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Mass spectrometry-based proteomics

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#	Paper	IF	Citations
2241	Bibliography. 255-272		
2240	Television Pickup Tubes and the Problem of Vision. <b>1948</b> , 131-166		100
2239	Chapter 8 Colchicine and Related Compounds. <b>1960</b> , 6, 247-288		4
2238	Innervation of spinal dura mater and dura mater of the posterior cranial fossa. <b>1961</b> , 11, 800-9		92
2237	The Fate of Nitrogen Applied to Soils. <b>1966</b> , 18, 219-258		205
2236	Paragonimus and paragonimiasis. <b>1969</b> , 7, 375-87		34
2235	Microbial transformations of antibiotics. <b>1971</b> , 14, 123-50		14
2234	Chapter 16 Integral and Differential Quadrature. <b>1973</b> , 221-254		
2233	Bacterial Glycolipids and Glycophospholipids. <b>1975</b> , 12, 141-167		42
2232	Mechanically Deboned Red Meat. 1981, 23-107		28
2231	16 Bacteriophage T4 Polynucleotide Kinase. <b>1981</b> , 299-314		25
2230	Biomass: Solar Energy Through Biology (Fuels Now and in the Future. <b>1982</b> , 16, 411-429		
2229	Morphogenesis and fine structure of Frankia (Actinomycetales): the microsymbiont of nitrogen-fixing actinorhizal root nodules. <b>1987</b> , 109, 1-88		7 <sup>2</sup>
2228	Purification of transforming growth factors beta 1 and beta 2 from bovine bone and cell culture assays. <b>1991</b> , 198, 317-27		24
2227	Chapter 95 Light scattering in intermetallic compounds. <b>1991</b> , 14, 163-223		1
2226	Visual Control of Human Locomotion. <b>1991</b> , 55-97		22
2225	Comparative Study of the Deactivation of Group Viii Metal Catalysts by Thiophene Poisoning in Ethylbenzene Hydrogenation. <b>1991</b> , 68, 557-564		23

2224 Copyright page. **1992**, 89, iv

2223 Organization and plasticity of GABA neurons and receptors in monkey visual cortex. <b>1992</b> , 90, 477-502		36
The Role of Cultural Schemata In Reading Comprehension. <b>1993</b> , 145-155		4
2221 Activation of reactants by hydroxyl groups of solid acids. An FTIR study. <b>1995</b> , 94, 509-516		12
2220 Chapter 11 Salt Marshes. <b>1995</b> , 53, 307-332		10
2219 The Discrete-Time Kalman Filter Under Uncertainty in Noise Covariances. <b>1996</b> , 363-415		
2218 Protein Analysis and Purification. <b>1996</b> ,		17
2217 Chapter 4. Melatonin Receptor Ligands and Their Potential Clinical Applications. <b>1997</b> , 31-40		6
2216 Glossary of Terms Used in Computational Drug Design (IUPAC Recommendations 1997). <b>1998</b> , 33, 397	-409	15
2215 3 Models of chromatography. <b>1998</b> , 21, 43-78		1
Adsorption of surfactants on diesel engine soot and its application in carbody washing. <b>1999</b> , 120, 177	-212	1
2213 Invariant scaling relations across tree-dominated communities. <i>Nature</i> , <b>2001</b> , 410, 655-60	50.4	490
Formation of residual NAPL in three-phase systems: Experiments and numerical simulations. <b>2002</b> , 47, 193-200		
Proteomics and transcriptomics analyses of secretagogin down-regulation in human non-functional pituitary adenomas. <b>2003</b> , 6, 189-202		35
2210 Update on chloroplast proteomics. <b>2003</b> , 78, 181-93		14
2209 Application of genomics and proteomics in Type 1 diabetes pathogenesis research. <b>2003</b> , 3, 743-57		18
High-throughput applications of phage display in proteomic analyses. <b>2003</b> , 2, 261-270		18
2207 Rediscovering the sweet spot in drug discovery. <b>2003</b> , 8, 1067-77		164

2206	Functional genomics: identifying drug targets for parasitic diseases. <b>2003</b> , 19, 538-43	21
2205	Peptide and protein de novo sequencing by mass spectrometry. <b>2003</b> , 13, 595-601	127
2204	Organelle proteomics: looking at less to see more. <b>2003</b> , 13, 629-38	150
2203	Systems biology in neuroscience: bridging genes to cognition. <b>2003</b> , 13, 577-82	44
2202	Targeting hepatocytes from liver tissue by laser capture microdissection and proteomics expression profiling. <b>2003</b> , 24, 3800-5	25
2201	A planar microfabricated nanoelectrospray emitter tip based on a capillary slot. <b>2003</b> , 24, 3640-7	30
2200	Current literature in mass spectrometry. <b>2003</b> , 38, 781-92	1
2199	Two-dimensional microfabricated sources for nanoelectrospray. <b>2003</b> , 38, 1259-64	19
2198	Current Awareness on Comparative and Functional Genomics. 2003, 4, 450-457	1
2197	Proposal for a standard representation of two-dimensional gel electrophoresis data. <b>2003</b> , 4, 492-501	6
2196	Native electron capture dissociation for the structural characterization of noncovalent interactions in native cytochrome C. <b>2003</b> , 42, 4900-4	76
2195	The complexity of complexes in signal transduction. <b>2003</b> , 84, 783-94	151
2194	Proteomics for cell protein expression profiling. <b>2003</b> , 121, XI-XII	1
2193	Strategic shotgun proteomics approach for efficient construction of an expression map of targeted protein families in hepatoma cell lines. <b>2003</b> , 3, 2472-86	88
2192	Generation of bioreagents for protein chips. <b>2003</b> , 3, 2123-34	41
2191	Targeted lipidomics using electron capture atmospheric pressure chemical ionization mass spectrometry. <b>2003</b> , 17, 2168-76	165
2190	A method for reducing the time required to match protein sequences with tandem mass spectra. <b>2003</b> , 17, 2310-6	408
2189	Mass spectrometric analysis of maleimide CyDye labelled model peptides. <b>2003</b> , 17, 2563-6	7

# (2003-2003)

2188	Correction: Corrigendum: Invariant scaling relations across tree-dominated communities. <i>Nature</i> , <b>2003</b> , 425, 741-741	50.4	0
2187	Global analysis of protein expression in yeast. <i>Nature</i> , <b>2003</b> , 425, 737-41	50.4	3045
2186	Protein kinase C switches the Raf kinase inhibitor from Raf-1 to GRK-2. <i>Nature</i> , <b>2003</b> , 426, 574-9	50.4	299
2185	Proteomic characterization of the human centrosome by protein correlation profiling. <i>Nature</i> , <b>2003</b> , 426, 570-4	50.4	1077
2184	Proteomic analysis of post-translational modifications. <b>2003</b> , 21, 255-61		1566
2183	Proteomics technologies: probing the proteome. <i>Nature</i> , <b>2003</b> , 424, 581-7	50.4	5
2182	Target discovery. <b>2003</b> , 2, 831-8		267
2181	Cancer diagnosis using proteomic patterns. <b>2003</b> , 3, 411-20		128
2180	Protein expression profiling arrays: tools for the multiplexed high-throughput analysis of proteins. <b>2003</b> , 1, 3		29
2179	In silico proteome analysis to facilitate proteomics experiments using mass spectrometry. <b>2003</b> , 1, 5		76
2178	Physiological and proteomic approaches to studying prefertilization events in the human. 2003, 7, 419-	27	28
2177	Heterogeneity analysis of the human pituitary proteome. <b>2003</b> , 49, 1740-51		35
2176	A microfluidic electrocapture device in sample preparation for protein analysis by MALDI mass spectrometry. <b>2003</b> , 75, 5213-9		38
2175	Direct atmospheric pressure coupling of polyacrylamide gel electrophoresis to mass spectrometry for rapid protein sequence analysis. <b>2003</b> , 2, 610-7		6
2174	Application of molecular beam deflection time-of-flight mass spectrometry to peptide analysis. <b>2003</b> , 75, 5512-6		15
2173	The impact of new technologies on human population studies. <b>2003</b> , 544, 349-60		15
2172	Neuropeptides in perisympathetic organs of Manduca sexta: specific composition and changes during the development. <b>2003</b> , 24, 1457-64		26
2171	Identification of Fyn-binding proteins in MC/9 mast cells using mass spectrometry. 2003, 310, 202-8		13

2170	Mass spectrometry-based clinical proteomics. <b>2003</b> , 4, 463-76	109
2169	Multiprotein signaling complexes and regulation of cardiac phenotype. <b>2003</b> , 35, 1027-33	11
2168	Integrated analysis of protein composition, tissue diversity, and gene regulation in mouse mitochondria. <b>2003</b> , 115, 629-40	742
2167	Dopamine receptor-interacting proteins: the Ca(2+) connection in dopamine signaling. <b>2003</b> , 24, 486-92	141
2166	Functional genomics and proteomics as a foundation for systems biology. <b>2003</b> , 2, 175-84	63
2165	What makes a mitochondrion?. <b>2003</b> , 4, 218	11
2164	Greedily building protein networks with confidence. <b>2003</b> , 19, 1869-74	49
2163	Inventories to insights. <b>2003</b> , 161, 465-9	20
2162	PROTEOME-3D: an interactive bioinformatics tool for large-scale data exploration and knowledge discovery. <b>2003</b> , 2, 1164-76	9
2161	Interactions between centromere complexes in Saccharomyces cerevisiae. 2003, 14, 4931-46	78
2160	The application of clinical proteomics to cancer and other diseases. <b>2003</b> , 41, 1562-70	40
2159	Identification of novel signaling complexes by functional proteomics. <b>2003</b> , 93, 595-603	50
2158	Integrating proteomic and functional genomic technologies in discovery-driven translational breast cancer research. <b>2003</b> , 2, 369-77	42
2157	Biotechnology: impact on biological warfare and biodefense. <b>2003</b> , 1, 161-8	44
2156	Rds3p is required for stable U2 snRNP recruitment to the splicing apparatus. <b>2003</b> , 23, 7339-49	24
2155	Identification of metal-binding proteins in human hepatoma lines by immobilized metal affinity chromatography and mass spectrometry. <b>2003</b> , 2, 1306-18	82
2154	Breast cancer: when proteomics challenges biological complexity. <b>2003</b> , 2, 281-91	54
2153	Toxicogenomics in drug development. <b>2003</b> , 31, 471-9	52

# (2004-2003)

2152	Finding partners: emerging protein interaction technologies applied to signaling networks. <b>2003</b> , 2003, pe56	10
2151	Funktionelle molekulare Analyse: Wie ist die Proteinvielfalt beherrschbar?. <b>2003</b> , 51, 1041-1046	1
2150	Bioinformatic analysis of the nucleolus. <b>2003</b> , 376, 553-69	114
2149	Identification of surrogate markers for determining drug activity using proteomics. 2003, 31, 1488-90	3
2148	Clinical applicability of mass spectrometry for inhaled carbon compounds and the characterization of trace element patterns in body fluids. <b>2004</b> , 5, 89-106	3
2147	Utility of Chemical Derivatization Schemes for Peptide Mass Fingerprinting. 52-82	
2146	2D DIGE. <b>2004</b> ,	
2145	Proteomic Studies of Human Lymphocytes: New Insights into HIV Lymphocyte Infection?. <b>2004</b> , 245-262	2
2144	. 2004,	7
2143	Tracking cell signaling protein expression and phosphorylation by innovative proteomic solutions. <b>2004</b> , 5, 69-77	34
2142	Immune systems biology: immunoprofiling of cells and molecules. <b>2004</b> , 36, 520-4	13
2141	Proteomic analyses using an accurate mass and time tag strategy. <b>2004</b> , 37, 621-4, 626-33, 636 passim	135
2140	Challenges in the Overall Analysis of Microbial Proteomes. <b>2004</b> , 2, 79-86	
2139	The use of laser capture microscopy in proteomics researcha review. <b>2004</b> , 20, 155-60	13
2138	Advancement of biomarker discovery and validation through the HUPO plasma proteome project. <b>2004</b> , 20, 131-4	39
2137	Integrated analysis of genetic, genomic and proteomic data. <b>2004</b> , 1, 67-75	43
2136	New approaches towards integrated proteomic databases and depositories. <b>2004</b> , 1, 267-74	7
2135	Proteomic analysis of mitochondrial proteins. <b>2004</b> , 61, 31-48	

2134	Proteomics: current techniques and potential applications to lung disease. <b>2004</b> , 287, L1-23	88
2133	Membrane protease proteomics: Isotope-coded affinity tag MS identification of undescribed MT1-matrix metalloproteinase substrates. <b>2004</b> , 101, 6917-22	245
2132	Oda5p, a novel axonemal protein required for assembly of the outer dynein arm and an associated adenylate kinase. <b>2004</b> , 15, 2729-41	75
2131	Electrophoretic Prefractionation for Comprehensive Analysis of Proteomes. <b>2004</b> , 93-118	9
2130	Chloroplast proteomics: potentials and challenges. <b>2004</b> , 55, 1213-20	68
2129	High-throughput proteomics using Fourier transform ion cyclotron resonance mass spectrometry. <b>2004</b> , 1, 87-95	40
2128	PINdb: a database of nuclear protein complexes from human and yeast. <b>2004</b> , 20, 1413-5	32
2127	Quantitative proteomic analysis of metabolic regulation by copper ions in Methylococcus capsulatus (Bath). <b>2004</b> , 279, 51554-60	71
2126	Protein stamping for MALDI mass spectrometry using an electrowetting-based microfluidic platform. <b>2004</b> ,	26
2125	Pleistocene glaciation in Spain. <b>2004</b> , 2, 389-394	13
2125	Pleistocene glaciation in Spain. 2004, 2, 389-394  Identification of biochemical adaptations in hyper- or hypocontractile hearts from phospholamban mutant mice by expression proteomics. 2004, 101, 2241-6	13 29
	Identification of biochemical adaptations in hyper- or hypocontractile hearts from phospholamban	
2124	Identification of biochemical adaptations in hyper- or hypocontractile hearts from phospholamban mutant mice by expression proteomics. <b>2004</b> , 101, 2241-6  How are we going to discover new cancer biomarkers? A proteomic approach for bladder cancer.	29
2124	Identification of biochemical adaptations in hyper- or hypocontractile hearts from phospholamban mutant mice by expression proteomics. <b>2004</b> , 101, 2241-6  How are we going to discover new cancer biomarkers? A proteomic approach for bladder cancer. <b>2004</b> , 50, 793-5	29
2124 2123 2122	Identification of biochemical adaptations in hyper- or hypocontractile hearts from phospholamban mutant mice by expression proteomics. 2004, 101, 2241-6  How are we going to discover new cancer biomarkers? A proteomic approach for bladder cancer. 2004, 50, 793-5  Genomics and proteomics tools for compound mode-of-action studies in drug discovery. 2004, 5, 395-404  Improved peptide identification in proteomics by two consecutive stages of mass spectrometric	29 30 11
2124 2123 2122 2121	Identification of biochemical adaptations in hyper- or hypocontractile hearts from phospholamban mutant mice by expression proteomics. 2004, 101, 2241-6  How are we going to discover new cancer biomarkers? A proteomic approach for bladder cancer. 2004, 50, 793-5  Genomics and proteomics tools for compound mode-of-action studies in drug discovery. 2004, 5, 395-404  Improved peptide identification in proteomics by two consecutive stages of mass spectrometric fragmentation. 2004, 101, 13417-22  The power and the limitations of cross-species protein identification by mass spectrometry-driven	29 30 11 288
2124 2123 2122 2121 2120	Identification of biochemical adaptations in hyper- or hypocontractile hearts from phospholamban mutant mice by expression proteomics. 2004, 101, 2241-6  How are we going to discover new cancer biomarkers? A proteomic approach for bladder cancer. 2004, 50, 793-5  Genomics and proteomics tools for compound mode-of-action studies in drug discovery. 2004, 5, 395-404  Improved peptide identification in proteomics by two consecutive stages of mass spectrometric fragmentation. 2004, 101, 13417-22  The power and the limitations of cross-species protein identification by mass spectrometry-driven sequence similarity searches. 2004, 3, 238-49  HysTaga novel proteomic quantification tool applied to differential display analysis of membrane	29 30 11 288 133

2116	Proteomic research: potential opportunities for clinical and physiological investigators. <b>2004</b> , 286, E863-74	32
2115	Molecular targets in immune-mediated diseases: focus on rheumatoid arthritis. <b>2004</b> , 8, 375-90	3
2114	Role of insulin action and cell size on protein expression patterns in adipocytes. <b>2004</b> , 279, 31902-9	78
2113	Analysis of curated and predicted plastid subproteomes of Arabidopsis. Subcellular compartmentalization leads to distinctive proteome properties. <b>2004</b> , 135, 723-34	71
2112	Proteomic mapping provides powerful insights into functional myelin biology. <b>2004</b> , 101, 4643-8	101
2111	Proteomic characterization of postmortem amyloid plaques isolated by laser capture microdissection. <b>2004</b> , 279, 37061-8	220
<b>21</b> 10	A tagging-via-substrate technology for detection and proteomics of farnesylated proteins. <b>2004</b> , 101, 12479-84	292
2109	Analyzing cellular biochemistry in terms of molecular networks. <b>2004</b> , 73, 1051-87	120
2108	Differential proteomics: an overview of gel and non-gel based approaches. <b>2004</b> , 3, 220-39	93
2107	MHC-bound antigens and proteomics for novel target discovery. <b>2004</b> , 5, 845-59	13
2106	Quantitative mass spectrometry reveals a role for the GTPase Rho1p in actin organization on the peroxisome membrane. <b>2004</b> , 167, 1099-112	132
2105	VHL-box and SOCS-box domains determine binding specificity for Cul2-Rbx1 and Cul5-Rbx2 modules of ubiquitin ligases. <b>2004</b> , 18, 3055-65	349
2104	Global investigation of p53-induced apoptosis through quantitative proteomic profiling using comparative amino acid-coded tagging. <b>2004</b> , 3, 998-1008	56
2103	Exploiting the kernel trick to correlate fragment ions for peptide identification via tandem mass spectrometry. <b>2004</b> , 20, 1948-54	86
2102	Application of the GA/KNN method to SELDI proteomics data. <b>2004</b> , 20, 1638-40	65
2101	Target class strategies in mass spectrometry-based proteomics. <b>2004</b> , 1, 57-66	10
2100	PathBLAST: a tool for alignment of protein interaction networks. <b>2004</b> , 32, W83-8	293
2099	Towards discovery-driven translational research in breast cancer. <b>2005</b> , 272, 2-15	42

	Tackling the plant proteome: practical approaches, hurdles and experimental tools. <b>2004</b> , 39, 715-33		264
2097	Scandinavian Congress of Physiology and Pharmacology, Odense, Denmark, October 11-14, 2003. <b>2004</b> , 181, 43-163		2
2096	Temporal analysis of phosphotyrosine-dependent signaling networks by quantitative proteomics. <b>2004</b> , 22, 1139-45		631
2095	Gaining confidence in high-throughput protein interaction networks. <b>2004</b> , 22, 78-85		372
2094	Intensity-based protein identification by machine learning from a library of tandem mass spectra. <b>2004</b> , 22, 214-9		256
2093	Proteomics in postgenomic neuroscience: the end of the beginning. <b>2004</b> , 7, 440-5		115
2092	Spread the word. <b>2004</b> , 5, 510-510		
2091	The ABC's (and XYZ's) of peptide sequencing. <b>2004</b> , 5, 699-711		829
2090	Serum protein profiling by SELDI mass spectrometry: detection of multiple variants of serum amyloid alpha in renal cancer patients. <b>2004</b> , 84, 845-56		184
2089	Predicting disease using genomics. <i>Nature</i> , <b>2004</b> , 429, 453-6	50.4	156
2088	The need for a public proteomics repository. <b>2004</b> , 22, 471-2		139
	The need for a public proteomics repository. <b>2004</b> , 22, 471-2  Genomics and proteomics: implications for inflammatory bowel diseases. <b>2004</b> , 10 Suppl 1, S1-6		139
2087			
2087	Genomics and proteomics: implications for inflammatory bowel diseases. <b>2004</b> , 10 Suppl 1, S1-6		6
2087 2086 2085	Genomics and proteomics: implications for inflammatory bowel diseases. <b>2004</b> , 10 Suppl 1, S1-6  High-throughput proteomics for alcohol research. <b>2004</b> , 28, 203-10		10
2087 2086 2085 2084	Genomics and proteomics: implications for inflammatory bowel diseases. 2004, 10 Suppl 1, S1-6  High-throughput proteomics for alcohol research. 2004, 28, 203-10  Proteomics of the Drosophila immune response. 2004, 22, 600-5		6 10 26
2087 2086 2085 2084	Genomics and proteomics: implications for inflammatory bowel diseases. 2004, 10 Suppl 1, S1-6  High-throughput proteomics for alcohol research. 2004, 28, 203-10  Proteomics of the Drosophila immune response. 2004, 22, 600-5  Functional genomics for parasitic nematodes and platyhelminths. 2004, 20, 178-84		6 10 26 24

2080	Proteomics in living cells. <b>2004</b> , 9, 262-7	21
2079	Proteomic approaches in brain research and neuropharmacology. <b>2004</b> , 500, 385-98	58
2078	Cell cycle goes global. <b>2004</b> , 16, 602-13	25
2077	Analysis of the human serum proteome. <b>2004</b> , 1, 101-225	89
2076	Recent advances in gel-based proteome profiling techniques. <b>2004</b> , 28, 63-76	23
2075	Application of microarrays in high-throughput enzymatic profiling. <b>2004</b> , 28, 227-39	5
2074	TANDEM: matching proteins with tandem mass spectra. <b>2004</b> , 20, 1466-7	2036
2073	Neuroproteomics: expression profiling of the brain's proteomes in health and disease. <b>2004</b> , 29, 1317-31	73
2072	Comparative proteomic analysis of human CD34+ stem/progenitor cells and mature CD15+ myeloid cells. <b>2004</b> , 22, 1003-14	36
2071	Mitochondria of protists. <b>2004</b> , 38, 477-524	261
2070	Open mass spectrometry search algorithm. <b>2004</b> , 3, 958-64	1191
2069	Strategies for automating top-down protein analysis with Q-FTICR MS. <b>2004</b> , 234, 175-184	19
2068	Selective enrichment of monospecific polyclonal antibodies for antibody-based proteomics efforts. <b>2004</b> , 1043, 33-40	46
2067	Focus on plant proteomics. <b>2004</b> , 42, 913-7	13
2066	A mini-review of mass spectrometry using high-performance FTICR-MS methods. <b>2004</b> , 378, 1048-58	46
2065	Proteomics for nasal secretion analysis. <b>2004</b> , 4, 224-9	11
2064	Plant proteome analysis. <b>2004</b> , 4, 285-98	235
2063	Improving large-scale proteomics by clustering of mass spectrometry data. <b>2004</b> , 4, 950-60	174

