trigger a differential proteomic response. **2020**, 15, e0242919
- 396 Registered report protocol: Quantitative analysis of septin Cdc10-associated proteome in *Cryptococcus neoformans*. **2020**, 15, e0242381 1
- 395 Fatty acid and proteomic analysis of *Sterculia striata* nut. **2020**, 40, 489-495
- 394 Open search algorithms discover patterns of chemical modifications via LC-MS/MS. **2022**, 95-125
- 393 Uterine infusion of conceptus fragments changes the protein profile from cyclic mares. **2020**, 17, e20200552
- 392 The Amniotic Fluid Proteome Differs Significantly between Donor and Recipient Fetuses in Pregnancies Complicated by Twin-to-Twin Transfusion Syndrome. **2020**, 35, e73 1
- 391 Pinpointing of cysteine oxidation sites in vivo by high-resolution proteomics reveals mechanism of redox-dependent inhibition of STING. 1
- 390 Fast quantitative analysis of timsTOF PASEF data with MSFragger and IonQuant. 3
- 389 Quantitative proteomics links the LRR59 interactome to mRNA translation on the ER membrane.
- 388 A comprehensive proteomic SWATH-MS workflow for profiling blood extracellular vesicles: a new avenue for glioma tumour surveillance. 0
- 387 Mechanisms of up-regulation of Ubiquitin-Proteasome activity in the absence of NatA dependent N-terminal acetylation.
- 386 Bioinformatic and experimental evidence for suicidal and catalytic plant THI4s.
- 385 Organization and composition of apicomplexan kinetochores reveal plasticity in chromosome segregation across parasite modes of division. 1
- 384 Identification of Bi-2-naphthol and Its Phosphate Derivatives Complexed with Cyclodextrin and Metal Ions Using Trapped Ion Mobility Spectrometry. *Analytical Chemistry*, **2021**, 93, 15096-15104 7.8 3
- 383 Malaria transmission relies on concavin-mediated maintenance of *Plasmodium* sporozoite cell shape.
- 382 APOBEC2 is a Transcriptional Repressor required for proper Myoblast Differentiation. 1
- 381 Current Omics Technologies in Biomarker Discovery. 465-497

380 Modules in Biological Networks. 637-663

- 379 Improved Ranking Functions for Protein and Modification-Site Identifications. **2007**, 444-458 1
- 378 A High-Throughput Bioinformatics Platform for Mass Spectrometry-Based Proteomics. **2007**, 71-88
- 377 Proximity Biotin Labeling Reveals KSHV Interferon Regulatory Factor Networks.
- 376 Sericin-Induced Melanogenesis in Cultured Retinal Pigment Epithelial Cells Is Associated with Elevated Levels of Hydrogen Peroxide and Inflammatory Proteins. **2020**, 25,
- 375 A wide-ranging *Pseudomonas aeruginosa* PeptideAtlas build: a useful proteomic resource for a versatile pathogen.
- 374 Annotated proteome of a human T-cell lymphoma. **2005**, 16, 341-6 3
- 373 Optimization of proteomic sample preparation procedures for comprehensive protein characterization of pathogenic systems. **2008**, 19, 285-95 13
- 372 The zebrafish lens proteome during development and aging. **2009**, 15, 2313-25 36
- 371 The 2M6 antigen is a Müller cell-specific intracellular membrane-associated protein of the sarcolemmal-membrane-associated protein family and is also TopAP. **2010**, 16, 961-9 7
- 370 A comparative study of in-gel digestions using microwave and pressure-accelerated technologies. **2010**, 21, 148-55 10
- 369 Alterations in the aqueous humor proteome in patients with Fuchs endothelial corneal dystrophy. **2010**, 16, 2376-83 23
- 368 Alterations in the aqueous humor proteome in patients with a glaucoma shunt device. **2011**, 17, 1891-900 55
- 367 Use of recombinant purified protein derivative (PPD) antigens as specific skin test for tuberculosis. **2012**, 136, 799-807 1
- 366 Analysis of endoscopic pancreatic function test (ePFT)-collected pancreatic fluid proteins precipitated via ultracentrifugation. **2013**, 14, 176-86 3
- 365 Distinctive and pervasive alterations in aqueous humor protein composition following different types of glaucoma surgery. **2015**, 21, 911-8 22
- 364 Gene Expression in the Three-Spined Stickleback (*Gasterosteus aculeatus*) of Marine and Freshwater Ecotypes. **2018**, 10, 66-74 3
- 363 Medial prefrontal cortex exacerbates gastric dysfunction of rats upon restraint water-immersion stress. **2019**, 20, 2303-2315 2