2062	Quantification of C-reactive protein in the serum of patients with rheumatoid arthritis using multiple reaction monitoring mass spectrometry and 13C-labeled peptide standards. <b>2004</b> , 4, 1175-86	373
2061	Identification of novel and downregulated biomarkers for alcoholism by surface enhanced laser desorption/ionization-mass spectrometry. <b>2004</b> , 4, 1187-94	83
2060	Has the yo-yo stopped? An assessment of human protein-coding gene number. <b>2004</b> , 4, 1712-26	75
2059	PhosphoSite: A bioinformatics resource dedicated to physiological protein phosphorylation. <b>2004</b> , 4, 1551-61	453
2058	Applications of proteomic methodologies to human pregnancy research: a growing gestation approaching delivery?. <b>2004</b> , 4, 1909-17	27
2057	Database-independent, database-dependent, and extended interpretation of peptide mass spectra in VEMS V2.0. <b>2004</b> , 4, 2583-93	56
2056	Characterization of a digested protein complex with quantitative aspects: an approach based on accurate mass chromatographic analysis with Fourier transform-ion cyclotron resonance mass spectrometry. <b>2004</b> , 4, 2558-66	17
2055	Challenges in mass spectrometry-based proteomics. <b>2004</b> , 4, 3686-703	149
2054	Current two-dimensional electrophoresis technology for proteomics. <b>2004</b> , 4, 3665-85	1355
2053	New mass spectrometric methods for the quantification of protein-ligand binding in solution. <b>2004</b> , 43, 22-5	26
2052	BioLogic gates enable logical transcription control in mammalian cells. <b>2004</b> , 87, 478-84	155
2051	Functional genomics studied by proteomics. <b>2004</b> , 26, 901-15	39
2050	Shared components of protein complexesversatile building blocks or biochemical artefacts?. <b>2004</b> , 26, 1333-43	38
2049	Neue massenspektrometrische Methoden zur Quantifizierung der Protein-Ligand-Assoziation in Läung. <b>2004</b> , 116, 22-25	4
2048	Immobilized pH gradients as a first dimension in shotgun proteomics and analysis of the accuracy of pI predictability of peptides. <b>2004</b> , 25, 936-45	139
2047	Genome-based proteomics. <b>2004</b> , 25, 1280-8	22
2046	New directions of miniaturization within the biomarker research area. <b>2004</b> , 25, 3479-91	23
2045	Proteomics and regulomics: the yin and yang of functional genomics. <b>2004</b> , 23, 25-33	18

2044 Application of proteomics technologies in the investigation of the brain. <b>2004</b> , 23, 231-58	111
$_{2043}$ Studying the interactome with the yeast two-hybrid system and mass spectrometry. <b>2004</b> , 23, 350-67	51
2042 Investigation of intact protein complexes by mass spectrometry. <b>2004</b> , 23, 368-89	503
The potentials of MS-based subproteomic approaches in medical science: the case of lysosomes and breast cancer. <b>2004</b> , 23, 393-442	16
2040 Selected reviews on Mass Spectrometric Topics XIII. <b>2004</b> , 23, 390-392	
2039 MALDI-TOF MS: a platform technology for genetic discovery. <b>2004</b> , 238, 173-188	15
2038 Impact of 'ome' analyses on inverse metabolic engineering. <b>2004</b> , 6, 204-11	85
2037 Fragmentation of amidinated peptide ions. <b>2004</b> , 15, 158-67	24
Selective molecular recognition of arginine by anionic salt bridge formation with bis-phosphate crown ethers: implications for gas phase peptide acidity from adduct dissociation. <b>2004</b> , 15, 616-24	23
2035 Development of an LC-MALDI method for the analysis of protein complexes. <b>2004</b> , 15, 803-22	72
Disposable chromatography for a high-throughput nano-ESI/MS and nano-ESI/MS-MS platform. <b>2004</b> , 15, 1333-40	13
2033 Modeling the resolution and sensitivity of FAIMS analyses. <b>2004</b> , 15, 1487-1498	81
Chemical probes and tandem mass spectrometry: a strategy for the quantitative analysis of proteomes and subproteomes. <b>2004</b> , 8, 66-75	132
2031 Native protein mass spectrometry: from intact oligomers to functional machineries. <b>2004</b> , 8, 519-26	247
Effect of buffer on peak shape of peptides in reversed-phase high performance liquid chromatography. <b>2004</b> , 1038, 77-84	64
Fully automated online multi-dimensional protein profiling system for complex mixtures. <b>2004</b> , 1057, 107-13	34
Proceedings of the 3rd International Conference on metals and genetics: metals and biochemistry, disease, environment Toronto, Ontario May 25\( \bar{\pi} \)9, 2004. <b>2004</b> , 37, 1122-1142	
2027 Proteomics/genomics and signaling in lymphocytes. <b>2004</b> , 16, 337-44	11

2026	Proteomicsapplication to the brain. <b>2004</b> , 61, 285-311	22
2025	Comparison of discrimination methods for peptide classification in tandem mass spectrometry.	3
2024	An Endorsement to Create Open Access Databases for Analytical Data of Complex Carbohydrates. <b>2004</b> , 23, 277-297	13
2023	A 'molecular switchboard'covalent modifications to proteins and their impact on transcription. <b>2004</b> , 2, 1-7	83
2022	Fast automatic registration of images using the phase of a complex wavelet transform: application to proteome gels. <b>2004</b> , 129, 542-52	21
2021	What mass spectrometry can reveal about protein function. <b>2004</b> , 129, 290-6	6
2020	Modeling protein tandem mass spectrometry data with an extended linear regression strategy. <b>2004</b> , 2004, 3055-9	1
2019		
2018	Separation of ion types in tandem mass spectrometry data interpretation a graph-theoretic approach. <b>2004</b> , 236-44	
2017	SPIDER: software for protein identification from sequence tags with de novo sequencing error. <b>2004</b> , 206-15	13
2017		2
	2004, 206-15  2003 Fred Beamish Award Lecture ? Exploring the dynamics of biological systems by mass	
2016	2004, 206-15  2003 Fred Beamish Award Lecture? Exploring the dynamics of biological systems by mass spectrometry. 2004, 82, 1565-1580  Mass spectrometry as a diagnostic and a cancer biomarker discovery tool: opportunities and	2
2016	2004, 206-15  2003 Fred Beamish Award Lecture? Exploring the dynamics of biological systems by mass spectrometry. 2004, 82, 1565-1580  Mass spectrometry as a diagnostic and a cancer biomarker discovery tool: opportunities and potential limitations. 2004, 3, 367-78  Informatics platform for global proteomic profiling and biomarker discovery using liquid	498
2016 2015 2014	2004, 206-15  2003 Fred Beamish Award Lecture? Exploring the dynamics of biological systems by mass spectrometry. 2004, 82, 1565-1580  Mass spectrometry as a diagnostic and a cancer biomarker discovery tool: opportunities and potential limitations. 2004, 3, 367-78  Informatics platform for global proteomic profiling and biomarker discovery using liquid chromatography-tandem mass spectrometry. 2004, 3, 984-97  Development of a protein chip: a MS-based method for quantitation of protein expression and	2 498 177
2016 2015 2014 2013	2004, 206-15  2003 Fred Beamish Award Lecture? Exploring the dynamics of biological systems by mass spectrometry. 2004, 82, 1565-1580  Mass spectrometry as a diagnostic and a cancer biomarker discovery tool: opportunities and potential limitations. 2004, 3, 367-78  Informatics platform for global proteomic profiling and biomarker discovery using liquid chromatography-tandem mass spectrometry. 2004, 3, 984-97  Development of a protein chip: a MS-based method for quantitation of protein expression and modification levels using an immunoaffinity approach. 2004, 76, 4082-92  Molecule-specific imaging with mass spectrometry and a buckminsterfullerene probe: application	2 498 177 33
2016 2015 2014 2013 2012	2004, 206-15  2003 Fred Beamish Award Lecture? Exploring the dynamics of biological systems by mass spectrometry. 2004, 82, 1565-1580  Mass spectrometry as a diagnostic and a cancer biomarker discovery tool: opportunities and potential limitations. 2004, 3, 367-78  Informatics platform for global proteomic profiling and biomarker discovery using liquid chromatography-tandem mass spectrometry. 2004, 3, 984-97  Development of a protein chip: a MS-based method for quantitation of protein expression and modification levels using an immunoaffinity approach. 2004, 76, 4082-92  Molecule-specific imaging with mass spectrometry and a buckminsterfullerene probe: application to characterizing solid-phase synthesized combinatorial libraries. 2004, 126, 3902-9  Semiquantitative proteomic analysis of rat forebrain postsynaptic density fractions by mass	2 498 177 33 43

### (2004-2004)

2008	Human serum proteins preseparated by electrophoresis or chromatography followed by tandem mass spectrometry. <b>2004</b> , 3, 364-82	76
2007	Understanding and designing field asymmetric waveform ion mobility spectrometry separations in gas mixtures. <b>2004</b> , 76, 7366-74	85
2006	Parallel identification of O-GlcNAc-modified proteins from cell lysates. <b>2004</b> , 126, 10500-1	97
2005	Mining disease susceptibility genes through SNP analyses and expression profiling using MALDI-TOF mass spectrometry. <b>2004</b> , 3, 218-27	45
2004	Synchrotron radiolysis and mass spectrometry: a new approach to research on the actin cytoskeleton. <b>2004</b> , 37, 221-9	33
2003	Multidimensional protein profiling technology and its application to human plasma proteome. <b>2004</b> , 3, 712-8	70
2002	Probity: a protein identification algorithm with accurate assignment of the statistical significance of the results. <b>2004</b> , 3, 32-6	43
2001	Multidimensional proteome analysis of human mammary epithelial cells. <b>2004</b> , 3, 68-75	84
2000	Proteomics in pancreatic disease. <b>2004</b> , 4, 67-75	14
1999	A structural perspective on protein protein interactions. <b>2004</b> , 14, 313-313	
	A structural perspective on protein protein interactions. <b>2004</b> , 14, 313-313  Trypsin cleaves exclusively C-terminal to arginine and lysine residues. <b>2004</b> , 3, 608-14	804
		804
1998	Trypsin cleaves exclusively C-terminal to arginine and lysine residues. <b>2004</b> , 3, 608-14  Application of peptide LC retention time information in a discriminant function for peptide	ŕ
1998 1997	Trypsin cleaves exclusively C-terminal to arginine and lysine residues. <b>2004</b> , 3, 608-14  Application of peptide LC retention time information in a discriminant function for peptide identification by tandem mass spectrometry. <b>2004</b> , 3, 760-9  Proteomics: how to control highly dynamic patterns of millions of molecules and interpret changes	127
1998 1997 1996	Trypsin cleaves exclusively C-terminal to arginine and lysine residues. <b>2004</b> , 3, 608-14  Application of peptide LC retention time information in a discriminant function for peptide identification by tandem mass spectrometry. <b>2004</b> , 3, 760-9  Proteomics: how to control highly dynamic patterns of millions of molecules and interpret changes correctly?. <b>2004</b> , 1, 1-8	127
1998 1997 1996 1995	Trypsin cleaves exclusively C-terminal to arginine and lysine residues. 2004, 3, 608-14  Application of peptide LC retention time information in a discriminant function for peptide identification by tandem mass spectrometry. 2004, 3, 760-9  Proteomics: how to control highly dynamic patterns of millions of molecules and interpret changes correctly?. 2004, 1, 1-8  Element-coded affinity tags for peptides and proteins. 2004, 15, 3-6	127 17 100
1998 1997 1996 1995	Trypsin cleaves exclusively C-terminal to arginine and lysine residues. 2004, 3, 608-14  Application of peptide LC retention time information in a discriminant function for peptide identification by tandem mass spectrometry. 2004, 3, 760-9  Proteomics: how to control highly dynamic patterns of millions of molecules and interpret changes correctly?. 2004, 1, 1-8  Element-coded affinity tags for peptides and proteins. 2004, 15, 3-6  Bioinformatics in mass spectrometry data analysis for proteomics studies. 2004, 1, 469-83	127 17 100

1990	Proteomic analysis of integral plasma membrane proteins. <b>2004</b> , 76, 1817-23	222
1989	Membrane Dynamics and Domains. 2004,	6
1988	Large-scale proteomic analysis of membrane proteins. <b>2004</b> , 1, 293-302	17
1987	Absolute quantitation of proteins by a combination of acid hydrolysis and matrix-assisted laser desorption/ionization mass spectrometry. <b>2004</b> , 76, 3569-75	18
1986	Dopamine transporter network and pathways. <b>2004</b> , 61, 79-96	7
1985	Open source system for analyzing, validating, and storing protein identification data. <b>2004</b> , 3, 1234-42	584
1984	Histidine-rich peptide selection and quantification in targeted proteomics. <b>2004</b> , 3, 37-45	32
1983	Towards a systems biology understanding of human health: interplay between genotype, environment and nutrition. <b>2004</b> , 10, 51-84	37
1982	Integration with the human genome of peptide sequences obtained by high-throughput mass spectrometry. <b>2005</b> , 6, R9	233
1981	The synovial proteome: analysis of fibroblast-like synoviocytes. <b>2004</b> , 6, R161-8	73
1980	Advances in recombinant antibody microarrays. <b>2004</b> , 343, 17-35	107
1979	Applications of eTag trade mark assay platform to systems biology approaches in molecular oncology and toxicology studies. <b>2004</b> , 111, 162-74	21
1978	Applying proteomics to signaling networks. <b>2004</b> , 14, 492-8	30
1977	Mammalian phospholipase Czeta induces oocyte activation from the sperm perinuclear matrix. <b>2004</b> , 274, 370-83	133
1976	The MTG proteins: chromatin repression players with a passion for networking. <b>2004</b> , 84, 1-9	29
1975	Understanding global changes in histone H1 phosphorylation using mass spectrometry. <b>2004</b> , 33, 53-8	9
1974	A systems approach to dissecting immunity and inflammation. <b>2004</b> , 16, 55-67	63
1973	LEnalyse protòmique: intfts et perspectives en biologie clinique. <b>2004</b> , 19, 313-322	1

1972 Proteomics on its way to study host-pathogen interaction in Candida albicans. <b>2004</b> , 7, 330-5	29
1971 Molecular oncology in the post-genomic era: the challenge of proteomics. <b>2004</b> , 10, 24-32	23
Potential for false positive identifications from large databases through tandem mass spectrometry. <b>2004</b> , 3, 1082-5	171
Large-scale quantitative proteomic study of PUMA-induced apoptosis using two-dimensional liquid chromatography-mass spectrometry coupled with amino acid-coded mass tagging. <b>2004</b> , 3, 1191-200	26
Hardware and software systems for accelerating common bioinformatics sequence analysis algorithms. <b>2004</b> , 2, 12-17	12
1967 Factors that contribute to the complexity of protein digests. <b>2004</b> , 3, 3-10	10
1966 Q TRAPImass spectrometer technology for proteomics applications. <b>2004</b> , 3, 31-36	3
1965 PRISM: a new strategy to analyze the mammalian proteome. <b>2004</b> , 3, 37-42	
RNA and RNA binding proteins participate in early stages of cell spreading through spreading initiation centers. <b>2004</b> , 117, 649-62	216
Metabolomics in the opening decade of the 21st century: building the roads to individualized health. <b>2004</b> , 134, 2729-32	62
1962 Research: advances in cell biology relevant to critical illness. <b>2004</b> , 10, 279-91	10
1961 Charting gene regulatory networks: strategies, challenges and perspectives. <b>2004</b> , 381, 1-12	61
1960 Large Gel Two-Dimensional Electrophoresis: Improving Recovery of Cellular Proteome. <b>2004</b> , 1, 35-39	18
1959 Genetic testing for malignant hyperthermia in North America. <b>2004</b> , 100, 212-4	9
Discharge criteria for children sedated by nonanesthesiologists: is "safe" really safe enough?. <b>2004</b> , 100, 207-9	24
Use of genomics and proteomics to develop better diagnostic tools for use in infectious diseases. <b>2004</b> , 15, 103-108	1
On the technicalities of discovering and applying protein biomarkers for cancer prevention. <b>2004</b> , 13, 437-46	4
1955 Long-lasting changes in brain protein expression after exposure to an anesthetic. <b>2004</b> , 100, 209-12	1

1954	Investigation of methods suitable for the matrix-assisted laser desorption/ionization mass spectrometric analysis of proteins from ribonucleoprotein complexes. <b>2004</b> , 10, 89-99	24
1953	Proteomics techniques and their application to hematology. <b>2004</b> , 103, 3624-34	90
1952	Comparative proteomic analysis of all-trans-retinoic acid treatment reveals systematic posttranscriptional control mechanisms in acute promyelocytic leukemia. <b>2004</b> , 104, 1314-23	101
1951	The use of isotope-coded affinity tags (ICAT) to study organelle proteomes in Arabidopsis thaliana. <b>2004</b> , 32, 520-3	54
1950	Genomic and proteomic approaches for studying human cancer: prospects for true patient-tailored therapy. <b>2004</b> , 1, 134-40	49
1949	Proteomic analysis of pulmonary edema fluid and plasma in patients with acute lung injury. <b>2004</b> , 286, L1095-104	73
1948	Mass-Spectrometry-Based Proteomics for Cancer Biology. <b>2005</b> , 91-107	
1947	Contributions of proteomics to diagnosis, treatment, and prevention of candidiasis. <b>2006</b> , 49, 331-61	5
1946	Two-dimensional gel electrophoresis. 2005,	
1945	The Use of Mass Spectrometry in Studying Protein-Protein Interaction. <b>2005</b> , 33-48	Ο
1944	Principles of Nanoflow Liquid Chromatography and Applications to Proteomics. 2005, 1, 65-71	22
1943	Protein, Antibody and Small Molecule Microarrays. <b>2005</b> , 279-295	1
1942	Emerging studies of the urinary proteome: the end of the beginning?. <b>2005</b> , 14, 579-85	27
1941	Proteomics. <b>2005</b> , 33, S444-8	19
1940	Proteomics in prostate cancer. <b>2005</b> , 15, 151-6	21
1939	Miniaturized Formats for Efficient Liquid Chromatography Mass Spectrometry ${f B}$ as ed Proteomics and Therapeutic Development. <b>2005</b> , 1-26	1
1938	Systems Biology: Applications in Drug Discovery. <b>2005</b> , 123-183	14
1937	Preprocessing of tandem mass spectrometric data based on decision tree classification. <b>2005</b> , 3, 231-7	3

1936 ICAT and other labeling strategies for semiquantitative LC-based expression profiling. 2005,

1935	Metabolic Networks from a Systems Perspective. <b>2005</b> , 265-289	1
1934	PROTEOMIC ANALYSIS AND FRUIT RIPENING. <b>2005</b> , 211-224	3
1933	Protein-Protein Docking Methods. <b>2005</b> , 115-146	11
1932	Application of Bis(terpyridine)ruthenium(II) to N-Terminal Amino Acid Sequencing. 2005, 34, 332-333	11
1931	Functional aberrant expression of CCR2 receptor on chronically activated NK cells in patients with TAP-2 deficiency. <b>2005</b> , 106, 3465-73	22
1930	Mass-Coded Abundance Tagging for Protein Identification and Relative Abundance Determination in Proteomic Experiments. <b>2005</b> , 407-415	
1929	Proteomics in clinical laboratory diagnosis. <b>2005</b> , 39, 159-84	4
1928	Marine proteomics: generation of sequence tags for dissolved proteins in seawater using tandem mass spectrometry. <b>2005</b> , 95, 183-198	49
1927	Algorithm for accurate similarity measurements of peptide mass fingerprints and its application. <b>2005</b> , 16, 13-21	23
1926	Statistical evaluation of electrospray tandem mass spectra for optimized peptide fragmentation. <b>2005</b> , 16, 505-14	10
1925	MALDI-TOF MS analysis of soluble PEG based multi-step synthetic reaction mixtures with automated detection of reaction failure. <b>2005</b> , 16, 670-8	15
1924	Multidimensional protein identification technology (MudPIT): technical overview of a profiling method optimized for the comprehensive proteomic investigation of normal and diseased heart tissue. <b>2005</b> , 16, 1207-20	107
1923	Increasing peptide identification in tandem mass spectrometry through automatic function switching optimization. <b>2005</b> , 16, 1818-26	2
1922	Proteomic approaches in the search for disease biomarkers. <b>2005</b> , 814, 11-9	57
1921	Is it biologically relevant to measure the structures of small peptides in the gas-phase?. <b>2005</b> , 240, 273-284	64
1920	Ion mobilitythass spectrometry: a new paradigm for proteomics. <b>2005</b> , 240, 301-315	262
1919	Proteomic LC-MS systems using nanoscale liquid chromatography with tandem mass spectrometry. <b>2005</b> , 1067, 73-83	140

1918	Limitations of current proteomics technologies. <b>2005</b> , 1077, 1-18	173
1917	An affinity-based probe for the proteomic profiling of aspartic proteases. <b>2005</b> , 46, 4053-4056	23
1916	Differential signatures of protein expression in marmoset liver and thymus induced by single-dose TCDD treatment. <b>2005</b> , 206, 33-48	27
1915	Capturing SDS-treated biotinylated protein and peptide by avidin functional affinity electrophoresis with or without SDS in the gel running buffer. <b>2005</b> , 336, 312-5	7
1914	Microfluidic systems and proteomics: applications of the electrocapture technology to protein and peptide analysis. <b>2005</b> , 345, 10-7	18
1913	Genomic medicine: bringing biomarkers to clinical medicine. <b>2005</b> , 9, 381-6	22
1912	Integrated microfabricated systems including a purification module and an on-chip nano electrospray ionization interface for biological analysis. <b>2005</b> , 1071, 213-22	52
1911	Solid-phase capture and release of arginine peptides by selective tagging and boronate affinity chromatography. <b>2005</b> , 1079, 187-96	23
1910	Separation, detection, and identification of peptides by ion-pair reversed-phase high-performance liquid chromatography-electrospray ionization mass spectrometry at high and low pH. <b>2005</b> , 1079, 274-86	88
1909	Genotyping single nucleotide polymorphisms by MALDI mass spectrometry in clinical applications. <b>2005</b> , 38, 335-50	132
		132 32
1908	<b>2005</b> , 38, 335-50	
1908 1907	2005, 38, 335-50  Characterisation of kinase-selective inhibitors by chemical proteomics. 2005, 1754, 183-90  Differential expression of the fast skeletal muscle proteome following chronic low-frequency	32
1908 1907	2005, 38, 335-50  Characterisation of kinase-selective inhibitors by chemical proteomics. 2005, 1754, 183-90  Differential expression of the fast skeletal muscle proteome following chronic low-frequency stimulation. 2005, 1752, 166-76	32
1908 1907 1906	Characterisation of kinase-selective inhibitors by chemical proteomics. 2005, 1754, 183-90  Differential expression of the fast skeletal muscle proteome following chronic low-frequency stimulation. 2005, 1752, 166-76  Macro/nao-structured silicon as solid support for antibody arrays. 2005, 1, 093-104  High-throughput identification of in-gel digested proteins by rapid, isocratic HPLC/MS/MS. 2005,	32 42 31
1908 1907 1906	Characterisation of kinase-selective inhibitors by chemical proteomics. 2005, 1754, 183-90  Differential expression of the fast skeletal muscle proteome following chronic low-frequency stimulation. 2005, 1752, 166-76  Macro/nao-structured silicon as solid support for antibody arrays. 2005, 1, 093-104  High-throughput identification of in-gel digested proteins by rapid, isocratic HPLC/MS/MS. 2005, 77, 8179-84	32 42 31 8
1908 1907 1906 1905	Characterisation of kinase-selective inhibitors by chemical proteomics. 2005, 1754, 183-90  Differential expression of the fast skeletal muscle proteome following chronic low-frequency stimulation. 2005, 1752, 166-76  Macro/nao-structured silicon as solid support for antibody arrays. 2005, 1, 093-104  High-throughput identification of in-gel digested proteins by rapid, isocratic HPLC/MS/MS. 2005, 77, 8179-84  From proteins to proteomics. 2005, 57, 267-72	32 42 31 8