362	Reduced Toxicity of (Say, 1821) May Result from Lowered Sodium α -Toxin Gene Expression and Toxin Protein Production. 2021 , 13,	1
361	Enrichment of membrane curvature-sensing proteins from Escherichia coli using spherical supported lipid bilayers. 2021 ,	
360	Molecular cloning, heterologous expression, and in silico sequence analysis of Enterobacter GH19 class I chitinase (chiRAM gene). 2021 , 49, 951	0
359	Supramolecular arrangement of protein in nanoparticle structures predicts nanoparticle tropism for neutrophils in acute lung inflammation. 2021 ,	13
358	Transcriptomic taxonomy and neurogenic trajectories of adult human, macaque, and pig hippocampal and entorhinal cells. 2021 ,	16
357	Up-regulation of ubiquitin-proteasome activity upon loss of NatA-dependent N-terminal acetylation. 2022 , 5,	0
356	Symbiotic responses of Lotus japonicus to two isogenic lines of a mycorrhizal fungus differing in the presence/absence of an endobacterium. 2021 , 108, 1547	2
355	Quantitative isotope-labeled crosslinker proteomics reveals developmental variation in protein interactions and posttranslational modifications in Diaphorina citri, the citrus greening insect vector.	
354	The Marine Neurotoxin Brevetoxin (PbTx-2) Inhibits and Mammalian Thioredoxin Reductases by Targeting Different Residues. 2021 , 84, 2961-2970	1
353	Comparison of Sample Preparation Methods for Shotgun Proteomic Studies in Aquaculture Species. 2021 , 9,	1
352	Saliva Protein Profiling for Subject Identification and Potential Medical Applications. 2021 , 3, 100012	0
351	Vesicular and extravesicular protein analyses from the airspaces of ozone-exposed mice revealed signatures associated with mucoinflammatory lung disease. 2021 , 11, 23203	1
350	Progressive polysomal association of Upf1, Upf2, and Upf3 as ribosomes traverse mRNA coding regions.	
349	Catalytic Cycling of Human Mitochondrial Lon Protease.	
348	Cryo-EM structure of native human thyroglobulin.. 2022 , 13, 61	1
347	Proximity Proteomics Reveals New Roles of Abelson Interactor 1 in Centrosome Function and Inflammatory Signaling.	
346	Multifaceted roles of the egg perivitelline layer in avian reproduction: Functional insights from the proteomes of chicken egg inner and outer sublayers.. 2022 , 258, 104489	0
345	Day and night isotope labelling reveal metabolic pathway specific regulation of protein synthesis rates in Arabidopsis.. 2022 ,	1

- 344 The C-terminal domain of SEC-10 is fundamental for exocyst function, Spitzenkörper organization and cell morphogenesis in *Neurospora crassa*.
- 343 Cryo-EM reconstruction of the human 40S ribosomal subunit at 2.15 Å resolution. 0
- 342 T cell activation decreases microRNA-15a/16 levels to promote MEK1-ERK1/2-Elk1 signaling and promote proliferative capacity.. **2022**, 101634 0
- 341 HIF-1 Interacts with TRIM28 and DNA-PK to release paused RNA polymerase II and activate target gene transcription in response to hypoxia.. **2022**, 13, 316 4
- 340 Fine-tuned method to extract high purified proteins from the seagrass *Halophila stipulacea* to be used for proteome analyses. 1-9
- 339 SCP4-STK35/PDIK1L complex is a dual phospho-catalytic signaling dependency in acute myeloid leukemia.. **2022**, 38, 110233
- 338 Multi-attribute Glycan Identification and FDR Control for Glycoproteomics.. **2022**, 100205 1
- 337 Bacterial gasdermins reveal an ancient mechanism of cell death.. **2022**, 375, 221-225 11
- 336 Interaction with mammalian enteric viruses alters outer membrane vesicle production and content by commensal bacteria.. **2022**, 11, e12172 3
- 335 Ionizing Radiation Activates Mitochondrial Function in Osteoclasts and Causes Bone Loss in Young Adult Male Mice.. **2022**, 23, 0
- 334 Maternal Fructose Intake Causes Developmental Reprogramming of Hepatic Mitochondrial Catalytic Activity and Lipid Metabolism in Weanling and Young Adult Offspring.. **2022**, 23, 0
- 333 SymRK-dependent phosphorylation of Gβ protein and its role in signaling during soybean (*Glycine max*) nodulation.. **2022**, 1
- 332 Diagnosis of invasive non-functional pituitary adenomas using exosomal biomarkers.. **2022**, 529, 25-25 0
- 331 Identification of Piperlongumine (PL) as a new E3 ligase ligand to induce targeted protein degradation. 1
- 330 Salivary ZG16B expression loss follows exocrine gland dysfunction related to oral chronic graft-versus-host disease.. **2022**, 25, 103592 2
- 329 Structural basis for safe and efficient energy conversion in a respiratory supercomplex.. **2022**, 13, 545 1
- 328 A practical guide to interpreting and generating bottom-up proteomics data visualizations.. **2022**, e2100103 2
- 327 Integrating endometrial proteomic and single cell transcriptomic pipelines reveals distinct menstrual cycle and endometriosis-associated molecular profiles. 0

326	Venomomics and antivenomics of Indian spectacled cobra (<i>Naja naja</i>) from the Western Ghats.. 2022 , 106324	0
325	A blood atlas of COVID-19 defines hallmarks of disease severity and specificity.. 2022 , 185, 916-938.e58	17
324	Adipose-derived stem cell spheroids are superior to single-cell suspensions to improve fat autograft long-term survival.. 2022 ,	2
323	A validated analysis pipeline for mass spectrometry-based vitreous proteomics: new insights into proliferative diabetic retinopathy. 2021 , 18, 28	2
322	Piperlongumine as a Neuro-Protectant in Chemotherapy Induced Cognitive Impairment.. 2022 , 23,	0
321	Putting Humpty Dumpty Back Together Again: What Does Protein Quantification Mean in Bottom-Up Proteomics?. 2022 ,	3
320	Shotgun Proteomics Identifies Active Metabolic Pathways in Bleached Coral Tissue and Intraskelatal Compartments. 2022 , 9,	
319	Epigenomic and Proteomic Changes in Fetal Spleens Persistently Infected with Bovine Viral Diarrhea Virus: Repercussions for the Developing Immune System, Bone, Brain, and Heart.. 2022 , 14,	
318	Data From A Biocodological Analysis of the Medieval Library and Archive From Orval Abbey, Belgium. 2022 , 10,	0
317	Functional Study of Protein Arginine Methyltransferases (PRMTs) Reveals That PRMT1 and PRMT5 Are Required for Macrophage Infection.. 2022 ,	0
316	Evidence for a trap-and-flip mechanism in a proton-dependent lipid transporter.. 2022 , 13, 1022	0
315	AAV-delivered suppressor tRNA overcomes a nonsense mutation in mice.. 2022 ,	3
314	Soybean Leaf Proteomic Profile Influenced by Rhizobacteria Under Optimal and Salt Stress Conditions.. 2022 , 13, 809906	0
313	Skeletal muscle proteome expression differentiates severity of cancer cachexia in mice and identifies loss of fragile X mental retardation syndrome-related protein 1.. 2022 , e2100157	1
312	TIDD: tool-independent and data-dependent machine learning for peptide identification.. 2022 , 23, 109	0
311	Parallel kinase pathways stimulate actin polymerization at depolarized mitochondria.. 2022 ,	1
310	Purification and characterization of a fungal aspartic peptidase from <i>Trichoderma reesei</i> and its application for food and animal feed protein hydrolyses.. 2022 ,	0
309	Hematopoietic Stem Cell Transplant-Membranous Nephropathy is Associated with Protocadherin FAT1.. 2022 ,	1

308	Spatiotemporal profiling of the bovine oviduct fluid proteome around the time of ovulation.. 2022 , 12, 4135	1
307	Repurposing Live Attenuated Trivalent MMR Vaccine as Cost-effective Cancer Immunotherapy.	
306	Proteomic profiling of tear fluid as a promising non-invasive screening test for colon cancer.. 2022 ,	0
305	Dynamic Changes in the Proteome of Early Bovine Embryos Developed .. 2022 , 10, 863700	0
304	Enhanced protein isoform characterization through long-read proteogenomics.. 2022 , 23, 69	3
303	CsrA-Controlled Proteins Reveal New Dimensions of <i>Acinetobacter baumannii</i> Desiccation Tolerance.. 2022 , e0047921	1
302	The mitochondrion of <i>Plasmodium falciparum</i> generates essential acetyl-CoA for protein acetylation.	
301	Emergence and intensification of dairying in the Caucasus and Eurasian steppes.. 2022 ,	3
300	A dataset of proteins associated with mRNAs.. 2022 , 41, 107953	
299	ALS-associated KIF5A mutations abolish autoinhibition resulting in a toxic gain of function.. 2022 , 39, 110598	4
298	Spirocyclic dimer SpiD7 activates the unfolded protein response to selectively inhibit growth and induce apoptosis of cancer cells.. 2022 , 101890	0
297	Opportunities lost? Evolutionary causes and ecological consequences of the absence of trehalose digestion in birds.	0
296	Pancreatic ductal adenocarcinoma cells employ integrin $\beta 4$ to form hemidesmosomes and regulate cell proliferation.. 2022 ,	0
295	Proteomic analyses identify differences between bovine epididymal and ejaculated spermatozoa that contribute to longevity.. 2022 , 184, 51-60	1
294	Multi-Omics Approach Profiling Metabolic Remodeling in Early Systolic Dysfunction and in Overt Systolic Heart Failure.. 2021 , 23,	0
293	The Tongue Squamous Carcinoma Cell Line Cal27 Primarily Employs Integrin $\beta 4$ -Containing Type II Hemidesmosomes for Adhesion Which Contribute to Anticancer Drug Sensitivity.. 2021 , 9, 786758	1
292	Myosin VI regulates ciliogenesis by promoting the turnover of the centrosomal/satellite protein OFD1.. 2021 , e54160	2
291	Enzymatic degradation is an effective means to reduce aflatoxin contamination in maize.. 2021 , 21, 70	1

- 290 From fruit growth to ripening in plantain: a careful balance between carbohydrate synthesis and breakdown.
- 289 Investigation of Effects of the Spectral Library on Analysis of diaPASEF Data.. **2021**, 1
- 288 Mouse Organ-Specific Proteins and Functions.. **2021**, 10,
- 287 Multi-modal Profiling of the Extracellular Matrix of Human Fallopian Tubes and Serous Tubal Intraepithelial Carcinomas. **2021**, 221554211061359 0
- 286 Sperm Proteome Analysis to Investigate DNA Repair Mechanisms in Varicocele Patients.. **2021**, 12, 757592 0
- 285 Calreticulin Shortage Results in Disturbance of Calcium Storage, Mitochondrial Disease, and Kidney Injury.. **2022**, 11, 1
- 284 Localization of the Priming Factors CAPS1 and CAPS2 in Mouse Sensory Neurons Is Determined by Their N-Termini.. **2022**, 15, 674243
- 283 The PeptideAtlas of a widely cultivated fish *Labeo rohita*: A resource for the Aquaculture Community.. **2022**, 9, 171 2
- 282 Proteome-wide identification of amino acid substitutions deleterious for protein function. 0
- 281 Proteomics dataset of epididymal fluid, seminal plasma, and proteins loosely attached to epididymal and ejaculated sperm from Angus bulls.. **2022**, 42, 108150 0
- 280 p66Shc is an apoptotic rheostat whose targeted ROS inhibition improves MI outcomes. 0
- 279 Proteomes of primary skin fibroblasts from healthy individuals reveal altered cell responses across the life span.. **2022**, e13609 0
- 278 Protein and volatile contents in the mandibular gland of the sugarcane borer *Diatraea saccharalis* (Lepidoptera: Crambidae).. **2022**, e21904
- 277 Allosteric regulation of the soluble epoxide hydrolase by nitro fatty acids using a combined experimental and computational approach.. **2022**, 167600 0
- 276 Composition and abundance of midgut surface proteins in the Asian citrus psyllid, *Diaphorina citri*.. **2022**, 104580 0
- 275 Table_1.XLSX. **2019**,
- 274 Table_1.XLSX. **2020**,
- 273 Data_Sheet_1.docx. **2020**,