19	900	Regulation of metabolic networks: understanding metabolic complexity in the systems biology era. <b>2005</b> , 168, 9-24		125	
18	899	Proteomic approach in the search of new cardiovascular biomarkers. <b>2005</b> , S103-7		14	
18	898	The potential of proteomics and peptidomics for allergy and asthma research. <b>2005</b> , 60, 1227-37		35	
18	<sup>3</sup> 97	New insect order Mantophasmatodea: species differentiation by mass fingerprints of peptide hormones?. <b>2005</b> , 43, 149-156		20	
18	396	Multireflection planar time-of-flight mass analyzer. I: An analyzer for a parallel tandem spectrometer. <b>2005</b> , 50, 73		40	
18	<sup>3</sup> 95	Quantitative mouse brain proteomics using culture-derived isotope tags as internal standards. <b>2005</b> , 23, 617-21		203	
18	894	Assignment of protein function in the postgenomic era. <b>2005</b> , 1, 130-42		116	
18	893	Mass spectrometry-based proteomics turns quantitative. <b>2005</b> , 1, 252-62		1312	
18	892	Watching and weightingchaperone complexes in action. <b>2005</b> , 2, 331-2		3	
18	891	A new method for C-terminal sequence analysis in the proteomic era. <b>2005</b> , 2, 193-200		44	
18	890	Comparative evaluation of mass spectrometry platforms used in large-scale proteomics investigations. <b>2005</b> , 2, 667-75		612	
18	389	Elucidating mechanisms of drug-induced toxicity. <b>2005</b> , 4, 410-20		239	
18	888	Miniaturization in functional genomics and proteomics. <b>2005</b> , 6, 465-76		108	
18	887	Scoring proteomes with proteotypic peptide probes. <b>2005</b> , 6, 577-83		310	
18	886	Community genomics in microbial ecology and evolution. <b>2005</b> , 3, 489-98		182	
18	885	Quantitative functional analysis of protein complexes on surfaces. <b>2005</b> , 563, 61-71		41	
18	384	Vitamin C degradation in plant cells via enzymatic hydrolysis of 4-O-oxalyl-L-threonate. <i>Nature</i> , <b>2005</b> , 433, 83-7	50.4	208	
18	383	Nucleolar proteome dynamics. <i>Nature</i> , <b>2005</b> , 433, 77-83	50.4	946	

1882	Toward data standards for proteomics. <b>2005</b> , 23, 373-6	9
1881	Protein Modifications and Networks in Health and Disease. <b>2005</b> , 272, 408-448	
1880	Mitochondrial proteomics in free radical research. <b>2005</b> , 38, 175-88	57
1879	Structural characterization of assemblies from overall shape and subcomplex compositions. <b>2005</b> , 13, 435-45	25
1878	Structural proteomics of macromolecular assemblies using oxidative footprinting and mass spectrometry. <b>2005</b> , 30, 583-92	104
1877	Metabolome analysis: the potential of in vivo labeling with stable isotopes for metabolite profiling. <b>2005</b> , 23, 28-33	142
1876	Proteomics in developmental toxicology. <b>2005</b> , 19, 291-304	14
1875	Calibration of mass spectrometric peptide mass fingerprint data without specific external or internal calibrants. <b>2005</b> , 6, 203	18
1874	Transformation and other factors of the peptide mass spectrometry pairwise peak-list comparison process. <b>2005</b> , 6, 285	15
1873	Key challenges in proteomics and proteoinformatics. Progress in proteins. <b>2005</b> , 24, 34-40	11
1872	Mechanistic data and cancer risk assessment: the need for quantitative molecular endpoints. <b>2005</b> , 45, 214-21	10
1871	On-line counting of cysteine residues in peptides during electrospray ionization by electrogenerated tags and their application to protein identification. <b>2005</b> , 26, 238-47	38
1870	Combining capillary electrophoresis with mass spectrometry for applications in proteomics. <b>2005</b> , 26, 1291-305	168
1869	Discovery of biomarkers in human urine and cerebrospinal fluid by capillary electrophoresis coupled to mass spectrometry: towards new diagnostic and therapeutic approaches. <b>2005</b> , 26, 1476-87	113
1868	Capillary electrophoresis coupled to mass spectrometry for clinical diagnostic purposes. <b>2005</b> , 26, 2708-16	91
1867	Activity-based high-throughput screening of enzymes by using a DNA microarray. <b>2005</b> , 44, 1048-1053	19
1866	A serum proteomic approach to gauging the state of remission in Wegener's granulomatosis. <b>2005</b> , 52, 902-10	41
1865	Activity-Based High-Throughput Screening of Enzymes by Using a DNA Microarray. <b>2005</b> , 117, 1072-1077	7

1864	Intact-protein based sample preparation strategies for proteome analysis in combination with mass spectrometry. <b>2005</b> , 24, 413-26	72
1863	Biochemical applications of mass spectrometry in pharmaceutical drug discovery. <b>2005</b> , 24, 347-66	67
1862	Bacterial proteomics and its role in antibacterial drug discovery. <b>2005</b> , 24, 549-65	58
1861	Comparative proteomics analysis of human pituitary adenomas: current status and future perspectives. <b>2005</b> , 24, 783-813	29
1860	Mass spectrometric studies on brain metabolism, using stable isotopes. <b>2005</b> , 24, 865-86	14
1859	Applying proteomics technology to platelet research. <b>2005</b> , 24, 918-30	49
1858	Proteomics and peptidomics in neuroscience. Experience of capabilities and limitations in a neurochemical laboratory. <b>2005</b> , 40, 202-13	25
1857	Top-down identification of endogenous peptides up to 9 kDa in cerebrospinal fluid and brain tissue by nanoelectrospray quadrupole time-of-flight tandem mass spectrometry. <b>2005</b> , 40, 214-26	28
1856	Quantitative peptidomics of mouse pituitary: comparison of different stable isotopic tags. <b>2005</b> , 40, 238-49	108
1855	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. <b>2005</b> , 40, 475-88	5
1854	Performance of the computer algorithm COMPLX for the detection of protein complexes in the mass spectra of simulated biological mixtures. <b>2005</b> , 40, 1187-96	2
1853	Protein fishing with chiral molecular baits. <b>2005</b> , 17, 332-7	11
1852	A new chemical probe for proteomics of carbohydrate-binding proteins. <b>2005</b> , 6, 291-5	60
1851	Fluorescent multiplex analysis of carrier protein post-translational modification. 2005, 6, 1335-7	9
1850	Construction, verification and experimental use of two epitope-tagged collections of budding yeast strains. <b>2005</b> , 6, 2-16	64
1849	C alpha-C backbone fragmentation dominates in electron detachment dissociation of gas-phase polypeptide polyanions. <b>2005</b> , 11, 1803-12	106
1848	Dissociation of alkaliated alanine in the gas phase: the role of the metal cation. <b>2005</b> , 11, 5289-301	10
1847	Mesoporous silica nanoreactors for highly efficient proteolysis. <b>2005</b> , 11, 5391-6	76

1846	Mass spectrometry-based proteomics in the life sciences. <b>2005</b> , 62, 848-69	85
1845	Comprehensive post-genomic data analysis approaches integrating biochemical pathway maps. <b>2005</b> , 66, 413-51	61
1844	Proteomic analysis of TRPC5- and TRPC6-binding partners reveals interaction with the plasmalemmal Na(+)/K(+)-ATPase. <b>2005</b> , 451, 87-98	73
1843	A proteomic fingerprint of dissolved organic carbon and of soil particles. <b>2005</b> , 142, 335-43	133
1842	PRIME: A Mass Spectrum Data Mining Tool for De Nova Sequencing and PTMs Identification. <b>2005</b> , 20, 483-490	6
1841	Application of mass spectrometry in proteomics. <b>2005</b> , 25, 71-93	91
1840	A novel mass spectrometry-based assay for GSK-3beta activity. <b>2005</b> , 6, 29	10
1839	Lipoproteomics I: mapping of proteins in low-density lipoprotein using two-dimensional gel electrophoresis and mass spectrometry. <b>2005</b> , 5, 551-65	117
1838	A subcellular prefractionation protocol for minute amounts of mammalian cell cultures and tissue. <b>2005</b> , 5, 35-45	88
1837	Differential protein expression by Porphyromonas gingivalis in response to secreted epithelial cell components. <b>2005</b> , 5, 198-211	56
1836	Increased quantitative proteome coverage with (13)C/(12)C-based, acid-cleavable isotope-coded affinity tag reagent and modified data acquisition scheme. <b>2005</b> , 5, 380-7	105
1835	Single-step Strep-tag purification for the isolation and identification of protein complexes from mammalian cells. <b>2005</b> , 5, 1199-203	96
1834	Silicone/graphite coating for on-target desalting and improved peptide mapping performance of matrix-assisted laser desorption/ionization-mass spectrometry targets in proteomic experiments. <b>2005</b> , 5, 1460-71	37
1833	A proteomic tool for protein identification from tandem mass spectral data. <b>2005</b> , 5, 853-5	2
1832	Large-scale identification of proteins in human salivary proteome by liquid chromatography/mass spectrometry and two-dimensional gel electrophoresis-mass spectrometry. <b>2005</b> , 5, 1714-28	296
1831	Distinct proteome features of plasma microparticles. <b>2005</b> , 5, 1940-52	77
1830	Sample preparation and digestion for proteomic analyses using spin filters. <b>2005</b> , 5, 1742-5	322
1829	Comprehensive proteomics in yeast using chromatographic fractionation, gas phase fractionation, protein gel electrophoresis, and isoelectric focusing. <b>2005</b> , 5, 2018-28	81

1828	Proteome analysis of Escherichia coli using high-performance liquid chromatography and Fourier transform ion cyclotron resonance mass spectrometry. <b>2005</b> , 5, 2029-42	9
1827	Proteomic changes in rice leaves during development of field-grown rice plants. <b>2005</b> , 5, 961-72	66
1826	Sequence tag scanning: a new explorative strategy for recognition of unexpected protein alterations by nanoelectrospray ionization-tandem mass spectrometry. <b>2005</b> , 5, 667-74	6
1825	Subproteomic analysis of metal-interacting proteins in human B cells. <b>2005</b> , 5, 3614-22	44
1824	Comparison of alternative analytical techniques for the characterisation of the human serum proteome in HUPO Plasma Proteome Project. <b>2005</b> , 5, 3423-41	97
1823	ProbIDtree: an automated software program capable of identifying multiple peptides from a single collision-induced dissociation spectrum collected by a tandem mass spectrometer. <b>2005</b> , 5, 4096-106	65
1822	Design, construction, and characterization of a large synthetic human antibody phage display library. <b>2005</b> , 5, 2340-50	146
1821	Proteomic analysis of neural differentiation of mouse embryonic stem cells. <b>2005</b> , 5, 4414-26	59
1820	2-D reference map of Bacillus anthracis vaccine strain A16R proteins. <b>2005</b> , 5, 4488-95	35
1819	Isolation of viral ribonucleoprotein complexes from infected cells by tandem affinity purification. <b>2005</b> , 5, 4483-7	16
1818	Extending ribosomal protein identifications to unsequenced bacterial strains using matrix-assisted laser desorption/ionization mass spectrometry. <b>2005</b> , 5, 4818-31	45
1817	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. <b>2005</b> , 5, 3226-45	672
1816	Proteome imaging: a closer look at life's organization. <b>2005</b> , 5, 4316-26	16
1815	Average peptide score: a useful parameter for identification of proteins derived from database searches of liquid chromatography/tandem mass spectrometry data. <b>2005</b> , 19, 9-14	16
1814	Applications of a matrix-assisted laser desorption/ionization orthogonal time-of-flight mass spectrometer. l. Metastable decay and collision-induced dissociation for sequencing peptides. <b>2005</b> , 19, 213-20	10
1813	Characterisation of intact recombinant human erythropoietins applied in doping by means of planar gel electrophoretic techniques and matrix-assisted laser desorption/ionisation linear time-of-flight mass spectrometry. <b>2005</b> , 19, 728-42	44
1812	Mass spectrometric detection of biotinylated peptides captured by avidin functional affinity electrophoresis. <b>2005</b> , 19, 886-92	7
1811	An algorithm for interpretation of low-energy collision-induced dissociation product ion spectra for de novo sequencing of peptides. <b>2005</b> , 19, 1084-96	9

In-source fragmentation and analysis of polysaccharides by capillary electrophoresis/mass spectrometry. <b>2005</b> , 19, 1305-14	44
New conditions for matrix-assisted laser desorption/ionization mass spectrometry of native bacterial R-type lipopolysaccharides. <b>2005</b> , 19, 1829-34	59
Large-scale identification of human biliary proteins from a cholesterol stone patient using a proteomic approach. <b>2005</b> , 19, 3569-78	36
1807 Liquid Chromatography Coupled to MS for Proteome Analysis. <b>2005</b> , 375-383	
1806 Functional clustering algorithm for high-dimensional proteomics data. <b>2005</b> , 2005, 80-6	6
1805 Bioinformatics: Genomics, Functional Genomics, and Proteomics. <b>2005</b> , 203-228	
1804 Biochemistry of protein complexes. <b>2005</b> ,	
1803 . <b>2005</b> ,	13
1802 . <b>2005</b> ,	71
1801 FT-ICR. <b>2005</b> ,	
1801 FT-ICR. 2005,  1800 Mass spectrometric data mining for protein sequences. 2005,	
1800 Mass spectrometric data mining for protein sequences. <b>2005</b> ,	15
1800 Mass spectrometric data mining for protein sequences. <b>2005</b> ,  1799 Arrays and Proteomics. <b>2005</b> , 34, 109-114	15
1800 Mass spectrometric data mining for protein sequences. 2005,  1799 Arrays and Proteomics. 2005, 34, 109-114  1798 Absolute quantitation of cancer-related proteins using an MS-based peptide chip. 2005, Suppl, 7-11	
1800 Mass spectrometric data mining for protein sequences. 2005,  1799 Arrays and Proteomics. 2005, 34, 109-114  1798 Absolute quantitation of cancer-related proteins using an MS-based peptide chip. 2005, Suppl, 7-11  1797 Peptide Sequence Tags for Fast Database Search in Mass-Spectrometry. 2005, 326-341	3
1800 Mass spectrometric data mining for protein sequences. 2005,  1799 Arrays and Proteomics. 2005, 34, 109-114  1798 Absolute quantitation of cancer-related proteins using an MS-based peptide chip. 2005, Suppl, 7-11  1797 Peptide Sequence Tags for Fast Database Search in Mass-Spectrometry. 2005, 326-341  1796 Proteomics of Signal Transduction Pathways. 2005, 417-431  Evidence for the presence of disease-perturbed networks in prostate cancer cells by genomic and	3 1 96

1792	A graph-theoretic approach for the separation of b and y ions in tandem mass spectra. <b>2005</b> , 21, 563-74	35
1791	Integrative Physiology in the Proteomics and Post-Genomics Age. 2005,	4
1790	Systematic comparison of a two-dimensional ion trap and a three-dimensional ion trap mass spectrometer in proteomics. <b>2005</b> , 4, 214-23	49
1789	Proteomic characterization of evolutionarily conserved and variable proteins of Arabidopsis cytosolic ribosomes. <b>2005</b> , 137, 848-62	127
1788	Biomarkers: mining the biofluid proteome. <b>2005</b> , 4, 409-18	191
1787	The agony and ecstasy of "OMIC" technologies in drug development. <b>2005</b> , 5, 39-52	85
1786	Proteome dynamics during C2C12 myoblast differentiation. <b>2005</b> , 4, 887-901	104
1785	Functional genomic analysis of cancer metastasis: biologic insights and clinical implications. <b>2005</b> , 5, 385-95	25
1784	Phosphoproteomics in analyzing signaling pathways. <b>2005</b> , 2, 117-28	28
1783	Proteomics in cancer vaccine development. <b>2005</b> , 2, 229-41	8
1782	Understanding protein trafficking in plant cells through proteomics. <b>2005</b> , 2, 781-92	11
1781	Mass spectrometry of the M. smegmatis proteome: protein expression levels correlate with function, operons, and codon bias. <b>2005</b> , 15, 1118-26	61
1780	Decreased asialotransferrin in cerebrospinal fluid of patients with childhood-onset ataxia and central nervous system hypomyelination/vanishing white matter disease. <b>2005</b> , 51, 2031-42	40
1779	Proteomic analysis of SRm160-containing complexes reveals a conserved association with cohesin. <b>2005</b> , 280, 42227-36	26
1778	Double standards in quantitative proteomics: direct comparative assessment of difference in gel electrophoresis and metabolic stable isotope labeling. <b>2005</b> , 4, 255-66	75
1777	Statistical and computational methods for comparative proteomic profiling using liquid chromatography-tandem mass spectrometry. <b>2005</b> , 4, 419-34	232
1776	Integrating global proteomic and genomic expression profiles generated from islet alpha cells: opportunities and challenges to deriving reliable biological inferences. <b>2005</b> , 4, 458-74	22
1775	A Heuristic method for assigning a false-discovery rate for protein identifications from Mascot database search results. <b>2005</b> , 4, 762-72	162

1774	Proteome analysis of prostate cancer. <b>2005</b> , 8, 14-21	22
1773	Functional differentiation of bundle sheath and mesophyll maize chloroplasts determined by comparative proteomics. <b>2005</b> , 17, 3111-40	186
1772	Contents. <b>2005</b> , v	
1771	Membranes, ions, and clocks: testing the Njus-Sulzman-Hastings model of the circadian oscillator. <b>2005</b> , 393, 682-93	29
1770	Application of surface activity in therapeutics. 2005, 233-293	3
1769	Microarray Technology and Its Applications. 2005,	30
1768	Proteomic profiling of pancreatic cancer for biomarker discovery. <b>2005</b> , 4, 523-33	113
1767	Collisional activation by MALDI tandem time-of-flight mass spectrometry induces intramolecular migration of amide hydrogens in protonated peptides. <b>2005</b> , 4, 1910-9	34
1766	A software suite for the generation and comparison of peptide arrays from sets of data collected by liquid chromatography-mass spectrometry. <b>2005</b> , 4, 1328-40	147
1765	Advances in clinical cancer proteomics: SELDI-ToF-mass spectrometry and biomarker discovery. <b>2005</b> , 4, 16-26	82
1764	Combinatorial Pattern Matching. 2005,	2
1763	Quantitative mass spectral evidence for the absence of circulating brain natriuretic peptide (BNP-32) in severe human heart failure. <b>2005</b> , 102, 17442-7	235
1762	Interpretation of shotgun proteomic data: the protein inference problem. 2005, 4, 1419-40	756
1761	Active kinase proteome screening reveals novel signal complexity in cardiomyopathy. <b>2005</b> , 4, 673-82	8
1760	Mass Spectrometry Data Analysis for Early Detection of Inherited Breast Cancer. <b>2005</b> , 21-28	
1759	Biological and Artificial Intelligence Environments. 2005,	
1758	Mass Spectra Alignments and Their Significance. <b>2005</b> , 429-441	3
1757	Virus infection and the interferon response: a global view through functional genomics. <b>2005</b> , 116, 37-55	11

1756	Rarity gives a charm: evaluation of trace proteins in plasma and serum. <b>2005</b> , 2, 393-406	16
1755	Batch introduction techniques. <b>2005</b> , 405, 36-49	4
1754	Proteomic analysis of ubiquitin conjugates in yeast. <b>2005</b> , 399, 367-81	17
1753	Combinatorial complexity and dynamical restriction of network flows in signal transduction. <b>2005</b> , 2, 5-15	50
1752	Prefractionation of Complex Protein Mixture for 2-D PAGE Using Reversed-Phase Liquid Chromatography. <b>2005</b> , 87-95	
1751	Protein microarrays as a discovery tool for studying protein-protein interactions. <b>2005</b> , 2, 13-26	20
1750	SpecAlignprocessing and alignment of mass spectra datasets. <b>2005</b> , 21, 2088-90	147
1749	Research in Computational Molecular Biology. 2005,	2
1748	New insights into viral structure and virus-cell interactions through proteomics. <b>2005</b> , 2, 577-88	13
1747	Proteomic applications of surface plasmon resonance biosensors: analysis of protein arrays. <b>2005</b> , 37, 1-10	56
1746	Electrospraying from nanofluidic capillary slot. <b>2005</b> , 87, 134101	13
1745	Molecular Diagnosis and Biomarker Identification on SELDI proteomics data by ADTBoost method. <b>2005</b> , 2005, 4771-4	3
1744	Capillary-LC-µESI-MS/MS and Nano-LC-Nano ESI-MS/MS Analysis Using a Single Binary Pump Capillary LC System: Applications in Proteomics. <b>2005</b> , 28, 1271-1289	4
1743	Parts per million mass accuracy on an Orbitrap mass spectrometer via lock mass injection into a C-trap. <b>2005</b> , 4, 2010-21	1233
1742	Integration of metabolic and signaling networks. 235-256	1
1741	High throughput proteome screening for biomarker detection. <b>2005</b> , 4, 182-90	109
1740	The probability distribution for a random match between an experimental-theoretical spectral pair in tandem mass spectrometry. <b>2005</b> , 3, 455-76	13
1739	AN AUTOMATA APPROACH TO MATCH GAPPED SEQUENCE TAGS AGAINST PROTEIN DATABASE. <b>2005</b> , 16, 487-497	1

1738	Drosophila nutrigenomics can provide clues to human gene-nutrient interactions. <b>2005</b> , 25, 499-522	40
1737	Plant genome analysis: the state of the art. <b>2005</b> , 247, 223-84	13
1736	Application of immobilized metal affinity chromatography in proteomics. <b>2005</b> , 2, 649-57	64
1735	The application of proteomics to diabetes. <b>2005</b> , 2, 54-60	18
1734	High throughput quantitative analysis of serum proteins using glycopeptide capture and liquid chromatography mass spectrometry. <b>2005</b> , 4, 144-55	176
1733	Proteomics: A new research area for the biomedical field. <b>2005</b> , 1, 83-94	4
1732	Stable isotope labeling of Arabidopsis thaliana cells and quantitative proteomics by mass spectrometry. <b>2005</b> , 4, 1697-709	165
1731	Mass spectrometric evidence that proteolytic processing of rainbow trout egg vitelline envelope proteins takes place on the egg. <b>2005</b> , 280, 37585-98	48
1730	Proteomic analysis reveals hyperactivation of the mammalian target of rapamycin pathway in neurofibromatosis 1-associated human and mouse brain tumors. <b>2005</b> , 65, 2755-60	242
1729	Mass spectrometry-based expression profiling of clinical prostate cancer. <b>2005</b> , 4, 545-54	53
1728	SPIDER: software for protein identification from sequence tags with de novo sequencing error. <b>2005</b> , 3, 697-716	162
1727	DBToolkit: processing protein databases for peptide-centric proteomics. <b>2005</b> , 21, 3584-5	120
1726	Perspectives in Conceptual Modeling. 2005,	3
1725	Mass spectrometry-based quantitative proteomic profiling. <b>2005</b> , 4, 27-38	83
1724	Precise and parallel characterization of coding polymorphisms, alternative splicing, and modifications in human proteins by mass spectrometry. <b>2005</b> , 4, 1002-8	85
1723	Optimal construction of theoretical spectra for MS/MS spectra identification. <b>2005</b> , 9, 380-90	
1722	High-resolution functional proteomics by active-site peptide profiling. <b>2005</b> , 102, 4996-5001	91
1721	Diagnosis and biomarker identification on SELDI proteomics data by ADTBoost.	