272 Presentation_1.PDF. **2018,**

271 Table_1.pdf. **2018,**

270 Image1.PDF. **2018,**

269 Image2.PDF. **2018,**

268 Image3.PDF. **2018,**

267 Image4.PDF. **2018,**

266 Image5.PDF. **2018,**

265 Table1.DOCX. **2018,**

264 Table10.XLSX. **2018,**

263 Table11.XLSX. **2018,**

262 Table12.XLSX. **2018,**

261 Table13.XLSX. **2018,**

260 Table2.XLSX. **2018,**

259 Table3.XLSX. **2018,**

258 Table4.XLSX. **2018,**

257 Table5.XLSX. **2018,**

256 Table6.XLSX. **2018,**

255 Table7.XLSX. **2018,**

254 Table8.XLSX. 2018,

253 Table9.XLSX. 2018,

252 Data_Sheet_1.PDF. 2019,

251 Data_Sheet_2.PDF. 2019,

250 Data_Sheet_3.PDF. 2019,

249 Image_1.TIFF. 2019,

248 Data_Sheet_1.pdf. 2018,

247 Data_Sheet_2.xlsx. 2018,

246 Table_1.XLSX. 2018,

245 Table_2.XLSX. 2018,

244 Data_Sheet_1.PDF. 2020,

243 Table_2.xlsx. 2020,

242 Image_1.TIFF. 2018,

241 Image_2.TIFF. 2018,

240 Image_3.TIFF. 2018,

239 Table_1.DOCX. 2018,

238 Table_2.DOCX. 2018,

237 Table_3.XLSX. 2018,

236 Data_Sheet_1.pdf. **2019**,

235 Data_Sheet_1.PDF. **2018**,

234 Table_1.XLSX. **2018**,

233 Data_Sheet_1.FASTA. **2019**,

232 Data_Sheet_2.xls. **2019**,

231 Image_1.JPEG. **2019**,

230 Image_2.TIFF. **2019**,

229 Table_1.docx. **2019**,

228 Data_Sheet_1.docx. **2020**,

227 Data_Sheet_2.zip. **2020**,

226 Image_1.TIF. **2020**,

225 DataSheet_1.xlsx. **2020**,

224 DataSheet_2.xlsx. **2020**,

223 DataSheet_3.docx. **2020**,

222 Data_Sheet_1.docx. **2020**,

221 Data_Sheet_2.xlsx. **2020**,

220 Data_Sheet_1.xlsx. **2020**,

219 Data_Sheet_2.pdf. **2020**,

218 Data_Sheet_1.PDF. 2019,

217 Table_2.xlsx. 2019,

216 Table_1.xlsx. 2020,

215 Table_2.xlsx. 2020,

214 Table_3.xlsx. 2020,

213 Image_1.TIF. 2018,

212 Image_2.TIF. 2018,

211 Image_3.TIF. 2018,

210 Image_4.TIF. 2018,

209 Image_5.TIF. 2018,

208 Image_6.TIF. 2018,

207 Table_1.xlsx. 2018,

206 Table_1.XLSX. 2020,

205 Data_Sheet_1.PDF. 2020,

204 Image_1.jpeg. 2020,

203 Image_2.jpeg. 2020,

202 Image_3.jpeg. 2020,

201 Image_4.jpeg. 2020,

200 Table_1.docx. **2020**,

199 Presentation_1.PDF. **2018**,

198 Table_1.xls. **2018**,

197 Table_2.xls. **2018**,

196 Data_Sheet_1.PDF. **2020**,

195 Data_Sheet_2.PDF. **2020**,

194 Table_1.pdf. **2020**,

193 Table_2.pdf. **2020**,

192 Table_3.pdf. **2020**,

191 Table_4.pdf. **2020**,

190 Table_5.pdf. **2020**,

189 Tear Proteomics of Children and Young Adult Soft Contact Lens, Orthokeratology and Spectacle Wearers - A Pilot Study.. **2022**, 1-11

188 Inhibition of growth by masarimycin.. **2022**, 168,

187 CROP: a retromer-PROPPIN complex mediating membrane fission in the endo-lysosomal system.. **2022**, e109646 2

186 Quantitative Isotope-Labeled Cross-Linker Proteomics Reveals Developmental Variation in Protein Interactions and Post-Translational Modifications in Diaphorina citri, the Citrus Greening Insect Vector. 0

185 E3 ligase HUWE1 promotes PDGF D-mediated osteoblastic differentiation of mesenchymal stem cells by effecting polyubiquitination of EPDGFR.. **2022**, 101981 1

184 Integrin-ECM interactions and membrane-associated Catalase cooperate to promote resilience of the Drosophila intestinal epithelium.. **2022**, 20, e3001635 0

183 Inositol polyphosphate multikinase physically binds to the SWI/SNF complex and modulates BRG1 occupancy in mouse embryonic stem cells.. **2022**, 11, 0

182	From fruit growth to ripening in plantain: a careful balance between carbohydrate synthesis and breakdown.. 2022 ,	0
181	Shotgun Proteomics for the Identification and Profiling of the Tear Proteome of Keratoconus Patients.. 2022 , 63, 12	0
180	Enzymes degraded under high light maintain proteostasis by transcriptional regulation in .. 2022 , 119, e2121362119	0
179	Differential mitochondrial protein interaction profile between human translocator protein and its A147T polymorphism variant.. 2022 , 17, e0254296	1
178	KSHV episome tethering sites on host chromosomes and regulation of latency-lytic switch by CHD4.. 2022 , 39, 110788	1
177	Fasciola hepatica Gastrodermal Cells Selectively Release Extracellular Vesicles via a Novel Atypical Secretory Mechanism. 2022 , 23, 5525	1
176	Kir7.1 disease mutant T153I within the inner pore affects K ⁺ conduction.. 2022 ,	0
175	Differential excretory/secretory proteome of the adult female and male stages of the human blood fluke, <i>Schistosoma mansoni</i> .	
174	Novel reusable animal model for comparative evaluation of in vivo growth and protein-expression of <i>Escherichia coli</i> O157 strains in the bovine rumen. 2022 , 17, e0268645	
173	COR27/28 Regulate the Evening Transcriptional Activity of the RVE8-LNK1/2 Circadian Complex.	
172	O-GlcNAc modification of leucyl-tRNA synthetase 1 integrates leucine and glucose availability to regulate mTORC1 and the metabolic fate of leucine. 2022 , 13,	0
171	Influence of Short and Medium Distance Road Transport on the Acute Phase Proteins in Horses.	
170	Preparation and Curation of Omics Data for Genome-Wide Association Studies. 2022 , 127-150	
169	PAF1 and FACT cooperate with MLL-AF4 to drive enhancer activity in leukemia.	
168	A Chloroplast Protein Atlas Reveals Novel Structures and Spatial Organization of Biosynthetic Pathways.	0
167	SFPQ Promotes Lung Cancer Malignancy via Regulation of CD44 v6 Expression. 12,	1
166	Rapid and in-depth coverage of the (phospho-)proteome with deep libraries and optimal window design for dia-PASEF.	2
165	Proteomic analysis of the IPF mesenchymal progenitor cell nuclear proteome identifies abnormalities in key nodal proteins that underlie their fibrogenic phenotype. 2200018	