1720	Proteomics and Protein-Protein Interactions. 2005,	10
1719	Elimination of redundant protein identifications in high throughput proteomics. <b>2005</b> , 2005, 4803-6	8
1718	Peptidomics of Cpe fat/fat mouse hypothalamus: effect of food deprivation and exercise on peptide levels. <b>2005</b> , 280, 4451-61	60
1717	Update on proteomics in Arabidopsis. Where do we go from here?. <b>2005</b> , 138, 591-9	67
1716	Low molecular weight proteomic information distinguishes metastatic from benign pheochromocytoma. <b>2005</b> , 12, 263-72	40
1715	Molecular Beacon Aptamers for Protein Monitoring in Real-Time and in Homogeneous Solutions. <b>2005</b> , 2, 31-40	26
1714	Mass tag-assisted identification of naturally processed HLA class II-presented meningococcal peptides recognized by CD4+ T lymphocytes. <b>2005</b> , 174, 5636-43	20
1713	Conserved patterns of protein interaction in multiple species. <b>2005</b> , 102, 1974-9	586
1712	"Subcellular proteomics" of neuromelanin granules isolated from the human brain. <b>2005</b> , 4, 945-57	79
1711	Quantitative phosphoproteomics applied to the yeast pheromone signaling pathway. <b>2005</b> , 4, 310-27	665
1710	Unraveling the pathogenesis of type 1 diabetes with proteomics: present and future directions. <b>2005</b> , 4, 441-57	41
1709	New data base-independent, sequence tag-based scoring of peptide MS/MS data validates Mowse scores, recovers below threshold data, singles out modified peptides, and assesses the quality of MS/MS techniques. <b>2005</b> , 4, 1180-8	81
1708	A uniform proteomics MS/MS analysis platform utilizing open XML file formats. <b>2005</b> , 1, 2005.0017	574
1707	Proteomic analysis of the Arabidopsis nucleolus suggests novel nucleolar functions. <b>2005</b> , 16, 260-9	313
1706	Improving protein identification using complementary fragmentation techniques in fourier transform mass spectrometry. <b>2005</b> , 4, 835-45	123
1705	Composition of clogging material in pancreatic endoprostheses. <b>2005</b> , 61, 862-6	26
1704	Two-dimensional gas-phase separations coupled to mass spectrometry for analysis of complex mixtures. <b>2005</b> , 77, 6381-8	111
1703	The opportunistic pathogen Toxoplasma gondii deploys a diverse legion of invasion and survival proteins. <b>2005</b> , 280, 34233-44	100

1702	The Proteomics Protocols Handbook. <b>2005</b> ,	204
1701	Prediction of physical protein-protein interactions. <b>2005</b> , 2, S1-16	75
1700	Chemical Signals in Vertebrates 10. <b>2005</b> ,	3
1699	Charge-state resolved mid-infrared spectroscopy of a gas-phase protein. <b>2005</b> , 7, 1345-8	154
1698	A two-dimensional electrophoresis proteomic reference map and systematic identification of 1367 proteins from a cell suspension culture of the model legume Medicago truncatula. <b>2005</b> , 4, 1812-25	97
1697	Mass spectrometry in diagnostic oncoproteomics. <b>2005</b> , 23, 465-78	24
1696	Principles of Fourier transform ion cyclotron resonance mass spectrometry and its application in structural biology. <b>2005</b> , 130, 18-28	39
1695	A compendium of signals and responses triggered by prodeath and prosurvival cytokines. <b>2005</b> , 4, 1569-90	116
1694	Pathway proteomics: global and focused approaches. <b>2005</b> , 5, 113-22	5
1693	AUDENS: a tool for automated peptide de novo sequencing. <b>2005</b> , 4, 1768-74	60
1692	Analysis of the dorsal spinal cord synaptic architecture by combined proteome analysis and in situ hybridization. <b>2005</b> , 4, 238-49	8
1691	Diffusion-time distribution analysis reveals characteristic ligand-dependent interaction patterns of nuclear receptors in living cells. <b>2005</b> , 44, 11676-83	39
1690	Development and evaluation of a micro- and nanoscale proteomic sample preparation method. <b>2005</b> , 4, 2397-403	141
1689	Metabolic engineering in the -omics era: elucidating and modulating regulatory networks. <b>2005</b> , 69, 197-216	89
1688	Beyond quantitative proteomics: signal enhancement of the a1 ion as a mass tag for peptide sequencing using dimethyl labeling. <b>2005</b> , 4, 101-8	105
1687	Metabolic labeling of human primary retinal pigment epithelial cells for accurate comparative proteomics. <b>2005</b> , 4, 620-7	24
1686	Exponentially modified protein abundance index (emPAI) for estimation of absolute protein amount in proteomics by the number of sequenced peptides per protein. <b>2005</b> , 4, 1265-72	1582
1685	Randomized sequence databases for tandem mass spectrometry peptide and protein identification. <b>2005</b> , 9, 364-79	75

1684	glycine. <b>2005</b> , 122, 241104	23
1683	Immunoaffinity CE for proteomics studies. <b>2005</b> , 77, 61A-67A	75
1682	STEM: a software tool for large-scale proteomic data analyses. <b>2005</b> , 4, 1826-31	54
1681	MALDI-TOF MS of phosphorylated lipids in biological fluids using immobilized metal affinity chromatography and a solid ionic crystal matrix. <b>2005</b> , 77, 4439-47	77
1680	Comparison of statistical approaches for the analysis of proteome expression data of differentiating neural stem cells. <b>2005</b> , 4, 96-100	47
1679	P-Mod: an algorithm and software to map modifications to peptide sequences using tandem MS data. <b>2005</b> , 4, 358-68	89
1678	Global proteome discovery using an online three-dimensional LC-MS/MS. 2005, 4, 801-8	82
1677	Introduction to Biological Mass Spectrometry: Determining Identity and Species of Origin of Two Proteins. <b>2005</b> , 82, 1215	19
1676	Comparison of probability and likelihood models for peptide identification from tandem mass spectrometry data. <b>2005</b> , 4, 1687-98	24
1675	Strategy to design improved proteomic experiments based on statistical analyses of the chemical properties of identified peptides. <b>2005</b> , 4, 2201-6	5
1674	Human tissue profiling with multidimensional protein identification technology. 2005, 4, 1757-67	72
1673	Robust method for proteome analysis by MS/MS using an entire translated genome: demonstration on the ciliome of Tetrahymena thermophila. <b>2005</b> , 4, 909-19	98
1672	Novel approach for peptide quantitation and sequencing based on 15N and 13C metabolic labeling. <b>2005</b> , 4, 578-85	61
1671	Sequence similarity-based proteomics in insects: characterization of the larvae venom of the Brazilian moth Cerodirphia speciosa. <b>2005</b> , 4, 862-9	34
1670	Proteomic profiling of surface proteins on Th1 and Th2 cells. <b>2005</b> , 4, 400-9	45
1669	MS-Analyzer: Intelligent Preprocessing, Management, and Data Mining Analysis of Mass Spectrometry Data on the Grid. <b>2005</b> ,	O
1668	Functional Genomics. <b>2005</b> , 7-25	1
1667	PROTEOMICS. <b>2005</b> , 383-393	

1666 De novo folding of GFP fusion proteins: high efficiency in eukaryotes but not in bacteria. 2005, 353, 397-409 76 Proteomic analysis of human natural killer cells: insights on new potential NK immune functions. 1665 23 2005, 42, 425-31 1664 The use of proteomics in meat science. **2005**, 71, 138-49 103 Mass spectrometric analysis of single identified neurons of an insect. 2005, 327, 640-5 48 Electron capture dissociation mass spectrometry in characterization of post-translational 1662 28 modifications. 2005, 334, 1-8 1661 The clinical application of proteomics. 2005, 357, 151-8 60 1660 The role of proteomics in the assessment of premature rupture of fetal membranes. 2005, 360, 27-36 51 1659 From proteomic inventory to architecture. **2005**, 579, 933-7 70 1658 Proteomic survey of bovine neutrophils. 2005, 103, 53-65 54 Peptide mass fingerprinting. 2005, 35, 237-47 179 1656 Purifying protein complexes for mass spectrometry: applications to protein translation. 2005, 35, 274-90 28 1655 Integrating gene and protein expression data: pattern analysis and profile mining. 2005, 35, 303-14 132 1654 Mass spectrometric analysis of histone posttranslational modifications. 2005, 36, 383-94 37 Cultivating the uncultivated: a community genomics perspective. 2005, 13, 411-5 76 Techniques: application of systems biology to absorption, distribution, metabolism, excretion and 1652 156 toxicity. 2005, 26, 202-9 Malaria vaccines: using models of immunity and functional genomics tools to accelerate the 1651 7 development of vaccines against Plasmodium falciparum. 2005, 23, 2235-42 Molecular weight assessment of proteins in total proteome profiles using 1D-PAGE and LC/MS/MS. 1650 21 **2005**, 3, 6 Pharmaceutical Applications of Liquid Chromatography Coupled with Mass Spectrometry (LC/MS). 1649 32 **2005**, 28, 1161-1202

1648	Comparative proteomics using 2-D gel electrophoresis and mass spectrometry as tools to dissect stimulons and regulons in bacteria with sequenced or partially sequenced genomes. <b>2005</b> , 7, 117-35	32
1647	Chemically modified, immobilized trypsin reactor with improved digestion efficiency. <b>2005</b> , 4, 1805-13	69
1646	Peptide sequence analysis. 2005, 402, 209-44	118
1645	Mass spectrometry-based peptide quantification: applications and limitations. <b>2005</b> , 2, 381-92	36
1644	SELDI-TOF proteomic analysis and cancer detection. <b>2005</b> , 3, 383-90, 422	15
1643	Physiologie des cellules monocytaires et macrophagiques. <b>2005</b> , 2, 240-258	
1642	Molecular approaches to the identification of biomarkers of exposure and effectreport of an expert meeting organized by COST Action B15. November 28, 2003. <b>2005</b> , 156, 227-40	23
1641	Toward defining the human parotid gland salivary proteome and peptidome: identification and characterization using 2D SDS-PAGE, ultrafiltration, HPLC, and mass spectrometry. <b>2005</b> , 44, 2885-99	148
1640	Chapter 1 Emerging technologies The way forward on improving protein analysis. 2005, 1-67	1
1639	Chapter 6 Microtechnology principles and platforms for proteomic analysis. <b>2005</b> , 46, 351-383	
1638	Chapter 5 Phosphorylation-specific analysis strategies for mass spectrometry: enhanced detection of phosphorylated proteins and peptides. <b>2005</b> , 46, 275-349	1
1637	Chapter 13 Simulation as a tool for optimizing proteome analysis. <b>2005</b> , 46, 523-534	
1636	Chapter 14 Proteomics and remodeling of extracellular matrix in lung diseases. <b>2005</b> , 46, 535-556	
1635	Chapter 15 Mammalian cell biology and proteomics. <b>2005</b> , 46, 557-596	
1634	Analysis of shotgun proteomics and RNA profiling data from Arabidopsis thaliana chloroplasts. <b>2005</b> , 4, 637-40	39
1633	Mass Spectrometry on the March: Where next? from Molecular Biophysics to Structural Biology, Perspectives and Challenges. <b>2005</b> , 382-441	
1632	Peptide sequence tags for fast database search in mass-spectrometry. <b>2005</b> , 4, 1287-95	103
1631	Comprehensive label-free method for the relative quantification of proteins from biological samples. <b>2005</b> , 4, 1442-50	194

1630	A strategy to investigate the plant meiotic proteome. <b>2005</b> , 109, 181-9	36
1629	Proteomics. <b>2005</b> , 402, 245-89	34
1628	Mechanism of divergent growth factor effects in mesenchymal stem cell differentiation. 2005, 308, 1472-7	495
1627	Proteomics-grade de novo sequencing approach. <b>2005</b> , 4, 2348-54	142
1626	Integrated approach for manual evaluation of peptides identified by searching protein sequence databases with tandem mass spectra. <b>2005</b> , 4, 998-1005	156
1625	11 Isoelectric focusing and proteomics. <b>2005</b> , 247-264	O
1624	Multidimensional protein identification technology: current status and future prospects. <b>2005</b> , 2, 27-39	32
1623	Amyotrophic lateral sclerosis: new developments in diagnostic markers. <b>2005</b> , 2, 177-84	24
1622	High-throughput proteomics using matrix-assisted laser desorption/ionization mass spectrometry. <b>2005</b> , 2, 407-20	30
1621	Use of lysozyme as a standard for evaluating the effectiveness of a proteomics process. <b>2005</b> , 4, 153-60	12
1620	Discovery of biomarker candidates within disease by protein profiling: principles and concepts. <b>2005</b> , 4, 1200-12	59
1619	High-accuracy proteome maps of human body fluids. <b>2006</b> , 7, 242	44
1618	Identification of 491 proteins in the tear fluid proteome reveals a large number of proteases and protease inhibitors. <b>2006</b> , 7, R72	276
1617	The elusive yeast interactome. <b>2006</b> , 7, 223	59
1616	Status of complete proteome analysis by mass spectrometry: SILAC labeled yeast as a model system. <b>2006</b> , 7, R50	224
1615	Bioinformatics and Drug Discovery. <b>2006</b> ,	1
1614	Mass Spectrometry-based Methods of Proteome Analysis. 2006,	
1613	Proteomic profiling of differentiating osteoblasts. <b>2006</b> , 3, 483-96	20

1612	Plant Proteomics. 2006,	2
1611	Conceptual Modeling - ER 2006. <b>2006</b> ,	3
1610	Cardiovascular Proteomics. 2006,	2
1609	Mass Spectrometry Data Analysis in Proteomics. 2006,	2
1608	RNA Towards Medicine. <b>2006</b> ,	
1607	Embryonic stem cell proteomics. <b>2006</b> , 3, 427-37	34
1606	Ionizable isotopic labeling reagent for relative quantification of amine metabolites by mass spectrometry. <b>2006</b> , 78, 6398-403	58
1605	Orbitrap mass analyzeroverview and applications in proteomics. <b>2006</b> , 6 Suppl 2, 16-21	161
1604	Prospective care: a personalized, preventative approach to medicine. <b>2006</b> , 7, 5-9	37
1603	Transcriptomics, proteomics and interactomics: unique approaches to track the insights of bioremediation. <b>2006</b> , 4, 355-62	56
1602	Toxicogenomics in regulatory ecotoxicology. <b>2006</b> , 40, 4055-65	221
1601	Analyzing the cardiac muscle proteome by liquid chromatography-mass spectrometry-based expression proteomics. <b>2007</b> , 357, 15-31	13
1600	Improved immobilized metal affinity chromatography for large-scale phosphoproteomics applications. <b>2006</b> , 5, 2789-99	109
1599	Synthesis of acid-cleavable light isotope-coded affinity tags (ICAT-L) for potential use in proteomic expression profiling analysis. <b>2006</b> , 17, 248-54	39
1598	Cleavable hydrophilic linker for one-bead-one-compound sequencing of oligomer libraries by tandem mass spectrometry. <b>2006</b> , 8, 417-26	78
1597	Analysis of the cGMP/cAMP interactome using a chemical proteomics approach in mammalian heart tissue validates sphingosine kinase type 1-interacting protein as a genuine and highly abundant AKAP. <b>2006</b> , 5, 1435-47	101
1596	Functional genomics and proteomics in the clinical neurosciences: data mining and bioinformatics. <b>2006</b> , 158, 83-108	22
1595	Arabidopsis Protocols. <b>2006</b> ,	2

1594	Protein mass measurement combined with mass spectrometric sequencing of protein digests for detection and characterization of protein modifications1. <b>2006</b> , 84, 986-997	1
1593	Proteomics of the human malaria parasite Plasmodium falciparum. <b>2006</b> , 3, 87-95	23
1592	A Grid Service for Pattern Extraction from Mass Spectrometry Data. 2006,	1
1591	Label-free quantitative proteomics using large peptide data sets generated by nanoflow liquid chromatography and mass spectrometry. <b>2006</b> , 5, 1338-47	169
1590	Experimental standards for high-throughput proteomics. <b>2006</b> , 10, 152-7	20
1589	Contribution of mass spectrometry-based proteomics to immunology. <b>2006</b> , 3, 653-64	24
1588	A hydrophilic interaction chromatography coupled to a mass spectrometry for the determination of glutathione in plant somatic embryos. <b>2006</b> , 131, 1167-74	72
1587	Mass spectrometry: uncovering the cancer proteome for diagnostics. <b>2007</b> , 96, 23-50	59
1586	Protein separation and characterization by np-RP-HPLC followed by intact MALDI-TOF mass spectrometry and peptide mass mapping analyses. <b>2006</b> , 5, 1688-700	27
1585	Proteomic approaches to dissect platelet function: Half the story. <b>2006</b> , 108, 3983-91	63
1584	High-resolution field asymmetric waveform ion mobility spectrometry using new planar geometry analyzers. <b>2006</b> , 78, 3706-14	151
1583	Identification of glycoproteins in human cerebrospinal fluid with a complementary proteomic approach. <b>2006</b> , 5, 2769-79	85
1582	Molecular biology of bladder cancer: prognostic and clinical implications. <b>2006</b> , 5, 67-77	43
1581	Proteomic analysis of GPI-anchored membrane proteins. <b>2006</b> , 3, 339-46	1
1580	Modular stop and go extraction tips with stacked disks for parallel and multidimensional Peptide fractionation in proteomics. <b>2006</b> , 5, 988-94	231
1579	Evaluation of multiprotein immunoaffinity subtraction for plasma proteomics and candidate biomarker discovery using mass spectrometry. <b>2006</b> , 5, 2167-74	188
1578	Current challenges and developments in GC-MS based metabolite profiling technology. <b>2006</b> , 124, 312-22	159
1577	Dynamical Simulations of Photoionization of Small Biological Molecules. <b>2006</b> , 213-237	

1576	A new chemical probe for the detection of the cancer-linked galectin-3. <b>2006</b> , 4, 4387-94	48
1575	Analytical model of peptide mass cluster centres with applications. <b>2006</b> , 4, 18	20
1574	Metabolic labeling of plant cell cultures with K(15)NO3 as a tool for quantitative analysis of proteins and metabolites. <b>2006</b> , 2, 14	83
1573	Detection and identification of protein isoforms using cluster analysis of MALDI-MS mass spectra. <b>2006</b> , 5, 785-92	60
1572	Multiplexed two-dimensional liquid chromatography for MALDI and nanoelectrospray ionization mass spectrometry in proteomics. <b>2006</b> , 5, 1803-7	32
1571	Molecular analysis of maturation processes by protein and phosphoprotein profiling during in vitro maturation of bovine oocytes: a proteomic approach. <b>2006</b> , 8, 259-74	30
1570	Spatially resolved non-invasive chemical stimulation for modulation of signalling in reconstructed neuronal networks. <b>2006</b> , 3, 333-43	6
1569	Identifying and quantifying sites of protein methylation by heavy methyl SILAC. <b>2006</b> , Chapter 14, Unit 14.9	19
1568	Introduction to proteomics. 2007, 367, 1-35	7
1567	Methods for proteomics in neuroscience. <b>2006</b> , 158, 41-82	58
1567 1566	Methods for proteomics in neuroscience. <b>2006</b> , 158, 41-82  Bioinformatics and data mining in proteomics. <b>2006</b> , 3, 333-43	58
,		
1566	Bioinformatics and data mining in proteomics. <b>2006</b> , 3, 333-43  Rapid validation of protein identifications with the borderline statistical confidence via de novo	23
1566 1565	Bioinformatics and data mining in proteomics. <b>2006</b> , 3, 333-43  Rapid validation of protein identifications with the borderline statistical confidence via de novo sequencing and MS BLAST searches. <b>2006</b> , 5, 2448-56  Electroelution of intact proteins from SDS-PAGE gels and their subsequent MALDI-TOF MS analysis.	23
1566 1565 1564	Bioinformatics and data mining in proteomics. <b>2006</b> , 3, 333-43  Rapid validation of protein identifications with the borderline statistical confidence via de novo sequencing and MS BLAST searches. <b>2006</b> , 5, 2448-56  Electroelution of intact proteins from SDS-PAGE gels and their subsequent MALDI-TOF MS analysis. <b>2007</b> , 355, 353-63	<ul><li>23</li><li>37</li><li>7</li></ul>
1566 1565 1564	Bioinformatics and data mining in proteomics. 2006, 3, 333-43  Rapid validation of protein identifications with the borderline statistical confidence via de novo sequencing and MS BLAST searches. 2006, 5, 2448-56  Electroelution of intact proteins from SDS-PAGE gels and their subsequent MALDI-TOF MS analysis. 2007, 355, 353-63  Proteomics in antitumor research. 2006, 3, 441-449  Aqueous two-phase partitioning for proteomic monitoring of cell surface biomarkers in human	<ul><li>23</li><li>37</li><li>7</li><li>2</li></ul>
1566 1565 1564 1563	Bioinformatics and data mining in proteomics. 2006, 3, 333-43  Rapid validation of protein identifications with the borderline statistical confidence via de novo sequencing and MS BLAST searches. 2006, 5, 2448-56  Electroelution of intact proteins from SDS-PAGE gels and their subsequent MALDI-TOF MS analysis. 2007, 355, 353-63  Proteomics in antitumor research. 2006, 3, 441-449  Aqueous two-phase partitioning for proteomic monitoring of cell surface biomarkers in human peripheral blood mononuclear cells. 2006, 5, 1168-75  Quantitative proteomic and genomic profiling reveals metastasis-related protein expression	23 37 7 2
1566 1565 1564 1563 1562	Bioinformatics and data mining in proteomics. 2006, 3, 333-43  Rapid validation of protein identifications with the borderline statistical confidence via de novo sequencing and MS BLAST searches. 2006, 5, 2448-56  Electroelution of intact proteins from SDS-PAGE gels and their subsequent MALDI-TOF MS analysis. 2007, 355, 353-63  Proteomics in antitumor research. 2006, 3, 441-449  Aqueous two-phase partitioning for proteomic monitoring of cell surface biomarkers in human peripheral blood mononuclear cells. 2006, 5, 1168-75  Quantitative proteomic and genomic profiling reveals metastasis-related protein expression patterns in gastric cancer cells. 2006, 5, 2727-42  Trade-off between high sensitivity and increased potential for false positive peptide sequence matches using a two-dimensional linear ion trap for tandem mass spectrometry-based proteomics.	23 37 7 2 19