- 164 A plant tethering system for the functional study of protein-RNA interactions in vivo. **2022**, 18,
- 163 MRG proteins are shared by multiple protein complexes with distinct functions. **2022**, 100253 0
- 162 10,12-conjugated linoleic acid supplementation improves HDL composition and function in mice. **2022**, 100241 0
- 161 Mass spectrometry-based draft of the mouse proteome. 2
- 160 Identification of secreted proteins by comparison of protein abundance in conditioned media and cell lysates.
- 159 Deproteinization of Chitin Extracted with the Help of Ionic Liquids. **2022**, 27, 3983 0
- 158 Feline Adipose Derived Multipotent Stromal Cell Transdifferentiation Into Functional Insulin Producing Cell Clusters. 10,
- 157 MicroID2: A Novel Biotin Ligase Enables Rapid Proximity Dependent Proteomics. **2022**, 100256 1
- 156 An analysis of proteogenomics and how and when transcriptome-informed reduction of protein databases can enhance eukaryotic proteomics. **2022**, 23, 1
- 155 Modification of G-protein biochemistry and its effect on plant/environment interaction. **2022**,
- 154 The structure of EXTL3 helps to explain the different roles of bi-domain exostosins in heparan sulfate synthesis. **2022**, 13, 2
- 153 Protease inhibitors from *Solanum chacoense* inhibit *Pectobacterium* virulence by reducing bacterial protease activity and motility. 2
- 152 GTSF1 accelerates target RNA cleavage by PIWI-clade Argonaute proteins. 1
- 151 Defects in autophagy lead to selective in vivo changes in turnover of cytosolic and organelle proteins in *Arabidopsis*. 0
- 150 Influence of short and medium distance road transport on the acute phase proteins in horses. **2022**, 104061
- 149 dia-PASEF data analysis using FragPipe and DIA-NN for deep proteomics of low sample amounts. **2022**, 13, 3
- 148 Systems-level patterns in biological processes are changed under prolongevity interventions and across biological age.
- 147 The p97 segregase cofactor Ubxn7 facilitates replisome disassembly during S-phase. **2022**, 102234 0

146	IGDQ motogenic peptide gradient induces directional cell migration through integrin $\alpha 5 \beta 1$ activation in MDA-MB-231 metastatic breast cancer cells. 2022 , 31, 100816	0
145	Pan-Cancer Analysis Reveals Recurrent BCAR4 Gene Fusions across Solid Tumors. OF1-OF8	
144	Catalytic cycling of human mitochondrial Lon protease. 2022 ,	1
143	Bioinformatic Analysis to Investigate Metaproteome Composition Using Trans-Proteomic Pipeline. 2022 , 2,	0
142	Dominant-Negative Form of SIGIRR: SIGIRRE8 Promotes Tumor Growth Through Regulation of Metabolic Pathways.	
141	Differential Excretory/Secretory Proteome of the Adult Female and Male Stages of the Human Blood Fluke, <i>Schistosoma mansoni</i> . 1,	0
140	Quantitative comparison of manuka and clover honey proteomes with royal jelly.	
139	An Sfi1-like centrin-interacting centriolar plaque protein affects nuclear microtubule homeostasis.	
138	Health Beneficial Bioactivities of Faba Bean Gastrointestinal (In Vitro) Digestate in Comparison to Soybean and Pea. 2022 , 23, 9210	0
137	High-throughput mass spectrometry maps the sepsis plasma proteome and differences in response.	1
136	Regulation of the Signal-Dependent E Protein HEBA1t Through a YYY Motif Is Required for Progression Through T Cell Development. 13,	0
135	Isolation of a virus causing a chronic infection in the archaeal model organism <i>Haloferax volcanii</i> reveals antiviral activities of a provirus. 2022 , 119,	0
134	Vimentin intermediate filaments provide structural stability to the mammalian Golgi apparatus.	
133	Tandem mass tag labeling to assess proteome differences between intermediate and very tender beef steaks. 2022 , 100,	0
132	Maturation and substrate processing topography of the <i>Plasmodium falciparum</i> invasion/egress protease plasmepsin X. 2022 , 13,	0
131	Composition and organization of kinetochores show plasticity in apicomplexan chromosome segregation. 2022 , 221,	1
130	Extracellular vesicles enriched in connexin 43 promote a senescent phenotype in bone and synovial cells contributing to osteoarthritis progression. 2022 , 13,	2
129	Metaproteome plasticity sheds light on the ecology of the rumen microbiome and its connection to host traits.	0