1558	Insulin-dependent interactions of proteins with GLUT4 revealed through stable isotope labeling by amino acids in cell culture (SILAC). <b>2006</b> , 5, 64-75	98
1557	Accurate mass-driven analysis for the characterization of protein phosphorylation. Study of the human Chk2 protein kinase. <b>2006</b> , 78, 2171-81	33
1556	Comparison of the protein profile of established and regressed hypertension-induced left ventricular hypertrophy. <b>2006</b> , 5, 404-13	28
1555	In-Gel Stable-Isotope Labeling (ISIL): a strategy for mass spectrometry-based relative quantification. <b>2006</b> , 5, 155-63	29
1554	MODi: a powerful and convenient web server for identifying multiple post-translational peptide modifications from tandem mass spectra. <b>2006</b> , 34, W258-63	51
1553	Top-down protein sequencing and MS3 on a hybrid linear quadrupole ion trap-orbitrap mass spectrometer. <b>2006</b> , 5, 949-58	163
1552	Miniaturized solid-phase extraction and sample preparation for MALDI MS using a microfabricated integrated selective enrichment target. <b>2006</b> , 5, 1071-81	49
1551	Systematic identification of functional orthologs based on protein network comparison. <b>2006</b> , 16, 428-35	142
1550	An integrated mass spectrometry-based proteomic approach: quantitative analysis of tandem affinity-purified in vivo cross-linked protein complexes (QTAX) to decipher the 26 S proteasome-interacting network. <b>2006</b> , 5, 366-78	221
1549	Analysis of complex protein mixtures with improved sequence coverage using (CE-MS/MS)n. <b>2006</b> , 78, 7309-16	41
1548	Biological network analyses: computational genomics and systems approaches. <b>2006</b> , 32, 203-209	
1547	Quantitative profiling of drug-associated proteomic alterations by combined 2-nitrobenzenesulfenyl chloride (NBS) isotope labeling and 2DE/MS identification. <b>2006</b> , 5, 2194-206	37
1546	Mass spectrometry technologies for proteomics. <b>2006</b> , 4, 295-320	86
1545	Multiple isoforms of myosin light chain 1 in pig diaphragm slow fibers: correlation with maximal shortening velocity and force generation. <b>2006</b> , 456, 112-8	10
1544	Ex vivo cancer chemoprevention research possibilities. <b>2006</b> , 21, 204-14	14
1543	A novel yeast two-hybrid approach to identify CDPK substrates: characterization of the interaction between AtCPK11 and AtDi19, a nuclear zinc finger protein. <b>2006</b> , 580, 904-11	62
1542	Global survey of organ and organelle protein expression in mouse: combined proteomic and transcriptomic profiling. <b>2006</b> , 125, 173-86	400
1541	A mammalian organelle map by protein correlation profiling. <b>2006</b> , 125, 187-99	477

1540	Global, in vivo, and site-specific phosphorylation dynamics in signaling networks. <b>2006</b> , 127, 635-48	2797
1539	From genes to systems: new global strategies for the characterization of NCL biology. <b>2006</b> , 1762, 934-44	13
1538	Complement C3c and related protein biomarkers in amyotrophic lateral sclerosis and Parkinson's disease. <b>2006</b> , 342, 1034-9	96
1537	Expression proteomics to p53 mutation reactivation with PRIMA-1 in breast cancer cells. <b>2006</b> , 349, 1117-24	14
1536	Proteome analysis of signaling cascades in human platelets. <b>2006</b> , 36, 152-6	31
1535	The emerging complexity of the vertebrate cilium: new functional roles for an ancient organelle. <b>2006</b> , 11, 9-19	119
1534	High-throughput techniques in breast cancer: a clinical perspective. <b>2006</b> , 42, 598-607	11
1533	In-gel isoelectric focusing of peptides as a tool for improved protein identification. <b>2006</b> , 5, 1721-30	101
1532	A clean, more efficient method for in-solution digestion of protein mixtures without detergent or urea. <b>2006</b> , 5, 3446-52	83
1531	Detecting differential and correlated protein expression in label-free shotgun proteomics. <b>2006</b> , 5, 2909-18	338
1531 1530	Detecting differential and correlated protein expression in label-free shotgun proteomics. <b>2006</b> , 5, 2909-18  Bioinformatics and its applications in plant biology. <b>2006</b> , 57, 335-60	338 78
1530	Bioinformatics and its applications in plant biology. <b>2006</b> , 57, 335-60  2D gel blood serum biomarkers reveal differential clinical proteomics of the neurodegenerative	78
1530 1529	Bioinformatics and its applications in plant biology. <b>2006</b> , 57, 335-60  2D gel blood serum biomarkers reveal differential clinical proteomics of the neurodegenerative diseases. <b>2006</b> , 3, 45-62  Differential expression analysis of proteins from neutrophils in the periparturient period and	78 42
1530 1529 1528	Bioinformatics and its applications in plant biology. <b>2006</b> , 57, 335-60  2D gel blood serum biomarkers reveal differential clinical proteomics of the neurodegenerative diseases. <b>2006</b> , 3, 45-62  Differential expression analysis of proteins from neutrophils in the periparturient period and neutrophils from dexamethasone-treated dairy cows. <b>2006</b> , 111, 149-64	78 42 44
1530 1529 1528 1527	Bioinformatics and its applications in plant biology. 2006, 57, 335-60  2D gel blood serum biomarkers reveal differential clinical proteomics of the neurodegenerative diseases. 2006, 3, 45-62  Differential expression analysis of proteins from neutrophils in the periparturient period and neutrophils from dexamethasone-treated dairy cows. 2006, 111, 149-64  Proteomic identification of palmitoylated proteins. 2006, 40, 135-42	78 42 44 34
1530 1529 1528 1527 1526	Bioinformatics and its applications in plant biology. 2006, 57, 335-60  2D gel blood serum biomarkers reveal differential clinical proteomics of the neurodegenerative diseases. 2006, 3, 45-62  Differential expression analysis of proteins from neutrophils in the periparturient period and neutrophils from dexamethasone-treated dairy cows. 2006, 111, 149-64  Proteomic identification of palmitoylated proteins. 2006, 40, 135-42  Quantitative proteomics to study mitogen-activated protein kinases. 2006, 40, 243-50	78 42 44 34 73

1522 Managing ontologies for Grid computing. <b>2006</b> , 2, 29-44	4
Comprehensive phenotyping in multiple sclerosis: discovery based proteomics and the curre understanding of putative biomarkers. <b>2006</b> , 22, 213-25	nt <sub>18</sub>
1520 Isotope Labeling in Quantitative Proteomics. <b>2006</b> , 47-61	
1519 Stable Isotope Labeling by Amino Acids in Cell Culture for Quantitative Proteomics. <b>2006</b> , 42	27-436
1518 Engineering RNA-based circuits. <b>2006</b> , 423-45	
1517 [Proteomics of breast cancer: From differential to functional analysis]. <b>2006</b> , 200, 199-202	
1516 Proteomics. 281-298	
1515 The use of Proteomics in the Study of Metabolic Control. 24-59	1
1514 The process chain for peptidomic biomarker discovery. <b>2006</b> , 22, 27-37	37
1513 . <b>2006</b> ,	5
1512 . <b>2006</b> ,	23
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. <b>2006</b> , 1-35	3
1510 . <b>2006</b> ,	8
1509 Proteomics. <b>2006</b> ,	
1508 . <b>2006</b> ,	4
1507 . <b>2006</b> ,	6
1506 Proteomic analysis of cytochromes P450: a mass spectrometry approach. <b>2006</b> , 34, 1246-51	23
1505 Proteomics. <b>2006</b> ,	O

1504	Proteomics in pulmonary medicine. <b>2006</b> , 130, 567-74	57
1503	Single Cell Proteomics: Challenge for Current Analytical Science. <b>2006</b> , 2, 67-76	10
1502	Screening the brain: molecular fingerprints of neural stem cells. <b>2006</b> , 1, 65-77	10
1501	Physiologie des cellules monocytaires et macrophagiques. <b>2006</b> , 1, 1-13	
1500	Isotope-Coded Affinity Tagging Technique Using Avidin Functional Affinity Electrophoresis: An Alternative to an Avidin Affinity Column. <b>2006</b> , 53, 745-750	2
1499	Identification and characterization of DNA-binding proteins by mass spectrometry. 2007, 104, 111-95	1
1498	Identification of glycosylated marker proteins of epithelial polarity in MDCK cells by homology driven proteomics. <b>2006</b> , 7, 8	30
1497	RT-PSM, a real-time program for peptide-spectrum matching with statistical significance. <b>2006</b> , 20, 1199-208	16
1496	Detection of artifacts and peptide modifications in liquid chromatography/mass spectrometry data using two-dimensional signal intensity map data visualization. <b>2006</b> , 20, 1558-62	17
1495	Enhanced detection of sulfo-peptides as onium salts in matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <b>2006</b> , 20, 1615-20	10
1494	Combined infrared multiphoton dissociation and electron-capture dissociation using co-linear and overlapping beams in Fourier transform ion cyclotron resonance mass spectrometry. <b>2006</b> , 20, 1838-44	22
1493	Top-down analysis of basic proteins by microchip capillary electrophoresis mass spectrometry. <b>2006</b> , 20, 1932-8	30
1492	An evaluation for cross-species proteomics research by publicly available expressed sequence tag database search using tandem mass spectral data. <b>2006</b> , 20, 2635-40	7
1491	Intact cell matrix-assisted laser desorption/ionization mass spectrometry as a tool to screen drugs in vivo for regulation of protein expression. <b>2006</b> , 20, 2769-72	7
1490	Direct structural assignment of neutral and sialylated N-glycans of glycopeptides using collision-induced dissociation MSn spectral matching. <b>2006</b> , 20, 3557-65	33
1489	Proteomic analysis of the tetraspanin web using LC-ESI-MS/MS and MALDI-FTICR-MS. <b>2006</b> , 6, 1437-49	8o
1488	Proteomic analysis of estrogen response of premalignant human breast cells using a 2-D liquid separation/mass mapping technique. <b>2006</b> , 6, 3847-61	21
1487	Analysis of the dynamic Bacillus subtilis Ser/Thr/Tyr phosphoproteome implicated in a wide variety of cellular processes. <b>2006</b> , 6, 2157-73	77

1486	SPLASH: systematic proteomics laboratory analysis and storage hub. <b>2006</b> , 6, 1758-69	5
1485	Differential proteome profiles in E2F2-deficient T lymphocytes. <b>2006</b> , 6 Suppl 1, S42-50	10
1484	Optimizing search conditions for the mass fingerprint-based identification of proteins. <b>2006</b> , 6, 2079-85	14
1483	Ligand profiling and identification technology for searching bioactive ligands. 2006, 6, 1741-9	1
1482	Systematical evaluation of the effects of sample collection procedures on low-molecular-weight serum/plasma proteome profiling. <b>2006</b> , 6, 3189-98	198
1481	Comparative proteomic studies on the pathogenesis of human ulcerative colitis. 2006, 6, 5322-31	98
1480	Selective detection of 2-nitrobenzenesulfenyl-labeled peptides by matrix-assisted laser desorption/ionization-time of flight mass spectrometry using a novel matrix. <b>2006</b> , 6, 2042-9	22
1479	Characterization of the phosphorylation sites of Mycobacterium tuberculosis serine/threonine protein kinases, PknA, PknD, PknE, and PknH by mass spectrometry. <b>2006</b> , 6, 3754-66	25
1478	Proteomic analysis of cold adaptation in a Siberian permafrost bacteriumExiguobacterium sibiricum 255-15 by two-dimensional liquid separation coupled with mass spectrometry. <b>2006</b> , 6, 5221-33	28
1477	Metabolomics: current technologies and future trends. <b>2006</b> , 6, 4716-23	402
	Metabolomics: current technologies and future trends. <b>2006</b> , 6, 4716-23  Advances in plant proteomics. <b>2006</b> , 6, 5504-16	188
1476	Advances in plant proteomics. <b>2006</b> , 6, 5504-16  Gaining knowledge from previously unexplained spectra-application of the PTM-Explorer software	188
1476 1475	Advances in plant proteomics. <b>2006</b> , 6, 5504-16  Gaining knowledge from previously unexplained spectra-application of the PTM-Explorer software to detect PTM in HUPO BPP MS/MS data. <b>2006</b> , 6, 5048-58	188
1476 1475 1474	Advances in plant proteomics. 2006, 6, 5504-16  Gaining knowledge from previously unexplained spectra-application of the PTM-Explorer software to detect PTM in HUPO BPP MS/MS data. 2006, 6, 5048-58  The pitfalls of proteomics experiments without the correct use of bioinformatics tools. 2006, 6, 5577-96  Mass spectrometry-based proteomic analysis of the epitope-tag affinity purified protein complexes	188 13 77
1476 1475 1474 1473	Advances in plant proteomics. 2006, 6, 5504-16  Gaining knowledge from previously unexplained spectra-application of the PTM-Explorer software to detect PTM in HUPO BPP MS/MS data. 2006, 6, 5048-58  The pitfalls of proteomics experiments without the correct use of bioinformatics tools. 2006, 6, 5577-96  Mass spectrometry-based proteomic analysis of the epitope-tag affinity purified protein complexes in eukaryotes. 2006, 6, 6158-66  High resolution proteome/peptidome analysis of body fluids by capillary electrophoresis coupled	188 13 77 57
1476 1475 1474 1473	Advances in plant proteomics. 2006, 6, 5504-16  Gaining knowledge from previously unexplained spectra-application of the PTM-Explorer software to detect PTM in HUPO BPP MS/MS data. 2006, 6, 5048-58  The pitfalls of proteomics experiments without the correct use of bioinformatics tools. 2006, 6, 5577-96  Mass spectrometry-based proteomic analysis of the epitope-tag affinity purified protein complexes in eukaryotes. 2006, 6, 6158-66  High resolution proteome/peptidome analysis of body fluids by capillary electrophoresis coupled with MS. 2006, 6, 5615-27	188 13 77 57 90

1468	A comparison of the HUPO Brain Proteome Project pilot with other proteomics studies. <b>2006</b> , 6, 5076-86	25
1467	Selective enrichment of Ser-/Thr-phosphorylated peptides in the presence of Ser-/Thr-glycosylated peptides. <b>2006</b> , 6, 6394-9	17
1466	Nanotechnology for genomics & proteomics. <b>2006</b> , 1, 38-45	16
1465	Charting protein complexes, signaling pathways, and networks in the immune system. <b>2006</b> , 210, 187-207	43
1464	Proteomic analysis of rat hippocampal plasma membrane: characterization of potential neuronal-specific plasma membrane proteins. <b>2006</b> , 98, 1126-40	55
1463	Computer-assisted mass spectrometric analysis of naturally occurring and artificially introduced cross-links in proteins and protein complexes. <b>2006</b> , 273, 281-91	49
1462	Toward the systems biology of vesicle transport. <b>2006</b> , 7, 761-8	7
1461	Challenges in deriving high-confidence protein identifications from data gathered by a HUPO plasma proteome collaborative study. <b>2006</b> , 24, 333-8	288
1460	Protein biomarker discovery and validation: the long and uncertain path to clinical utility. <b>2006</b> , 24, 971-83	1347
1459	Analyzing phosphoinositides and their interacting proteins. <b>2006</b> , 3, 251-8	97
1459 1458	Analyzing phosphoinositides and their interacting proteins. <b>2006</b> , 3, 251-8  Dynamic proteomics in individual human cells uncovers widespread cell-cycle dependence of nuclear proteins. <b>2006</b> , 3, 525-31	97
,	Dynamic proteomics in individual human cells uncovers widespread cell-cycle dependence of	
1458	Dynamic proteomics in individual human cells uncovers widespread cell-cycle dependence of nuclear proteins. <b>2006</b> , 3, 525-31  An efficient tandem affinity purification procedure for interaction proteomics in mammalian cells.	117
1458 1457	Dynamic proteomics in individual human cells uncovers widespread cell-cycle dependence of nuclear proteins. <b>2006</b> , 3, 525-31  An efficient tandem affinity purification procedure for interaction proteomics in mammalian cells. <b>2006</b> , 3, 1013-9  Protein interaction screening by quantitative immunoprecipitation combined with knockdown	117 326
1458 1457 1456	Dynamic proteomics in individual human cells uncovers widespread cell-cycle dependence of nuclear proteins. 2006, 3, 525-31  An efficient tandem affinity purification procedure for interaction proteomics in mammalian cells. 2006, 3, 1013-9  Protein interaction screening by quantitative immunoprecipitation combined with knockdown (QUICK). 2006, 3, 981-3	117 326 214
1458 1457 1456 1455	Dynamic proteomics in individual human cells uncovers widespread cell-cycle dependence of nuclear proteins. 2006, 3, 525-31  An efficient tandem affinity purification procedure for interaction proteomics in mammalian cells. 2006, 3, 1013-9  Protein interaction screening by quantitative immunoprecipitation combined with knockdown (QUICK). 2006, 3, 981-3  Quantitative proteome analysis using isotope-coded affinity tags and mass spectrometry. 2006, 1, 139-45  Two-dimensional fluorescence difference gel electrophoresis for comparative proteomics profiling.	117 326 214 158
1458 1457 1456 1455	Dynamic proteomics in individual human cells uncovers widespread cell-cycle dependence of nuclear proteins. 2006, 3, 525-31  An efficient tandem affinity purification procedure for interaction proteomics in mammalian cells. 2006, 3, 1013-9  Protein interaction screening by quantitative immunoprecipitation combined with knockdown (QUICK). 2006, 3, 981-3  Quantitative proteome analysis using isotope-coded affinity tags and mass spectrometry. 2006, 1, 139-45  Two-dimensional fluorescence difference gel electrophoresis for comparative proteomics profiling. 2006, 1, 1732-42	117 326 214 158

1450	In-gel stable isotope labeling for relative quantification using mass spectrometry. <b>2006</b> , 1, 46-51	14
1449	Tumour microenvironment - opinion: validating matrix metalloproteinases as drug targets and anti-targets for cancer therapy. <b>2006</b> , 6, 227-39	1005
1448	A visual approach to proteomics. <b>2006</b> , 7, 225-30	196
1447	Interpreting the protein language using proteomics. <b>2006</b> , 7, 391-403	392
1446	Collecting and organizing systematic sets of protein data. <b>2006</b> , 7, 803-12	90
1445	Functional and quantitative proteomics using SILAC. <b>2006</b> , 7, 952-8	775
1444	Quantitative proteomics and its applications for systems biology. <b>2006</b> , 71, 1060-72	7
1443	Robust Salmonella metabolism limits possibilities for new antimicrobials. <i>Nature</i> , <b>2006</b> , 440, 303-7 50.4	287
1442	Organellar proteomics: turning inventories into insights. <b>2006</b> , 7, 874-9	175
1441	Molecular predictors of response and outcome in ovarian cancer. <b>2006</b> , 60, 19-37	33
1440	A network model of early events in epidermal growth factor receptor signaling that accounts for combinatorial complexity. <b>2006</b> , 83, 136-51	127
1439	Peptide, domain, and DNA affinity selection in the identification and quantitation of proteins from complex biological samples. <b>2006</b> , 356, 1-11	1
1438	In situ phosphorylation of immobilized receptors on biosensor surfaces: application to E-cadherin/beta-catenin interactions. <b>2006</b> , 357, 277-88	21
1437	Improved analysis of membrane protein by PVDF-aided, matrix-assisted laser desorption/ionization mass spectrometry. <b>2006</b> , 556, 237-46	11
1436	Analysis of protein interaction networks using mass spectrometry compatible techniques. <b>2006</b> , 564, 10-8	16
1435	Protein-sensing assay formats and devices. <b>2006</b> , 568, 232-47	70
1434	Reduced expression of regucalcin in young and aged mdx diaphragm indicates abnormal cytosolic calcium handling in dystrophin-deficient muscle. <b>2006</b> , 1764, 773-85	42
1433	Dissecting the ubiquitin pathway by mass spectrometry. <b>2006</b> , 1764, 1940-7	66

1432	A biological approach to computational models of proteomic networks. <b>2006</b> , 10, 73-80	100
1431	Tandem mass spectrometry reveals the quaternary organization of macromolecular assemblies. <b>2006</b> , 13, 597-605	191
1430	Micro-separation toward systems biology. <b>2006</b> , 1106, 19-28	35
1429	Simplified gradient generator for micro- and nano-liquid chromatography. <b>2006</b> , 1123, 47-52	14
1428	Quantitative proteome analysis using D-labeled N-ethylmaleimide and 13C-labeled iodoacetanilide by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <b>2006</b> , 14, 8197-209	18
1427	Charge-state dependent dissociation of a trypsin/inhibitor complex via ion trap collisional activation. <b>2006</b> , 253, 147-155	6
1426	Atypical behavior in the electron capture induced dissociation of biologically relevant transition metal ion complexes of the peptide hormone oxytocin. <b>2006</b> , 253, 217-224	60
1425	Why donE biologists use SIMS?. <b>2006</b> , 252, 6827-6835	94
1424	Use of surface enhanced laser desorption/ionization-time of flight mass spectrometry (SELDI-TOF MS) to study protein expression in a rat model of cocaine withdrawal. <b>2006</b> , 158, 1-12	9
1423	Protein identification via surface-induced dissociation in an FT-ICR mass spectrometer and a patchwork sequencing approach. <b>2006</b> , 17, 700-9	18
1422	A new method for evaluation of intracellular protein kinase signals using mass spectrometry. <b>2006</b> , 7, 699-704	3
1421	Proteomic technology for biomarker profiling in cancer: an update. <b>2006</b> , 7, 411-20	37
1420	Mass spectrometry and protein analysis. <b>2006</b> , 312, 212-7	1552
1419	Chemistry. Mass spectrometry: bottom-up or top-down?. <b>2006</b> , 314, 65-6	314
1418	Protein profiling of sickle cell versus control RBC core membrane skeletons by ICAT technology and tandem mass spectrometry. <b>2006</b> , 11, 326-37	17
1417	Quantitative peptidomics in mice: effect of cocaine treatment. <b>2006</b> , 28, 265-75	34
1416	Protein identification by tandem mass spectrometry and sequence database searching. 2007, 367, 87-119	129
1415	Proteomics: a promising approach to study biotic interaction in legumes. A review. <b>2006</b> , 147, 37-47	54

1414 Degradomics: systems biology of the protease web. Pleiotropic roles of MMPs in cancer. <b>2006</b> , 25,	69-75 181
1413 Toward genomic cell culture engineering. <b>2006</b> , 50, 121-40	11
Proteomics of the human brain: sub-proteomes might hold the key to handle brain complexity. <b>2006</b> , 113, 1041-54	27
Electron capture dissociation mass spectrometry in characterization of peptides and proteins. <b>200</b> $^{1411}$ , 28, 1047-59	61
1410 [Proteome analysisbasis for individualized pancreatic carcinoma therapy?]. <b>2006</b> , 47 Suppl 1, S40-	-8 4
Spatially resolved ultra-trace analysis of elements combining resonance ionization with a MALDI-TOF spectrometer. <b>2006</b> , 386, 109-18	10
Direct determination of the ionization energy of histidine with VUV synchrotron radiation. <b>2006</b> , 249-250, 155-161	31
Mechanisms for the selective gas-phase fragmentation reactions of methionine side chain fixed charge sulfonium ion containing peptides. <b>2006</b> , 17, 1631-42	20
Enhanced nuclear factor-kappa B-associated Wnt-1 expression in hepatitis B- and C-related hepatocarcinogenesis: identification by functional proteomics. <b>2006</b> , 13, 27-39	26
1405 Stem cells and proteomics. <b>2006</b> , 18, 161-167	
1404 Toxicoproteomics in the study of aromatic hydrocarbon toxicity. <b>2006</b> , 11, 187-198	13
1403 Mass spectrometry of protein modifications by reactive oxygen and nitrogen species. <b>2006</b> , 41, 15	<b>07-20</b> <i>73</i>
A machine learning perspective on the development of clinical decision support systems utilizing mass spectra of blood samples. <b>2006</b> , 39, 227-48	79
1401 Informatics solutions for high-throughput proteomics. <b>2006</b> , 11, 509-16	9
1400 Software for computational peptide identification from MS-MS data. <b>2006</b> , 11, 595-600	53
1399 Mass spectrometry of macromolecular assemblies: preservation and dissociation. <b>2006</b> , 16, 245-51	l 190
1398 Proteomics of transplant rejection. <b>2006</b> , 20, 195-207	8
1397 Serum proteomics study of the squamous cell carcinoma antigen 1 in tongue cancer. <b>2006</b> , 42, 26-3	31 19

1396	Integrative analysis of metabolic networks: from peaks to flux models?. <b>2006</b> , 9, 220-6	12
1395	Microbial identification by mass cataloging. <b>2006</b> , 7, 117	12
1394	QPath: a method for querying pathways in a protein-protein interaction network. <b>2006</b> , 7, 199	113
1393	MassSorter: a tool for administrating and analyzing data from mass spectrometry experiments on proteins with known amino acid sequences. <b>2006</b> , 7, 42	5
1392	Molecular phenotype of zebrafish ovarian follicle by serial analysis of gene expression and proteomic profiling, and comparison with the transcriptomes of other animals. <b>2006</b> , 7, 46	71
1391	Proteomics of metal transport and metal-associated diseases. <b>2006</b> , 12, 2410-22	40
1390	High-throughput localization of organelle proteins by mass spectrometry: a quantum leap for cell biology. <b>2006</b> , 28, 780-4	4
1389	MALDI-TOF/TOF de novo sequence analysis of 2-D PAGE-separated proteins from Halorhodospira halophila, a bacterium with unsequenced genome. <b>2006</b> , 27, 2702-11	31
1388	Proteomic analysis of cartilage- and bone-associated samples. <b>2006</b> , 27, 2687-701	23
1387	Using size exclusion chromatography-RPLC and RPLC-CIEF as two-dimensional separation strategies for protein profiling. <b>2006</b> , 27, 2722-33	46
1386	HepatoProteomics: applying proteomic technologies to the study of liver function and disease. <b>2006</b> , 44, 299-308	46
1385	Investigation of molecular interaction within biological macromolecular complexes by mass spectrometry. <b>2006</b> , 26, 339-68	25
1384	From multi-scale methodology to systems biology: to integrate strain improvement and fermentation optimization. <b>2006</b> , 81, 734-745	23
1383	Detecting and characterizing reactive metabolites by liquid chromatography/tandem mass spectrometry. <b>2006</b> , 41, 1121-39	124
1382	Tandem mass spectrometry of amidated peptides. <b>2006</b> , 41, 1470-83	34
1381	Rewiring enervated: thinking LARGEr than myodystrophy. <b>2006</b> , 84, 237-43	5
1380	Rice proteomics: a cornerstone for cereal food crop proteomes. <b>2006</b> , 25, 1-53	129
1379	The role of mass spectrometry in plant systems biology. <b>2006</b> , 25, 173-214	123

1378	Deciphering the human nucleolar proteome. <b>2006</b> , 25, 215-34	82
1377	Advances in proteomics data analysis and display using an accurate mass and time tag approach. <b>2006</b> , 25, 450-82	272
1376	Processing and classification of protein mass spectra. <b>2006</b> , 25, 409-49	136
1375	Studies of Malaria by Mass Spectrometry. <b>2006</b> , 161-180	
1374	Local Structure Comparison of Proteins. <b>2006</b> , 68, 177-251	1
1373	Proteomic identification of AP2 gamma as a rat placental lactogen II trophoblast cell-specific enhancer binding protein. <b>2006</b> , 147, 4319-29	19
1372	Analyses of homo-oligomer interfaces of proteins from the complementarity of molecular surface, electrostatic potential and hydrophobicity. <b>2006</b> , 19, 421-9	29
1371	Proteomic study of caveolae and rafts isolated from human endothelial cells. <b>2007</b> , 357, 199-213	16
1370	Two-dimensional polyacrylamide gel electrophoresis for cardiovascular proteomics. 2007, 357, 3-13	8
1369	Analysis of antihypertensive drugs in the heart of animal models: a proteomic approach. 2007, 357, 45-58	3
1368	Quantitative proteomics by stable isotope labeling and mass spectrometry. <b>2007</b> , 367, 209-18	23
1367	Inferring Transcriptional Networks by Mining Omics Data. <b>2006</b> , 1, 301-313	14
1366	Software Analysis of Two-Dimensional Electrophoretic Gels in Proteomic Experiments. 2006, 1, 255-262	16
1365	Technology Insight: renal proteomicsat the crossroads between promise and problems. <b>2006</b> , 2, 445-58	24
1364	Protein primary structure using orthogonal fragmentation techniques in Fourier transform mass spectrometry. <b>2006</b> , 3, 251-61	36
1363	Signal maps for mass spectrometry-based comparative proteomics. <b>2006</b> , 5, 423-32	96
1362	Hunting interactomes of a membrane protein: obtaining the largest set of voltage-dependent anion channel-interacting protein epitopes. <b>2006</b> , 5, 1667-80	23
1361	The role of mass spectrometry in biomarker discovery and measurement. <b>2006</b> , 7, 525-39	70

1360	IndexToolkit: an open source toolbox to index protein databases for high-throughput proteomics. <b>2006</b> , 22, 2572-3	4
1359	Proteomic strategies for individualizing therapy of acute myeloid leukemia (AML). <b>2006</b> , 7, 159-70	6
1358	Warm ischemia-induced alterations in oxidative and inflammatory proteins in hepatic Kupffer cells in rats. <b>2006</b> , 5, 979-86	32
1357	Biology of atherosclerotic plaques: what we are learning from proteomic analysis. <b>2006</b> , 72, 18-29	35
1356	Regulation of female fertility and identification of future contraceptive targets. <b>2006</b> , 12, 3915-28	6
1355	Three-dimensional compartmentalization of myosin heavy chain and myosin light chain isoforms in dog thyroarytenoid muscle. <b>2006</b> , 290, C1446-58	21
1354	Protein-protein interactions more conserved within species than across species. <b>2006</b> , 2, e79	85
1353	Differential label-free quantitative proteomic analysis of Shewanella oneidensis cultured under aerobic and suboxic conditions by accurate mass and time tag approach. <b>2006</b> , 5, 714-25	80
1352	Arabidopsis thaliana proteomics: from proteome to genome. <b>2006</b> , 57, 1485-91	43
1351	Probing genuine strong interactions and post-translational modifications in the heterogeneous yeast exosome protein complex. <b>2006</b> , 5, 1581-92	51
1350	SpecDB: A Database for Storing and Managing Mass Spectrometry Proteomics Data. <b>2006</b> , 236-245	1
1349	Advances and challenges in liquid chromatography-mass spectrometry-based proteomics profiling for clinical applications. <b>2006</b> , 5, 1727-44	281
1348	Joining high-throughput technology with in silico modelling advances genome-wide screening towards targeted discovery. <b>2006</b> , 5, 32-6	3
1347	Label-free semiquantitative peptide feature profiling of human breast cancer and breast disease sera via two-dimensional liquid chromatography-mass spectrometry. <b>2006</b> , 5, 1095-104	32
1346	Recombinant Protein Techniques. <b>2005</b> , 385-430	
1345	MASS SPECTROMETRY OUTGROWS SIMPLE BIOCHEMISTRY: NEW APPROACHES TO ORGANELLE PROTEOMICS. <b>2006</b> , 01, 209-221	7
1344	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. <b>2006</b> , 5, 652-70	143
1343	Reproducibility of LC-MS-based protein identification. <b>2006</b> , 57, 1509-14	24

1342	Proteomic analysis of early left ventricular hypertrophy secondary to hypertension: modulation by antihypertensive therapies. <b>2006</b> , 17, S159-64	23
1341	Processes and Machines for Nonwoven Production. <b>2006</b> , 167-187	1
1340	Analysis of posttranslational modifications of proteins by tandem mass spectrometry. <b>2006</b> , 40, 790-8	161
1339	A novel structure-based encoding for machine-learning applied to the inference of SH3 domain specificity. <b>2006</b> , 22, 2333-9	23
1338	Congress of Clinical Chemistry and Laboratory Medicine, Annual Congress of the Society of Clinical Chemistry and Laboratory Medicine (DGKL) in association with The Austrian Society for Laboratory Medicine and Clinical Chemistry, The Swiss Society for Clinical Chemistry (SGKC), The German	
1337	Association of Technical Assistants in Medicine (dvta), Mannheim, Germany, October 1st - 4th, Endogenous transforming growth factor-beta receptor-mediated Smad signaling complexes analyzed by mass spectrometry. <b>2006</b> , 5, 1245-60	16
1336	Preanalytical and analytical variation of surface-enhanced laser desorption-ionization time-of-flight mass spectrometry of human serum. <b>2006</b> , 44, 1243-52	43
1335	The Diabetic Kidney. <b>2006</b> ,	1
1334	A systems approach to model metastatic progression. <b>2006</b> , 66, 5537-9	8
1333	Proteomic identification of lower apolipoprotein A-I in Alzheimer's disease. <b>2006</b> , 21, 155-61	60
1332	Shotgun proteomics of cyanobacteriaapplications of experimental and data-mining techniques. <b>2006</b> , 5, 121-32	27
1331	Relative and absolute quantification of postsynaptic density proteome isolated from rat forebrain and cerebellum. <b>2006</b> , 5, 1158-70	367
1330	Molecular interactions between the specialist herbivore Manduca sexta (Lepidoptera, Sphingidae) and its natural host Nicotiana attenuata. VII. Changes in the plant's proteome. <b>2006</b> , 142, 1621-41	132
1329	Causes and Diagnosis of Alzheimers Disease: A Proteomics Approach. <b>2006</b> , 3, 81-112	2
1328	The application of DIGE-based proteomics to renal physiology. <b>2006</b> , 104, p61-72	23
1327	Characterizing phosphoproteins and phosphoproteomes using mass spectrometry. <b>2006</b> , 4, 363-76	35
1326	Purification and fractionation of membranes for proteomic analyses. <b>2006</b> , 323, 403-20	13
1325	Quality Assessment of Peptide Tandem Mass Spectra. <b>2006</b> ,	

1324	Quantitation in proteomic experiments utilizing mass spectrometry. <b>2006</b> , 22, 1-19	11
1323	Taking a Walk on the Wild Side with Planar Electrochromatography and Thin-Layer Electrophoresis: Of Peptides, Proteins, and Proteomics. <b>2006</b> , 29, 1177-1218	9
1322	Peptidomics Technologies and Applications in Drug Research. 2006, 113-135	2
1321	Robust Feature Extraction and Reduction of Mass Spectrometry Data for Cancer Classification. <b>2006</b> ,	1
1320	A tandem affinity tag for two-step purification under fully denaturing conditions: application in ubiquitin profiling and protein complex identification combined with in vivocross-linking. <b>2006</b> , 5, 737-48	292
1319	MS2DB: An Algorithmic Approach to Determine Disulfide Linkage Patterns. <b>2006</b> ,	1
1318	Compression of LC/MS Proteomic Data. 2006,	2
1317	Perspectives of proteomics in acute myeloid leukemia. <b>2006</b> , 6, 1663-75	9
1316	Analysis and Classification of Proteomics Data, a Case Study. 2006,	
1315	Proteomics for diabetes research: an update and future perspectives. <b>2006</b> , 1, 507-515	О
		O
1314	Ultrasensitive and absolute quantification of the phosphoinositide 3-kinase/Akt signal transduction pathway by mass spectrometry. <b>2006</b> , 103, 8959-64	43
1314	Ultrasensitive and absolute quantification of the phosphoinositide 3-kinase/Akt signal transduction	
	Ultrasensitive and absolute quantification of the phosphoinositide 3-kinase/Akt signal transduction pathway by mass spectrometry. <b>2006</b> , 103, 8959-64  CFBP is a novel tyrosine-phosphorylated protein that might function as a regulator of	43
1313	Ultrasensitive and absolute quantification of the phosphoinositide 3-kinase/Akt signal transduction pathway by mass spectrometry. <b>2006</b> , 103, 8959-64  CFBP is a novel tyrosine-phosphorylated protein that might function as a regulator of CIN85/CD2AP. <b>2006</b> , 281, 28919-31  Mitochondrial protein nitration primes neurodegeneration in experimental autoimmune	43 25
1313	Ultrasensitive and absolute quantification of the phosphoinositide 3-kinase/Akt signal transduction pathway by mass spectrometry. <b>2006</b> , 103, 8959-64  CFBP is a novel tyrosine-phosphorylated protein that might function as a regulator of CIN85/CD2AP. <b>2006</b> , 281, 28919-31  Mitochondrial protein nitration primes neurodegeneration in experimental autoimmune encephalomyelitis. <b>2006</b> , 281, 31950-62	43 25 110
1313 1312 1311	Ultrasensitive and absolute quantification of the phosphoinositide 3-kinase/Akt signal transduction pathway by mass spectrometry. 2006, 103, 8959-64  CFBP is a novel tyrosine-phosphorylated protein that might function as a regulator of CIN85/CD2AP. 2006, 281, 28919-31  Mitochondrial protein nitration primes neurodegeneration in experimental autoimmune encephalomyelitis. 2006, 281, 31950-62  Receptor-binding sites: bioinformatic approaches. 2006, 316, 291-358	43 25 110
1313 1312 1311 1310	Ultrasensitive and absolute quantification of the phosphoinositide 3-kinase/Akt signal transduction pathway by mass spectrometry. 2006, 103, 8959-64  CFBP is a novel tyrosine-phosphorylated protein that might function as a regulator of CIN85/CD2AP. 2006, 281, 28919-31  Mitochondrial protein nitration primes neurodegeneration in experimental autoimmune encephalomyelitis. 2006, 281, 31950-62  Receptor-binding sites: bioinformatic approaches. 2006, 316, 291-358  In-depth analysis of the membrane and cytosolic proteome of red blood cells. 2006, 108, 791-801	43 25 110 1 342

1306	Role and challenges of proteomics in pharma and biotech: technical, scientific and commercial perspective. <b>2006</b> , 3, 179-95	2
1305	Top down mass spectrometry of 2006, 5, 14-25	61
1304	Quantitative proteomics of the archaeon Methanococcus maripaludis validated by microarray analysis and real time PCR. <b>2006</b> , 5, 868-81	63
1303	Proteomic studies of the Singapore grouper iridovirus. <b>2006</b> , 5, 256-64	51
1302	Optimization and use of peptide mass measurement accuracy in shotgun proteomics. <b>2006</b> , 5, 1326-37	241
1301	Proteomic analysis of seed filling in Brassica napus. Developmental characterization of metabolic isozymes using high-resolution two-dimensional gel electrophoresis. <b>2006</b> , 141, 32-46	163
1300	Proteomic analysis of pluripotent stem cells. <b>2007</b> , Chapter 1, Unit 1B.1	2
1299	Functional specifications of an integrated proteomics information management and analysis platform. <b>2007</b> , 2007, 6065-9	1
1298	Genomics and proteomics approaches in understanding tumor angiogenesis. <b>2007</b> , 7, 133-47	9
1297	SWISS-TANDEM: A Web-Based Workspace for MS/MS Protein Identification on PC Grids. 2007,	1
1296	Two-dimensional blue native/SDS gel electrophoresis of multiprotein complexes from Helicobacter pylori. <b>2007</b> , 6, 193-206	40
1295	Systems Biology and Computational Proteomics. <b>2007</b> ,	
1294	Proteomics identification of proteins in human cortex using multidimensional separations and MALDI tandem mass spectrometer. <b>2007</b> , 6, 1818-23	40
1293	Thematic review series: systems biology approaches to metabolic and cardiovascular disorders. Proteomics approaches to the systems biology of cardiovascular diseases. <b>2007</b> , 48, 1-8	27
1292	EBP, a program for protein identification using multiple tandem mass spectrometry datasets. <b>2007</b> , 6, 527-36	45
1291	Overview of Proteomics. 1-61	1
1290	Identification of accessible human cancer biomarkers using ex vivo chemical proteomic strategies. <b>2007</b> , 4, 727-39	13
1289	Long-distance combinatorial linkage between methylation and acetylation on histone H3 N termini. <b>2007</b> , 104, 2086-91	149

1288	Breast cancer proteomics: clinical perspectives. <b>2007</b> , 7, 209-19	6
1287	Experiment-specific estimation of peptide identification probabilities using a randomized database. <b>2007</b> , 11, 351-65	23
1286	TandTRAQ: an open-source tool for integrated protein identification and quantitation. 2007, 23, 3394-6	14
1285	High-throughput and targeted in-depth mass spectrometry-based approaches for biofluid profiling and biomarker discovery. <b>2007</b> , 1, 541-65	26
1284	Defining primary and secondary progenitor disorders in the brain: proteomic approaches for analysis of neural progenitor cells. <b>2007</b> , 8, 117-25	1
1283	Deciphering protein-protein interactions. Part II. Computational methods to predict protein and domain interaction partners. <b>2007</b> , 3, e43	237
1282	Deciphering protein-protein interactions. Part I. Experimental techniques and databases. <b>2007</b> , 3, e42	255
1281	A metal-coded affinity tag approach to quantitative proteomics. <b>2007</b> , 6, 1907-16	142
1280	Introduction to computational proteomics. <b>2007</b> , 3, e114	44
1279	A geometric approach for the alignment of liquid chromatography-mass spectrometry data. <b>2007</b> , 23, i273-81	68
1278	A predictive model for identifying proteins by a single peptide match. <b>2007</b> , 23, 277-80	50
1277	Speeding up tandem mass spectrometry database search: metric embeddings and fast near neighbor search. <b>2007</b> , 23, 612-8	33
1276	Current Status of Computational Approaches for Protein Identification Using Tandem Mass Spectra. <b>2007</b> , 4, 121-130	7
1275	Mass Spectrometry-Based Approaches for Structural Studies on Protein Complexes at Low-Resolution. <b>2007</b> , 4, 1-16	9
1274	Identification of putative androgen receptor interaction protein modules: cytoskeleton and endosomes modulate androgen receptor signaling in prostate cancer cells. <b>2007</b> , 6, 252-71	46
1273	MAPU: Max-Planck Unified database of organellar, cellular, tissue and body fluid proteomes. <b>2007</b> , 35, D771-9	56
1272	Expanded protein information at SGD: new pages and proteome browser. <b>2007</b> , 35, D468-71	66
1271	PROTEIN INTERACTION NETWORKS. <b>2007</b> , 133-161	2

1270 Near-Lossless Compression of Mass Spectra for Proteomics. <b>2007</b> ,	2
1269 Proteomics and systems biology in exercise and sport sciences research. <b>2007</b> , 35, 5-11	15
1268 Signal transduction by growth factor receptors: signaling in an instant. <b>2007</b> , 6, 2913-6	9
Characterization of proteins associated with polyglutamine aggregates: a novel approach toward isolation of aggregates from protein conformation disorders. <b>2007</b> , 1, 128-35	ards 46
1266 Peptide detectability following ESI mass spectrometry. <b>2007</b> ,	7
1265 Proteomic diagnosis of Sjgren's syndrome. <b>2007</b> , 4, 757-67	31
1264 [Proteomics: biomarker research in psychiatry]. <b>2007</b> , 75, 579-86	11
1263 Technology insight: the application of proteomics in gastrointestinal disease. <b>2007</b> , 4, 372-85	9
SOI-based nanoelectrospray emitter tips for mass spectrometry: a coupled MEMS and microfludesign. <b>2007</b> , 17, 509-514	uidic 18
Bayesian estimation for molecular profile reconstruction in proteomics based on liquid chromatography and mass spectrometry. <b>2007</b> , 2007, 5980-3	5
1260 Network-centered view of coronary artery disease. <b>2007</b> , 5, 1095-103	2
Computational methods for the comparative quantification of proteins in label-free LCn-MS experiments. <b>2008</b> , 9, 156-65	62
An Interactive Tool for the Management and Visualization of Mass-Spectrometry Proteomics D <b>2007</b> , 635-642	Pata.
1257 Quantitative model for binary measurements of protein-protein interactions. <b>2007</b> , 14, 1011-2	3
Imaging mass spectrometry based exploration of biochemical tissue composition using peak intensity weighted PCA. <b>2007</b> ,	10
1255 Predictive modeling in proteomics-based disease detection. <b>2007</b> , 2007, 3308-11	
1254 Mass spectrometry-based quantitative proteomics. <b>2007</b> , 24, 147-63	21
1253 Algorithms and tools for analysis and management of mass spectrometry data. <b>2008</b> , 9, 144-55	5 12