128	Immunoproteome profiling of <i>Listeria monocytogenes</i> under mild acid and salt stress conditions. 2200082	
127	Proteomics reveals multiple effects of titanium dioxide and silver nanoparticles in the metabolism of turbot, <i>Scophthalmus maximus</i> . 2022, 136110	0
126	A multifaceted gradient in human cerebellum of structural and functional development.	0
125	Comparative proteomics of adult <i>Paragonimus kellicotti</i> excretion/secretion products released in vitro or present in the lung cyst nodule. 2022, 16, e0010679	0
124	Rapid and in-depth coverage of the (phospho-)proteome with deep libraries and optimal window design for dia-PASEF. 2022, 100279	3
123	Proteome of the Wood Decay Fungus <i>Fomitopsis pinicola</i> Is Altered by Substrate.	
122	Exogenous cholesterol acquisition signaling in LH-responsive MA-10 Leydig cells and in adult mice. 2022, 254, 187-199	0
121	Identification of secreted proteins by comparison of protein abundance in conditioned media and cell lysates. 2022, 655, 114846	0
120	Integrated Profiling of Gram-Positive and Gram-Negative Probiotic Genomes, Proteomes and Metabolomes Revealed Small Molecules with Differential Growth Inhibition of Antimicrobial-Resistant Pathogens. 1-23	0
119	Tandem mass tag proteomic and untargeted metabolomic profiling reveals altered serum and CSF biochemical datasets in iron deficient monkeys. 2022, 45, 108591	1
118	Bioinformatics Resources, Tools, and Strategies in Designing Therapeutic Proteins. 2022, 91-123	0
117	Outer Membrane Vesicles of <i>Actinobacillus pleuropneumoniae</i> Exert Immunomodulatory Effects on Porcine Alveolar Macrophages.	0
116	The SARS-CoV-2 Spike S1 Protein Induces Global Proteomic Changes in A11-Like Rat L2 Cells that are Attenuated by Hyaluronan.	0
115	Not4-dependent targeting of MMF1 mRNA to mitochondria limits its expression via ribosome pausing, Egd1 ubiquitination, Caf130, No-Go-Decay and autophagy.	0
114	In vivo Safety and Immunoactivity of Oncolytic Jurona Virus in Hepatocellular Carcinoma: A Comprehensive Proteogenomic Analysis.	0
113	A multifaceted proteomics strategy in combination with an updated proteome provides insights into the mechanism of calcification in coccolithophores.	0
112	An Aurora B-RPA signaling axis secures chromosome segregation fidelity.	0
111	Proteogenomic analysis of cancer aneuploidy and normal tissues reveals divergent modes of gene regulation across cellular pathways. 11,	0

110	Reduced SPAG17 expression in systemic sclerosis triggers myofibroblast transition and drives fibrosis. 2022 ,	0
109	Comparison of cat and human calcium oxalate monohydrate kidney stone matrix proteomes.	1
108	Proteomic and bioinformatic analyses of proteins in the outer membrane and extracellular compartments and outer membrane vesicles of <i>Candidatus Liberibacter</i> species. 13,	0
107	Circular RNA hsa_circ_0062682 Binds to YBX1 and Promotes Oncogenesis in Hepatocellular Carcinoma. 2022 , 14, 4524	0
106	Transcription factors interact with RNA to regulate genes.	0
105	Comparative Analysis of Co-Cultured Amniotic Cell-Conditioned Media with Cell-Free Amniotic Fluid Reveals Differential Effects on Epithelial-Mesenchymal Transition and Myofibroblast Activation. 2022 , 10, 2189	1
104	A Parallelization Strategy for the Time Efficient Analysis of Thousands of LC/MS Runs in High-Performance Computing Environment.	1
103	On the role of cell surface associated, mucin-like glycoproteins in the pennate diatom <i>Craspedostauros australis</i> (Bacillariophyceae).	1
102	C1orf112 is a novel regulator of interstrand crosslink that decreases FIGLN1-RAD51 interaction.	0
101	Genetic variation and structural diversity in major seed proteins among and within <i>Camelina</i> species. 2022 , 256,	0
100	MetaLP: An integrative linear programming method for protein inference in metaproteomics. 2022 , 18, e1010603	0
99	Subcellular localization of type IV pili regulates bacterial multicellular development. 2022 , 13,	2
98	Study on Tissue Homogenization Buffer Composition for Brain Mass Spectrometry-Based Proteomics. 2022 , 10, 2466	1
97	Proteomic consequences of TDA1 deficiency in <i>Saccharomyces cerevisiae</i> : Protein kinase Tda1 is essential for Hxk1 and Hxk2 serine 15 phosphorylation. 2022 , 12,	0
96	Mass Spectrometry-Based Proteomics of Human Milk to Identify Differentially Expressed Proteins in Women with Breast Cancer versus Controls. 2022 , 10, 36	1
95	PRAMEL7/CUL2 axis regulates NuRD stability to establish ground-state pluripotency in embryonic stem cells.	0
94	MSFragger-Labile: A Flexible Method to Improve Labile PTM Analysis in Proteomics.	0
93	Essential Functions of Calmodulin and Identification of Its Proximal Interacting Proteins in Tachyzoite-Stage <i>Toxoplasma gondii</i> via BiOID Technology. 2022 , 10,	0

92	MSBooster: Improving Peptide Identification Rates using Deep Learning-Based Features.	1
91	NIMA-related kinase 9 regulates the phosphorylation of the essential myosin light chain in the heart. 2022 , 13,	0
90	Dual roles of mTORC1-dependent activation of the ubiquitin-proteasome system in muscle proteostasis. 2022 , 5,	0
89	CKL2 mediates the crosstalk between abscisic acid and brassinosteroid signaling to promote swift growth recovery after stress in Arabidopsis.	0
88	Genetic Code Expansion in <i>Pseudomonas putida</i> KT2440.	0
87	One-stop analysis of DIA proteomics data using MSFragger-DIA and FragPipe computational platform.	0
86	Comparative Evaluation of Proteome Discoverer and FragPipe for the TMT-Based Proteome Quantification.	0
85	Identification of proteomic landscape of drug-binding proteins in live cells by proximity-dependent target ID. 2022 ,	0
84	RAD51AP1 regulates ALT-HDR through chromatin-directed homeostasis of TERRA. 2022 , 82, 4001-4017.e7	2
83	Novel antimicrobial activity of protein produced by <i>Streptomyces lividans</i> TK24 against the phytopathogen <i>Clavibacter michiganensis</i> . 2022 , 204,	0
82	Proteomics analysis of MSN, MWCNT and ZnO nanoparticle-induced alteration in prepubertal rat ovary.	0
81	Overview and considerations in bottom-up proteomics.	2
80	Systematic proximal mapping of the classical RAD51 paralogs unravel functionally and clinically relevant interactors for genome stability. 2022 , 18, e1010495	0
79	SEPeQuant enables comprehensive protein isoform characterization in shotgun proteomics.	0
78	Effects of an exogenous ketone ester using multi-omics in skeletal muscle of aging C57BL/6J male mice. 9,	1
77	Repurposing live attenuated trivalent MMR vaccine as cost-effective cancer immunotherapy. 12,	0
76	The Shared Proteome of the Apomictic Fern <i>Dryopteris affinis</i> ssp. <i>affinis</i> and Its Sexual Relative <i>Dryopteris oreades</i> . 2022 , 23, 14027	0
75	Gallic Acid has an inhibitory effect on skin squamous cell carcinoma and acts on the heat shock protein HSP90AB1. 2022 , 147041	0

74	The Ras GTPase -activating-like protein IQGAP1 bridges Gasdermin D to the ESCRT system to promote IL -1 β release via exosomes.	0
73	Vaping Additives Cannabinoid Oil and Vitamin E Acetate Adhere to and Damage the Human Airway Epithelium.	2
72	Dissecting Regulators of Aging and Age-Related Macular Degeneration in the Retinal Pigment Epithelium. 2022 , 2022, 1-19	2
71	Multi-omics endotype of preterm infants with bronchopulmonary dysplasia and pulmonary hypertension.	0
70	Functional divergence of the sarcomeric myosin, MYH7b, supports species-specific biological roles. 2022 , 102657	1
69	Mass Spectrometry-based Methodologies for Studying Proteolytic Networks and the Degradome. 2016 , 396-410	0
68	Decreased methylglyoxal-mediated protein glycation in the healthy aging mouse model of ectopic expression of UCP1 in skeletal muscle. 2023 , 59, 102574	0
67	Differential affinity chromatography reveals a link between Porphyromonas gingivalis-induced changes in vascular smooth muscle cell differentiation and the type 9 secretion system. 12,	0
66	Poly ADP-Ribose Signaling is Dysregulated in Huntington's Disease Patients.	0
65	Gilthead Seabream Liver Integrative Proteomics and Metabolomics Analysis Reveals Regulation by Different Prosurvival Pathways in the Metabolic Adaptation to Stress. 2022 , 23, 15395	0
64	Probiotic Properties and Proteomic Analysis of Pediococcus pentosaceus 1101. 2023 , 12, 46	0
63	Identification of the Collagen Types Essential for Mammalian Breast Acinar Structures. 2022 , 8, 837	0
62	Redox proteomics and structural analyses provide insightful implications for additional non-catalytic thiol-disulfide motifs in PDIs. 2022 , 102583	0
61	The proteomic analysis of bovine embryos developed in vivo or in vitro reveals the contribution of the maternal environment to early embryo. 2022 , 23,	1
60	Histopathologic and proteogenomic heterogeneity reveals features of clear cell renal cell carcinoma aggressiveness. 2022 ,	1
59	Secretome Analysis of the Plant Biostimulant Bacteria Strains Bacillus subtilis (EB2004S) and Lactobacillus helveticus (EL2006H) in Response to pH Changes. 2022 , 23, 15144	1
58	Slit2 signaling stimulates Ewing sarcoma growth. 2022 , 13, 88-99	0
57	Regional and disease specific human lung extracellular matrix composition. 2022 , 121960	0

- 56 HLA-Glyco: A large-scale interrogation of the glycosylated immunopeptidome. ○
- 55 Dietary sugar shifts mitochondrial metabolism and small RNA biogenesis in sperm. ○
- 54 Mink1 regulates spemann organizer cell fate in the xenopus gastrula via Hmga2. **2022**, ○
- 53 Genotypic and phenotypic differences among phase-variable colony variants conserved across *Gardnerella* spp. ○
- 52 Proximity proteomics reveals role of Abelson interactor 1 in the regulation of TAK1 / RIPK1 signaling. ○
- 51 Artificial extracellular matrix scaffolds of mobile molecules enhance maturation of human stem cell-derived neurons. **2023**, ○
- 50 Excretory/Secretory Proteome of Females and Males of the Hookworm *Ancylostoma ceylanicum*. **2023**, 12, 95 ○
- 49 Adaptive evolution of carnivory in *Nepenthes* pitcher plants: a comparative transcriptomics and proteomics perspective. ○
- 48 Trans-Proteomic Pipeline: Robust Mass Spectrometry-Based Proteomics Data Analysis Suite. ○
- 47 Benchmarking commonly used software suites and analysis workflows for DIA proteomics and phosphoproteomics. **2023**, 14, ○
- 46 Oridonin Induces Apoptosis in Esophageal Squamous Cell Carcinoma by Inhibiting Cytoskeletal Protein LASP1 and PDLIM1. **2023**, 28, 805 ○
- 45 Proteoglycans in breast cancer, identification and characterization by LC-MS/MS assisted proteomics approach: A review. 2200046 ○
- 44 Proximity-enhanced protein crosslinking through an alkene-tetrazine reaction. **2023**, 132, 106359 ○
- 43 The bovine uterine fluid proteome is more impacted by the stage of the estrous cycle than the proximity of the ovulating ovary in the periconception period. **2023**, 198, 332-343 ○
- 42 IDIA: An Integrative Signal Extractor for Data-Independent Acquisition Proteomics. **2022**, ○
- 41 Epigenetic regulation of Neuregulin 1 promotes breast cancer progression associated to hyperglycemia. **2023**, 14, ○
- 40 The use of serum protein analysis in the diagnosis of fatal envenomation via *Crotalus horridus* (timber rattlesnake). ○
- 39 Testis-enriched ferlin, FER1L5, is required for Ca²⁺-activated acrosome reaction and male fertility. **2023**, 9, 1