# (2007-2007)

1252	Identification of histidine phosphorylations in proteins using mass spectrometry and affinity-based techniques. <b>2007</b> , 423, 549-72	10
1251	Chapter 77 Experimental Studies of Dislocation Core Defects. <b>2007</b> , 419-452	5
1250	Information quality in proteomics. <b>2008</b> , 9, 174-88	25
1249	Cancer biomarker discovery in plasma using a tissue-targeted proteomic approach. <b>2007</b> , 16, 1915-7	39
1248	Proteomic profiling of intact proteins using WAX-RPLC 2-D separations and FTICR mass spectrometry. <b>2007</b> , 6, 602-10	73
1247	The implications of proteolytic background for shotgun proteomics. <b>2007</b> , 6, 1589-98	159
1246	A statistical method for chromatographic alignment of LC-MS data. <b>2007</b> , 8, 357-67	56
1245	The serine/threonine/tyrosine phosphoproteome of the model bacterium Bacillus subtilis. <b>2007</b> , 6, 697-707	309
1244	Zebrafish ovarian follicle transcriptome. <b>2007</b> , 77-97	3
1243	Improving gene annotation using peptide mass spectrometry. <b>2007</b> , 17, 231-9	144
1242	Quantitative, multiplexed assays for low abundance proteins in plasma by targeted mass spectrometry and stable isotope dilution. <b>2007</b> , 6, 2212-29	580
1241	The potential of proteomics for providing new insights into environmental impacts on human health. <b>2007</b> , 22, 175-94	18
1240	A Fast and Accurate Algorithm for the Quantification of Peptides from Mass Spectrometry Data. <b>2007</b> , 473-487	6
1239	Plant Proteomics. 2007,	6
1238	Assessing bias in experiment design for large scale mass spectrometry-based quantitative proteomics. <b>2007</b> , 6, 1741-8	44
1237	Structural analysis of multiprotein complexes by cross-linking, mass spectrometry, and database searching. <b>2007</b> , 6, 2200-11	185
1236	Proteomics analysis of the developing fish oocyte. <b>2007</b> , 99-111	1
1235	Diagnostic potential of urine proteome: a broken mirror of renal diseases. <b>2007</b> , 18, 2233-9	43

Anwendung der SELDI-TOF-Massenspektrometrie zur Identifizierung neuer Biomarker:

Mößlichkeiten und Grenzen / Application of SELDI-TOF-mass spectrometry for biomarker identification: potentials and limitations. **2007**, 31, 93-108

1233	PrestOMIC, an open source application for dissemination of proteomic datasets by individual laboratories. <b>2007</b> , 5, 8	4
1232	Application of Proteomics to Investigate Plant-Microbe Interactions. 2007, 4, 28-43	49
1231	Advances in urinary proteome analysis and biomarker discovery. <b>2007</b> , 18, 1057-71	241
1230	Managing information quality in e-science. 2007,	9
1229	Proteomics analysis of human coronary atherosclerotic plaque: a feasibility study of direct tissue proteomics by liquid chromatography and tandem mass spectrometry. <b>2007</b> , 6, 1088-102	129
1228	The Paragon Algorithm, a next generation search engine that uses sequence temperature values and feature probabilities to identify peptides from tandem mass spectra. <b>2007</b> , 6, 1638-55	1030
1227	Computational proteomics: management and analysis of proteomics data. <b>2008</b> , 9, 97-101	9
1226	Phytochrome-Interacting Factors. 81-105	4
1225	Urine proteomicsprospects for future diagnostics. <b>2007</b> , 94, 133-41	4
1224	Proteomics: Beyond cDNA. 1023-1059	
1223	Novel technologies for cancer biomarker discovery: humoral proteomics. <b>2007</b> , 3, 141-52	16
1222	Proteins and Peptides: Structure Determination. 287-342	
1221	MALDI-MS in Protein Chemistry and Proteomics. 83-108	1
1220	Neuropeptidomics: expanding proteomics downwards. <b>2007</b> , 35, 588-93	60
1219	Visualization of protein interactions inside the secretory pathway. <b>2007</b> , 35, 970-3	10
1218	Mass spectrometric approaches for elucidation of antigenantibody recognition structures in molecular immunology. <b>2007</b> , 13, 69-75	37
1217	Proteomic approach to breast cancer. <b>2007</b> , 14, 360-8	17

## (2007-2007)

1216	Plasticity of the central nervous system and formation of "auxiliary niches" after stem cell grafting: an essay. <b>2007</b> , 16, 263-71	7
1215	A proteome catalog of Drosophila melanogaster: an essential resource for targeted quantitative proteomics. <b>2007</b> , 1, 182-6	13
1214	Identification of secreted proteins during skeletal muscle development. <b>2007</b> , 6, 698-710	69
1213	Clinical proteomics: discovery of cancer biomarkers using mass spectrometry and bioinformatics approachesa prostate cancer perspective. <b>2007</b> , 25 Suppl 2, B110-21	23
1212	Proteomics in pediatric research and practice. <b>2007</b> , 54, 9-28	6
1211	Affinity-purification mass spectrometry (AP-MS) of serine/threonine phosphatases. 2007, 42, 298-305	85
<b>121</b> 0	Integrative analysis of transcriptomic and proteomic data: challenges, solutions and applications. <b>2007</b> , 27, 63-75	178
1209	Tools and strategies for visualization of large image data sets in high-resolution imaging mass spectrometry. <b>2007</b> , 78, 053716	28
1208	Stable-isotope dimethylation labeling combined with LC-ESI MS for quantification of amine-containing metabolites in biological samples. <b>2007</b> , 79, 8631-8	139
1207	Reconstruction of dynamic network models from metabolite measurements. <b>2007</b> , 97-127	4
,	Reconstruction of dynamic network models from metabolite measurements. <b>2007</b> , 97-127  High-Resolution Two-Dimensional Gel Electrophoresis: A Cornerstone of Plant Proteomics. <b>2007</b> , 14-28	5
,		
1206	High-Resolution Two-Dimensional Gel Electrophoresis: A Cornerstone of Plant Proteomics. 2007, 14-28  Proteomics-based identification of biomarkers for predicting sensitivity to a PI3-kinase inhibitor in cancer. 2007, 352, 514-21	5
1206 1205 1204	High-Resolution Two-Dimensional Gel Electrophoresis: A Cornerstone of Plant Proteomics. 2007, 14-28  Proteomics-based identification of biomarkers for predicting sensitivity to a PI3-kinase inhibitor in cancer. 2007, 352, 514-21	5
1206 1205 1204	High-Resolution Two-Dimensional Gel Electrophoresis: A Cornerstone of Plant Proteomics. 2007, 14-28  Proteomics-based identification of biomarkers for predicting sensitivity to a PI3-kinase inhibitor in cancer. 2007, 352, 514-21  Urinary proteomics. 2007, 375, 49-56  Systematic discovery of in vivo phosphorylation networks. 2007, 129, 1415-26	5 17 77
1206 1205 1204 1203	High-Resolution Two-Dimensional Gel Electrophoresis: A Cornerstone of Plant Proteomics. 2007, 14-28  Proteomics-based identification of biomarkers for predicting sensitivity to a Pl3-kinase inhibitor in cancer. 2007, 352, 514-21  Urinary proteomics. 2007, 375, 49-56  Systematic discovery of in vivo phosphorylation networks. 2007, 129, 1415-26	5 17 77 611
1206 1205 1204 1203	High-Resolution Two-Dimensional Gel Electrophoresis: A Cornerstone of Plant Proteomics. 2007, 14-28  Proteomics-based identification of biomarkers for predicting sensitivity to a PI3-kinase inhibitor in cancer. 2007, 352, 514-21  Urinary proteomics. 2007, 375, 49-56  Systematic discovery of in vivo phosphorylation networks. 2007, 129, 1415-26  Is proteomics the new genomics?. 2007, 130, 395-8  Selective anchoring of TFIID to nucleosomes by trimethylation of histone H3 lysine 4. 2007, 131, 58-69	5 17 77 611 350

1198	An introduction to mass spectrometry based proteomics-detection and characterization of gonadotropins and related molecules. <b>2007</b> , 260-262, 212-27	24
1197	Application of proteomics to understand the molecular mechanisms behind meat quality. <b>2007</b> , 77, 97-104	93
1196	Development of a one-step ELISA method using an affinity peptide tag specific to a hydrophilic polystyrene surface. <b>2007</b> , 127, 288-99	44
1195	Characterization of the proteins of bacterial strain isolated from contaminated site involved in heavy metal resistancea proteomic approach. <b>2007</b> , 128, 444-51	29
1194	Two-dimensional gel electrophoresis in platelet proteomics research. <b>2007</b> , 139, 339-53	26
1193	The human red blood cell proteome and interactome. <b>2007</b> , 232, 1391-408	140
1192	Absolute quantification of specific proteins in complex mixtures using visible isotope-coded affinity tags. <b>2007</b> , 359, 159-76	12
1191	Systems-level insights into cellular regulation: inferring, analysing, and modelling intracellular networks. <b>2007</b> , 1, 61-77	44
1190	Predict, prevent and personalize: Genomic and proteomic approaches to cardiovascular medicine. <b>2007</b> , 23 Suppl A, 28A-33A	21
1189	Principles of proteomics and its applications in cancer. <b>2007</b> , 5, 14-22	14
	Principles of proteomics and its applications in cancer. <b>2007</b> , 5, 14-22  Approaches to the study of the cell secretome. <b>2007</b> , 4, 239-48	138
		, i
1188	Approaches to the study of the cell secretome. <b>2007</b> , 4, 239-48  Electrospray ionization mass spectrometry in enzymology: uncovering the mechanisms of two-substrate reactions. <b>2007</b> , 132, 397-402	138
1188 1187 1186	Approaches to the study of the cell secretome. <b>2007</b> , 4, 239-48  Electrospray ionization mass spectrometry in enzymology: uncovering the mechanisms of two-substrate reactions. <b>2007</b> , 132, 397-402	138
1188 1187 1186 1185	Approaches to the study of the cell secretome. 2007, 4, 239-48  Electrospray ionization mass spectrometry in enzymology: uncovering the mechanisms of two-substrate reactions. 2007, 132, 397-402  Protein complexes in the gas phase: technology for structural genomics and proteomics. 2007, 107, 3544-67	138 3 342
1188 1187 1186 1185	Approaches to the study of the cell secretome. 2007, 4, 239-48  Electrospray ionization mass spectrometry in enzymology: uncovering the mechanisms of two-substrate reactions. 2007, 132, 397-402  Protein complexes in the gas phase: technology for structural genomics and proteomics. 2007, 107, 3544-67  Proteomics: a review and an example using the reticulocyte membrane proteome. 2007, 36, 13-24	138 3 342 9
1188 1187 1186 1185 1184	Approaches to the study of the cell secretome. 2007, 4, 239-48  Electrospray ionization mass spectrometry in enzymology: uncovering the mechanisms of two-substrate reactions. 2007, 132, 397-402  Protein complexes in the gas phase: technology for structural genomics and proteomics. 2007, 107, 3544-67  Proteomics: a review and an example using the reticulocyte membrane proteome. 2007, 36, 13-24  Proteomic analysis of Saccharomyces cerevisiae. 2007, 4, 793-813	138 3 342 9

1180	Proteomics of Human Body Fluids. <b>2007</b> ,	17
1179	Plant Systems Biology. <b>2007</b> ,	1
1178	Coverage and error models of protein-protein interaction data by directed graph analysis. <b>2007</b> , 8, R186	32
1177	Normalization of two-channel microarrays accounting for experimental design and intensity-dependent relationships. <b>2007</b> , 8, R44	19
1176	Beyond Structural Genomics for Plant Science. <b>2007</b> , 77-161	13
1175	Vascular Biology Protocols. 2007,	1
1174	Use of proteomics for the discovery of early markers of drug toxicity. <b>2007</b> , 3, 689-704	21
1173	Analysis of the mouse liver proteome using advanced mass spectrometry. <b>2007</b> , 6, 2963-72	75
1172	Self-assembled monolayers for MALDI-TOF mass spectrometry for immunoassays of human protein antigens. <b>2007</b> , 79, 5878-87	55
1171	Proteomics of Amniotic Fluid. <b>2007</b> , 415-436	2
1170	Proteomics. <b>2007</b> , 27-50	
1169	A systematic MS-based approach for identifying in vitro substrates of PKA and PKG in rat uteri. <b>2007</b> , 6, 2674-84	53
1168	A proteomics strategy to discover beta-glucosidases from Aspergillus fumigatus with two-dimensional page in-gel activity assay and tandem mass spectrometry. <b>2007</b> , 6, 4749-57	41
1167	Systematic evaluation of objective functions for predicting intracellular fluxes in Escherichia coli. <b>2007</b> , 3, 119	526
1166	Cell and Molecular Biology of Plastids. 2007,	14
1165	Bioarrays. 2007,	2
1164	Ab initio photoionization dynamics of beta-alanine. <b>2007</b> , 126, 141103	12
1163	Covalent capture of phospho-dependent protein oligomerization by site-specific incorporation of a diazirine photo-cross-linker. <b>2007</b> , 129, 8068-9	41

1162	The Fish Oocyte. 2007,	29
1161	Quantitative Proteomics by Mass Spectrometry. <b>2007</b> ,	12
1160	The low molecular weight proteome of Halobacterium salinarum. <b>2007</b> , 6, 1510-8	60
1159	Pathway analysis software as a tool for drug target selection, prioritization and validation of drug mechanism. <b>2007</b> , 11, 411-21	23
1158	Transcriptional regulation of protein complexes within and across species. <b>2007</b> , 104, 1283-8	44
1157	Centrality Measures for the Human Red Blood Cell Interactome. 2007,	3
1156	Gas-phase ions of solute species from charged droplets of solutions. <b>2007</b> , 104, 1111-7	179
1155	A Time Series Based Approach for Classifying Mass Spectrometry Data. 2007,	
1154	. 2007,	
	Proteomics of blood-based therapeutics: a promising tool for quality assurance in transfusion	
1153	medicine. <b>2007</b> , 21, 179-93	29
1153		10
1152	medicine. <b>2007</b> , 21, 179-93  Proteomics in uveal melanoma research: opportunities and challenges in biomarker discovery. <b>2007</b>	
1152	medicine. <b>2007</b> , 21, 179-93  Proteomics in uveal melanoma research: opportunities and challenges in biomarker discovery. <b>2007</b> , 4, 273-86	
1152 1151	Proteomics in uveal melanoma research: opportunities and challenges in biomarker discovery. 2007, 4, 273-86  Application of Wavelet Transform to the MS-based Proteomics Data Preprocessing. 2007,	10
1152 1151 1150 1149	Proteomics in uveal melanoma research: opportunities and challenges in biomarker discovery. 2007, 4, 273-86  Application of Wavelet Transform to the MS-based Proteomics Data Preprocessing. 2007,  Robust Estimation and Graph-Based Meta Clustering for LC-MS Feature Extraction. 2007,  Wash-free in-situ self-desalting and peptide enrichment by block copolymer analyzed with	10 2 1
1152 1151 1150 1149	Proteomics in uveal melanoma research: opportunities and challenges in biomarker discovery. 2007, 4, 273-86  Application of Wavelet Transform to the MS-based Proteomics Data Preprocessing. 2007,  Robust Estimation and Graph-Based Meta Clustering for LC-MS Feature Extraction. 2007,  Wash-free in-situ self-desalting and peptide enrichment by block copolymer analyzed with MALDI-TOFMS. 2007, 4468-70	10 2 1 12
1152 1151 1150 1149 1148	Proteomics in uveal melanoma research: opportunities and challenges in biomarker discovery. 2007, 4, 273-86  Application of Wavelet Transform to the MS-based Proteomics Data Preprocessing. 2007,  Robust Estimation and Graph-Based Meta Clustering for LC-MS Feature Extraction. 2007,  Wash-free in-situ self-desalting and peptide enrichment by block copolymer analyzed with MALDI-TOFMS. 2007, 4468-70  Visualizing Quantitative Proteomics Datasets using Treemaps. 2007,	10 2 1 1 12 2

## (2007-2007)

1144	fragments necessary for protein annotation. <b>2007</b> , 3, 554-66	15
1143	A novel quantitative proteomics reagent based on soluble nanopolymers. <b>2007</b> , 1251-3	20
1142	Targeted analysis of protein termini. <b>2007</b> , 6, 4634-45	85
1141	Carboxyl-terminated dendrimer-coated bioactive interface for protein microarray: high-sensitivity detection of antigen in complex biological samples. <b>2007</b> , 23, 5670-7	86
1140	Contribution of protein fractionation to depth of analysis of the serum and plasma proteomes. <b>2007</b> , 6, 3558-65	144
1139	Protein expression in the striatum and cortex regions of the brain for a mouse model of Huntington's disease. <b>2007</b> , 6, 3134-42	30
1138	Markedly increased urinary preprohaptoglobin and haptoglobin in passive Heymann nephritis: a differential proteomics approach. <b>2007</b> , 6, 3313-20	26
1137	Site-specific pyrolysis-induced cleavage at aspartic acid residue in peptides and proteins. <b>2007</b> , 6, 1700-4	23
1136	Supplemental activation method for high-efficiency electron-transfer dissociation of doubly protonated peptide precursors. <b>2007</b> , 79, 477-85	321
1135	Whole proteome analysis of post-translational modifications: applications of mass-spectrometry for proteogenomic annotation. <b>2007</b> , 17, 1362-77	155
1134	Proteome profile of cytosolic component of zebrafish liver generated by LC-ESI MS/MS combined with trypsin digestion and microwave-assisted acid hydrolysis. <b>2007</b> , 6, 263-72	63
1133	Identification of differentially secreted biomarkers using LC-MS/MS in isogenic cell lines representing a progression of breast cancer. <b>2007</b> , 6, 2993-3002	100
1132	Identifying pharmacodynamic protein markers of centrally active drugs in humans: a pilot study in a novel clinical model. <b>2007</b> , 6, 955-66	17
1131	Performance characteristics of electron transfer dissociation mass spectrometry. <b>2007</b> , 6, 1942-51	330
1130	Personalized medicine and proteomics: lessons from non-small cell lung cancer. <b>2007</b> , 6, 2925-35	51
1129	Examining the proteome of Drosophila across organism lifespan. <b>2007</b> , 6, 3637-47	26
1128	Comparative urine analysis by liquid chromatography-mass spectrometry and multivariate statistics: method development, evaluation, and application to proteinuria. <b>2007</b> , 6, 194-206	40
1127	Phosphopeptide enrichment by aliphatic hydroxy acid-modified metal oxide chromatography for nano-LC-MS/MS in proteomics applications. <b>2007</b> , 6, 1103-9	362

1126	YPED: a web-accessible database system for protein expression analysis. 2007, 6, 4019-24	34
1125	Relative specificities of water and ammonia losses from backbone fragments in collision-activated dissociation. <b>2007</b> , 6, 2669-73	20
1124	SwedCAD, a database of annotated high-mass accuracy MS/MS spectra of tryptic peptides. 2007, 6, 4063-7	27
1123	A minimalist model for exploring conformational effects on the electrospray charge state distribution of proteins. <b>2007</b> , 111, 6534-43	66
1122	Relative quantification of proteins across the species boundary through the use of shared peptides. <b>2007</b> , 6, 97-104	14
1121	Research in Computational Molecular Biology. 2007,	1
<b>112</b> 0	Molecular markers for bladder cancer: the road to a multimarker approach. <b>2007</b> , 7, 1717-27	70
1119	Novel neuroproteomic approaches to studying traumatic brain injury. <b>2007</b> , 161, 401-18	33
1118	Use of SELDI-TOF mass spectrometry for identification of new biomarkers: potential and limitations. <b>2007</b> , 45, 1435-49	73
1117	Protein markers of ischemic insult in brain endothelial cells identified using 2D gel electrophoresis and ICAT-based quantitative proteomics. <b>2007</b> , 6, 226-39	38
1116	Microbial proteomics: a mass spectrometry primer for biologists. <b>2007</b> , 6, 26	45
1115	Report on the workshop "New Technologies in Stem Cell Research," Society for Pediatric Research, San Francisco, California, April 29, 2006. <b>2007</b> , 25, 1070-88	1
1114	Concise review: trends in stem cell proteomics. <b>2007</b> , 25, 1888-903	74
1113	Proteomic analysis of secreted exosomes. <b>2007</b> , 43, 99-131	61
1112	Instrumental Methods. 76-156	
1111	Involvement of splicing factor-1 in beta-catenin/T-cell factor-4-mediated gene transactivation and pre-mRNA splicing. <b>2007</b> , 132, 1039-54	56
1110	Ecological potentials of biodiversity modelled from information entropies: Plant species diversity of North-Central European forests as an example. <b>2007</b> , 2, 328-336	4
1109	Low energy peptide fragmentations in an ESI-Q-Tof type mass spectrometer. <b>2007</b> , 6, 1378-91	59