- 38 Unraveling the Relevance of Tissue-Specific Decellularized Extracellular Matrix Hydrogels for Vocal Fold Regenerative Biomaterials: A Comprehensive Proteomic and In Vitro Study. 2200095 ○
- 37 Membranous Nephropathy in Syphilis is Associated with Neuron-Derived Neurotrophic Factor. **2023**, Publish Ahead of Print, ○
- 36 Microphysiological system recapitulating the pathophysiology of adipose tissue in obesity. **2023**, ○
- 35 Comparative- and network-based proteomic analysis of bacterial chondronecrosis with osteomyelitis lesions in broiler proximal tibiae identifies new molecular signatures of lameness. **2023**, 13, ○
- 34 Impact of Coenzyme Q10 Supplementation on Skeletal Muscle Respiration, Antioxidants, and the Muscle Proteome in Thoroughbred Horses. **2023**, 12, 263 ○
- 33 A large-scale proteogenomic atlas of pear. **2023**, 16, 599-615 ○
- 32 Human Serum Mediated Bacteriophage Life Cycle Switch in *Aggregatibacter actinomycetemcomitans* Is Linked to Pyruvate Dehydrogenase Complex. **2023**, 13, 436 ○
- 31 Piperlongumine conjugates induce targeted protein degradation. **2023**, 30, 203-213.e17 1
- 30 Vir1p, the Yeast Homolog of Virilizer, is Required for mRNA m6A Methylation and Meiosis. ○
- 29 Quantitative comparison of manuka and clover honey proteomes with royal jelly. **2023**, 18, e0272898 ○
- 28 Interactomes of Glycogen Synthase Kinase-3 Isoforms. **2023**, 22, 977-989 ○
- 27 Nitric oxide suppression by secreted frizzled-related protein 2 drives retinoblastoma. **2023**, 42, 112103 ○
- 26 The sperm-interacting proteome in the bovine isthmus and ampulla during the periovulatory period. **2023**, 14, ○
- 25 Embryonic poly(A)-binding protein interacts with translation-related proteins and undergoes phosphorylation on the serine, threonine, and tyrosine residues in the mouse oocytes and early embryos. ○
- 24 *Vibrio natriegens* genome-scale modeling reveals insights into halophilic adaptations and resource allocation. **2023**, 19, ○
- 23 Proteome Analysis of *Nicotiana tabacum* Cells following Isonitrosoacetophenone Treatment Reveals Defence-Related Responses Associated with Priming. **2023**, 12, 1137 ○
- 22 ARF-family global interactome mapping uncovers spatial organization of cellular signaling pathways. ○
- 21 The triticale mature pollen and stigma proteomes assembling the proteins for a productive encounter. **2023**, 278, 104867 ○

- 20 Developmental mRNA clearance by PIWI-bound endo-siRNAs in Paramecium. **2023**, 42, 112213 ○
- 19 Systematic Identification of Post-Transcriptional Regulatory Modules. ○
- 18 Acute ACAT1/SOAT1 Blockade Increases MAM Cholesterol and Strengthens ER-Mitochondria Connectivity. **2023**, 24, 5525 ○
- 17 ProInfer: An interpretable protein inference tool leveraging on biological networks. **2023**, 19, e1010961 ○
- 16 Vir1p, the yeast homolog of virilizer, is required for mRNA m6A methylation and meiosis. ○
- 15 MBNL1 regulates programmed postnatal switching between regenerative and differentiated cardiac states. ○
- 14 Cryo-EM reconstruction of the human 40S ribosomal subunit at 2.15 Å resolution. ○
- 13 Global detection of human variants and isoforms by deep proteome sequencing. ○
- 12 Enhanced Ca²⁺-channeling complex formation at the ER-mitochondria interface underlies the pathogenesis of alcohol-associated liver disease. **2023**, 14, ○
- 11 Proteomic Profiling of Fallopian Tube-Derived Extracellular Vesicles Using a Microfluidic Tissue-on-Chip System. **2023**, 10, 423 ○
- 10 MSFragger-Labile: A Flexible Method to Improve Labile PTM Analysis in Proteomics. **2023**, 100538 ○
- 9 Rothia from the Human Nose Inhibit Moraxella catarrhalis Colonization with a Secreted Peptidoglycan Endopeptidase. ○
- 8 COLD REGULATED GENE 27 and 28 antagonize the transcriptional activity of the RVE8/LNK1/LNK2 circadian complex. ○
- 7 Characterization of methionine dependence in melanoma cells. ○
- 6 Analysis of Ku70 S155 Phospho-Specific BioID2 Interactome Identifies Ku Association with TRIP12 in Response to DNA Damage. **2023**, 24, 7041 ○
- 5 A cell-free antigen processing system informs HIV-1 epitope selection and vaccine design. **2023**, 220, ○
- 4 A new window into fish welfare: A proteomic discovery study of stress biomarkers in the skin mucus of gilthead seabream (Sparus aurata). **2023**, 104904 ○
- 3 Mass Spectrometry based identification of site-specific proteomic alterations and potential pathways underlying the pathophysiology of schizophrenia. ○

- 2 Dataset on the proteomic response during ferroptosis induction via tamoxifen induced GPX4 KO in mouse embryonic fibroblasts. **2023**, 109170 ○
- 1 Organelle interactions compartmentalize hepatic fatty acid trafficking and metabolism. **2023**, 42, 112435 ○