1108 Analysis of Proteins and Other Biopolymers. 689-802

1107	Method development of efficient protein extraction in bone tissue for proteome analysis. <b>2007</b> , 6, 2287-94	103
1106	Ultrasensitive assays for proteins. <b>2007</b> , 132, 724-37	118
1105	The methodologies of systems biology. <b>2007</b> , 23-70	21
1104	Comprehensive peptidome analysis of mouse livers by size exclusion chromatography prefractionation and nanoLC-MS/MS identification. <b>2007</b> , 6, 801-8	36
1103	Proteome cataloging and relative quantification of Francisella tularensis tularensis strain Schu4 in 2D PAGE using preparative isoelectric focusing. <b>2007</b> , 6, 3484-90	5
1102	Detection and validation of non-synonymous coding SNPs from orthogonal analysis of shotgun proteomics data. <b>2007</b> , 6, 2331-40	44
1101	Network-based prediction of protein function. <b>2007</b> , 3, 88	743
1100	Clustering Methods in a Protein Protein Interaction Network. 319-355	10
1099	Accurate mass measurements in proteomics. <b>2007</b> , 107, 3621-53	92
1098	Analytical methods from the perspective of method standardization. <b>2007</b> , 11-52	16
1097	Spectral networks: a new approach to de novo discovery of protein sequences and posttranslational modifications. <b>2007</b> , 42, 687, 689, 691 passim	28
1096	Dual-tagging system for the affinity purification of mammalian protein complexes. <b>2007</b> , 43, 296, 298, 300 passim	25
1095	Insights into chloroplast proteomics: from basic principles to new horizons. <b>2007</b> , 371-407	
1094	Biomarker Discovery in Animal Health and Disease: The Application of Post-Genomic Technologies. <b>2007</b> , 2, 117727190700200	27
1093	Methodology and Applications of Disease Biomarker Identification in Human Serum. <b>2007</b> , 2, 1177271907002	20 <b>9</b> 9
1092	[Functional proteomics in oncology: to understand more than to describe]. <b>2007</b> , 23 Spec No 1, 27-30	3
1091	Platelet Genomics and Proteomics. <b>2007</b> , 99-116	3

1090	Innovative proteomic approaches for cancer biomarker discovery. <b>2007</b> , 43, 279, 281-3, 285	26
1089	Proteomics of Toxoplasma gondii. <b>2007</b> , 541-565	1
1088	. 2007,	82
1087	Proteomic Mapping of Endothelium and Vascular Targeting in Vivo. 881-897	4
1086	. 2007,	5
1085	Statistical Methods for Biomarker Discovery Using Mass Spectrometry. 465-486	2
1084	. 2007,	3
1083	Capillary Separation Techniques. 469-510	1
1082	Social behavior and the evolution of neuropeptide genes: lessons from the honeybee genome. <b>2007</b> , 29, 416-21	25
1081	Molecular portrait of high productivity in recombinant NS0 cells. <b>2007</b> , 97, 933-51	51
1080	Backbone carbonyl group basicities are related to gas-phase fragmentation of peptides and protein folding. <b>2007</b> , 46, 1481-4	25
1079	Boosting the throughput of separation techniques by "multiplexing". <b>2007</b> , 46, 5609-13	63
1078	Chemoenzymatic enrichment of phosphotyrosine-containing peptides. 2007, 46, 4751-3	12
1077	Reverse glycoblotting allows rapid-enrichment glycoproteomics of biopharmaceuticals and disease-related biomarkers. <b>2007</b> , 46, 8808-13	47
1076	Introduction to chemical proteomics for drug discovery and development. 2007, 340, 169-77	12
1075	Backbone Carbonyl Group Basicities Are Related to Gas-Phase Fragmentation of Peptides and Protein Folding. <b>2007</b> , 119, 1503-1506	
1074	Durchsatzsteigerung von Trenntechniken durch Multiplexing□ <b>2007</b> , 119, 5706-5710	15
1073	Chemoenzymatic Enrichment of Phosphotyrosine-Containing Peptides. <b>2007</b> , 119, 4835-4837	3

Reverse Glycoblotting Allows Rapid-Enrichment Glycoproteomics of Biopharmaceuticals and Disease-Related Biomarkers. <b>2007</b> , 119, 8964-8969	2
1071 Quantification of Polypeptides by Mass Spectrometry. 291-316	1
1070 Peptidomics of Short Linear Cytolytic Peptides from Spider Venom. 55-70	
1069 Peptidomics Approach to Proteomics. 153-175	1
1068 Toxicogenomics: a pivotal piece in the puzzle of toxicological research. <b>2007</b> , 27, 302-9	83
Development of an integrated approach for evaluation of 2-D gel image analysis: impact of multiple proteins in single spots on comparative proteomics in conventional 2-D gel/MALDI workflow. <b>2007</b> , 28, 2080-94	75
Optimization of a pressurized liquid junction nanoelectrospray interface between CE and MS for reliable proteomic analysis. <b>2007</b> , 28, 1964-9	26
High MS-compatibility of silver nitrate-stained protein spots from 2-DE gels using ZipPlates and AnchorChips for successful protein identification. <b>2007</b> , 28, 1607-14	27
1064 The resistance of metallothionein to proteolytic digestion: an LC-MS/MS analysis. <b>2007</b> , 28, 2942-52	4
1063 Spatially addressable protein array: ssDNA-directed assembly for antibody microarray. <b>2007</b> , 28, 4638-44	13
A fully automated 2-D LC-MS method utilizing online continuous pH and RP gradients for global proteome analysis. <b>2007</b> , 28, 4311-9	43
Peptidomics of identified neurons demonstrates a highly differentiated expression pattern of FXPRLamides in the neuroendocrine system of an insect. <b>2007</b> , 500, 498-512	31
MS-Analyzer: preprocessing and data mining services for proteomics applications on the Grid. <b>2007</b> , 19, 2047-2066	11
1059 Mass spectrometry for the quantification of bioactive peptides in biological fluids. <b>2007</b> , 26, 389-402	61
1058 Imaging mass spectrometry. <b>2007</b> , 26, 606-43	852
1057 Biomarker discovery in lung cancerpromises and challenges of clinical proteomics. <b>2007</b> , 26, 451-66	47
1056 Proteomics in neurosciences. <b>2007</b> , 26, 432-50	39
Proteomic analysis of the distribution of the major seed allergens in wild, landrace, ancestral, and modern soybean genotypes. <b>2007</b> , 87, 2511-2518	17

1054	Assessing a novel microfluidic interface for shotgun proteome analyses. <b>2007</b> , 30, 1468-76	22
1053	Disulfide bond cleavages observed in SORI-CID of three nonapeptides complexed with divalent transition-metal cations. <b>2007</b> , 42, 450-8	34
1052	Modification of aluminum chips for LDI mass spectrometry of proteins. <b>2007</b> , 42, 1504-13	1
1051	A novel pyrimidine-based stable-isotope labeling reagent and its application to quantitative analysis using matrix-assisted laser desorption/ionization mass spectrometry. <b>2007</b> , 42, 1514-21	19
1050	Polymeric integrated selective enrichment target (ISET) for solid-phase-based sample preparation in MALDI-TOF MS. <b>2007</b> , 42, 1445-52	24
1049	High-sensitivity analysis of specific peptides in complex samples by selected MS/MS ion monitoring and linear ion trap mass spectrometry: application to biological studies. <b>2007</b> , 42, 1391-403	65
1048	Global metabolic changes following loss of a feedback loop reveal dynamic steady states of the yeast metabolome. <b>2007</b> , 9, 8-20	16
1047	A wavelet-based data pre-processing analysis approach in mass spectrometry. <b>2007</b> , 37, 509-16	18
1046	Study of posttranslational non-enzymatic modifications of collagen using capillary electrophoresis/mass spectrometry and high performance liquid chromatography/mass spectrometry. <b>2007</b> , 1155, 125-33	30
1045	Trends in sample preparation for classical and second generation proteomics. <b>2007</b> , 1153, 235-58	150
1045	Multivariate comparison between peptide mass fingerprints obtained by liquid	150
	Multivariate comparison between peptide mass fingerprints obtained by liquid chromatography-electrospray ionization-mass spectrometry with different trypsin digestion	
1044	Multivariate comparison between peptide mass fingerprints obtained by liquid chromatography-electrospray ionization-mass spectrometry with different trypsin digestion procedures. <b>2007</b> , 1171, 69-79  Automated injection of uncleaned samples using a ten-port switching valve and a strong	10
1044	Multivariate comparison between peptide mass fingerprints obtained by liquid chromatography-electrospray ionization-mass spectrometry with different trypsin digestion procedures. 2007, 1171, 69-79  Automated injection of uncleaned samples using a ten-port switching valve and a strong cation-exchange trap column for proteome analysis. 2007, 1171, 56-62  Real-time monitoring of peptic and tryptic digestions of bovine beta-casein using quartz crystal microbalance. 2007, 584, 72-7  Advances in hyphenated analytical techniques for shotgun proteome and peptidome analysisa	10
1044 1043 1042	Multivariate comparison between peptide mass fingerprints obtained by liquid chromatography-electrospray ionization-mass spectrometry with different trypsin digestion procedures. 2007, 1171, 69-79  Automated injection of uncleaned samples using a ten-port switching valve and a strong cation-exchange trap column for proteome analysis. 2007, 1171, 56-62  Real-time monitoring of peptic and tryptic digestions of bovine beta-casein using quartz crystal microbalance. 2007, 584, 72-7  Advances in hyphenated analytical techniques for shotgun proteome and peptidome analysisa	10 20 14
1044 1043 1042	Multivariate comparison between peptide mass fingerprints obtained by liquid chromatography-electrospray ionization-mass spectrometry with different trypsin digestion procedures. 2007, 1171, 69-79  Automated injection of uncleaned samples using a ten-port switching valve and a strong cation-exchange trap column for proteome analysis. 2007, 1171, 56-62  Real-time monitoring of peptic and tryptic digestions of bovine beta-casein using quartz crystal microbalance. 2007, 584, 72-7  Advances in hyphenated analytical techniques for shotgun proteome and peptidome analysisa review. 2007, 598, 193-204	10 20 14 51
1044 1043 1042 1041	Multivariate comparison between peptide mass fingerprints obtained by liquid chromatography-electrospray ionization-mass spectrometry with different trypsin digestion procedures. 2007, 1171, 69-79  Automated injection of uncleaned samples using a ten-port switching valve and a strong cation-exchange trap column for proteome analysis. 2007, 1171, 56-62  Real-time monitoring of peptic and tryptic digestions of bovine beta-casein using quartz crystal microbalance. 2007, 584, 72-7  Advances in hyphenated analytical techniques for shotgun proteome and peptidome analysisa review. 2007, 598, 193-204  Using ontologies for preprocessing and mining spectra data on the Grid. 2007, 23, 55-60  Nanoelectrospray peptide mapping revisited: Composite survey spectra allow high dynamic range	10 20 14 51

1036	Marine microgels: Optical and proteomic fingerprints. <b>2007</b> , 105, 229-239	33
1035	Mass spectra alignments and their significance. <b>2007</b> , 5, 714-728	3
1034	A silicon beam-based microcantilever nanoelectrosprayer. <b>2007</b> , 125, 72-78	4
1033	Parallel processing of large datasets from NanoLC-FTICR-MS measurements. <b>2007</b> , 18, 152-61	14
1032	Hydrogen rearrangement to and from radical z fragments in electron capture dissociation of peptides. <b>2007</b> , 18, 113-20	113
1031	Quantitative analysis of complex peptide mixtures using FTMS and differential mass spectrometry. <b>2007</b> , 18, 226-33	66
1030	Liquid matrix deposition on conductive hydrophobic surfaces for tuning and quantitation in UV-MALDI mass spectrometry. <b>2007</b> , 18, 693-7	37
1029	Sequencing of T-superfamily conotoxins from Conus virgo: pyroglutamic acid identification and disulfide arrangement by MALDI mass spectrometry. <b>2007</b> , 18, 1396-404	32
1028	Mapping the human plasma proteome by SCX-LC-IMS-MS. <b>2007</b> , 18, 1249-64	158
1027	Evaluation of the influence of amino acid composition on the propensity for collision-induced dissociation of model peptides using molecular dynamics simulations. <b>2007</b> , 18, 1625-37	8
1026	Top-down quantitation and characterization of SILAC-labeled proteins. 2007, 18, 2058-64	74
1025	Analytical methodologies for the detection and structural characterization of phosphorylated proteins. <b>2007</b> , 849, 163-80	27
1024	Biomarker discovery from body fluids using mass spectrometry. <b>2007</b> , 849, 105-14	41
1023	Affinity chromatography: a useful tool in proteomics studies. <b>2007</b> , 849, 81-90	55
1022	The Mass Distance Fingerprint: a statistical framework for de novo detection of predominant modifications using high-accuracy mass spectrometry. <b>2007</b> , 854, 173-82	11
1021	Click Chemistry-Led Advances in High Content Functional Proteomics. <b>2007</b> , 26, 1229-1238	45
1020	Application of phenylboronic acid modified hydrogel affinity chips for high-throughput mass spectrometric analysis of glycated proteins. <b>2007</b> , 21, 1-6	31
1019	Evaluation of an on-target sample preparation system for matrix-assisted laser desorption/ionization time-of-flight mass spectrometry in conjunction with normal-flow peptide high-performance liquid chromatography for peptide mass fingerprint analyses. <b>2007</b> , 21, 44-58	16

1018	Recommended criteria for the mass spectrometric identification of target peptides and proteins (. <b>2007</b> , 21, 297-304	37
1017	Rapid protein identification using a disposable on-line clean-up/concentrating device and electrospray ionization mass spectrometry. <b>2007</b> , 21, 459-65	2
1016	Structural analysis of O-glycopeptides employing negative- and positive-ion multi-stage mass spectra obtained by collision-induced and electron-capture dissociations in linear ion trap time-of-flight mass spectrometry. <b>2007</b> , 21, 691-8	38
1015	Understanding the influence of post-excite radius and axial confinement on quantitative proteomic measurements using Fourier transform ion cyclotron resonance mass spectrometry. <b>2007</b> , 21, 1196-204	6
1014	Specific capture of phosphopeptides on matrix-assisted laser desorption/ionization time-of-flight mass spectrometry targets modified by magnetic affinity nanoparticles. <b>2007</b> , 21, 2407-14	24
1013	Simultaneous detection of N-terminal fragment ions in a protein mixture using a ruthenium(II) complex. <b>2007</b> , 21, 2647-53	4
1012	Quantitative analysis of a proteome by N-terminal stable-isotope labelling of tryptic peptides. <b>2007</b> , 21, 2671-9	5
1011	Detection of potential ion suppression for peptide analysis in nanoflow liquid chromatography/mass spectrometry. <b>2007</b> , 21, 2860-6	12
1010	pFind 2.0: a software package for peptide and protein identification via tandem mass spectrometry. <b>2007</b> , 21, 2985-91	158
1009	A protein-specifically adapted scoring function for the reranking of docking solutions. <b>2007</b> , 67, 98-111	10
1008	Proteomic profiling of animal models mimicking skeletal muscle disorders. <b>2007</b> , 1, 1169-84	27
1007	High-resolution proteome/peptidome analysis of peptides and low-molecular-weight proteins in urine. <b>2007</b> , 1, 792	49
1006	Phosphoproteomics for the discovery of kinases as cancer biomarkers and drug targets. <b>2007</b> , 1, 1042-57	38
1005	Clinical application of tear proteomics: Present and future prospects. <b>2007</b> , 1, 972-82	18
1004	Proteomic strategies in multiple sclerosis and its animal models. <b>2007</b> , 1, 1393-1405	9
1003	Clinical proteomics in neurodegenerative diseases. <b>2007</b> , 1, 1342-50	17
1002	Proteomics studies of pancreatic cancer. <b>2007</b> , 1, 1582-1591	27
1001	AFM fishing nanotechnology is the way to reverse the Avogadro number in proteomics. <b>2007</b> , 7, 4-9	62

1	000	Exploring proteasome complexes by proteomic approaches. <b>2007</b> , 7, 1047-58	47
9	999	From the genome sequence to the proteome and back: evaluation of E. coli genome annotation with a 2-D gel-based proteomics approach. <b>2007</b> , 7, 1097-106	24
9	998	Standardisation of rapid in-gel digestion by mass spectrometry. <b>2007</b> , 7, 642-54	33
9	997	Development and validation of a spectral library searching method for peptide identification from MS/MS. <b>2007</b> , 7, 655-67	405
9	996	Automation of nanoflow liquid chromatography-tandem mass spectrometry for proteome analysis by using a strong cation exchange trap column. <b>2007</b> , 7, 528-539	35
9	995	MascotDatfile: an open-source library to fully parse and analyse MASCOT MS/MS search results. <b>2007</b> , 7, 364-6	44
9	994	Proteomic and functional alterations in brain mitochondria from Tg2576 mice occur before amyloid plaque deposition. <b>2007</b> , 7, 605-616	106
Ş	993	A combined dataset of human cerebrospinal fluid proteins identified by multi-dimensional chromatography and tandem mass spectrometry. <b>2007</b> , 7, 469-73	100
9	992	Proteomic exploitation on prothymosin alpha-induced mononuclear cell activation. 2007, 7, 1814-24	37
9	991	A new strategy to filter out false positive identifications of peptides in SEQUEST database search results. <b>2007</b> , 7, 4036-44	19
9	990	Sequence similarity-driven proteomics in organisms with unknown genomes by LC-MS/MS and automated de novo sequencing. <b>2007</b> , 7, 2318-29	93
9	989	SuperHirn - a novel tool for high resolution LC-MS-based peptide/protein profiling. 2007, 7, 3470-80	269
9	988	Proteome of mesenchymal stem cells. <b>2007</b> , 7, 2881-94	62
ç	987	A la carte proteomics with an emphasis on gel-free techniques. <b>2007</b> , 7, 2698-718	79
9	986	A novel method for analyzing phosphoproteins using SELDI-TOF MS in combination with a series of recombinant proteins. <b>2007</b> , 7, 2350-4	8
Ş	985	Assessing peptide de novo sequencing algorithms performance on large and diverse data sets. <b>2007</b> , 7, 3051-4	42
9	984	Proteomic profiling of chronic low-frequency stimulated fast muscle. <b>2007</b> , 7, 3417-30	55
ç	983	Proteomic analysis of the cellular responses induced in uninfected immune cells by cell-expressed X4 HIV-1 envelope. <b>2007</b> , 7, 3116-30	28

982	Computational prediction of proteotypic peptides for quantitative proteomics. <b>2007</b> , 25, 125-31		582
981	Quantitative proteomic assessment of very early cellular signaling events. <b>2007</b> , 25, 566-8		103
980	Improving the success rate of proteome analysis by modeling protein-abundance distributions and experimental designs. <b>2007</b> , 25, 651-5		65
979	Executable cell biology. <b>2007</b> , 25, 1239-49		411
978	Higher-energy C-trap dissociation for peptide modification analysis. <b>2007</b> , 4, 709-12		727
977	Analysis and validation of proteomic data generated by tandem mass spectrometry. <b>2007</b> , 4, 787-97		523
976	Mass spectrometry-based functional proteomics: from molecular machines to protein networks. <b>2007</b> , 4, 807-15		193
975	Mapping protein post-translational modifications with mass spectrometry. <b>2007</b> , 4, 798-806		602
974	Imaging mass spectrometry at cellular length scales. <b>2007</b> , 2, 1185-96		98
973	Palmitoylated proteins: purification and identification. <b>2007</b> , 2, 1573-84		296
972	Protocol for micro-purification, enrichment, pre-fractionation and storage of peptides for proteomics using StageTips. <b>2007</b> , 2, 1896-906		2539
971	Determining the stoichiometry and interactions of macromolecular assemblies from mass spectrometry. <b>2007</b> , 2, 715-26		538
970	Analysis of protein complexes using mass spectrometry. <b>2007</b> , 8, 645-54		553
969	Clathrate nanostructures for mass spectrometry. <i>Nature</i> , <b>2007</b> , 449, 1033-6	50.4	426
968	The molecular sociology of the cell. <i>Nature</i> , <b>2007</b> , 450, 973-82	50.4	424
967	The biological impact of mass-spectrometry-based proteomics. <i>Nature</i> , <b>2007</b> , 450, 991-1000	50.4	564
966	A discrete neuropeptide difference between two hybridizing grasshopper subspecies. <b>2007</b> , 91, 541-54	8	5
965	Monitoring gene changes during antiepileptic drug therapy to widen the safety window and reduce pharmacoresistance. <b>2007</b> , 48 Suppl 1, 19-25		4

## (2007-2007)

964	A cotton ascorbate peroxidase is involved in hydrogen peroxide homeostasis during fibre cell development. <b>2007</b> , 175, 462-471	99
963	The 20S proteasome isolated from Alzheimer's disease brain shows post-translational modifications but unchanged proteolytic activity. <b>2007</b> , 101, 1483-90	35
962	Use of proteomics for the identification of novel drug targets in brain diseases. 2007, 102, 306-15	14
961	Novel insights in the use of hydrolytic enzymes secreted by fungi with biotechnological potential. <b>2007</b> , 44, 573-81	17
960	Top-down MS, a powerful complement to the high capabilities of proteolysis proteomics. <b>2007</b> , 274, 6256-68	147
959	Applications of diagonal chromatography for proteome-wide characterization of protein modifications and activity-based analyses. <b>2007</b> , 274, 6277-89	23
958	SAMPI: protein identification with mass spectra alignments. <b>2007</b> , 8, 102	5
957	AYUMS: an algorithm for completely automatic quantitation based on LC-MS/MS proteome data and its application to the analysis of signal transduction. <b>2007</b> , 8, 15	18
956	Multivariate analysis and visualization of splicing correlations in single-gene transcriptomes. <b>2007</b> , 8, 16	7
955	Precise protein quantification based on peptide quantification using iTRAQ. 2007, 8, 214	87
954	The EIPeptiDi tool: enhancing peptide discovery in ICAT-based LC MS/MS experiments. 2007, 8, 255	7
953	Optimization of filtering criterion for SEQUEST database searching to improve proteome coverage in shotgun proteomics. <b>2007</b> , 8, 323	23
952	msmsEval: tandem mass spectral quality assignment for high-throughput proteomics. <b>2007</b> , 8, 51	33
951	Time-series alignment by non-negative multiple generalized canonical correlation analysis. <b>2007</b> , 8 Suppl 10, S4	14
950	Prediction of peptides observable by mass spectrometry applied at the experimental set level. <b>2007</b> , 8 Suppl 7, S23	56
949	Sharing mass spectrometry data in a grid-based distributed proteomics laboratory. <b>2007</b> , 43, 577-591	21
948	Tools for computational processing of LC-MS datasets: a user's perspective. <b>2007</b> , 86, 281-90	23
947	Implications of salivary proteomics in drug discovery and development: a focus on cancer drug discovery. <b>2007</b> , 12, 911-6	27

946	Distribution of orphan metabolic activities. <b>2007</b> , 25, 343-8	37
945	Intestinal epithelial cell signalling and chronic inflammation: From the proteome to specific molecular mechanisms. <b>2007</b> , 622, 42-57	40
944	Proteomic analysis of macrophages: a new way to identify novel cell-surface antigens. <b>2007</b> , 321, 80-5	22
943	Bioinformatics and Proteomics: An Engineering Problem Solving-Based Approach. <b>2007</b> , 50, 49-54	3
942	Salivary proteome and its genetic polymorphisms. <b>2007</b> , 1098, 22-50	144
941	The application of proteomic techniques to fungal protein identification and quantification. <b>2007</b> , 1111, 133-46	7
940	PhosphoPepa phosphoproteome resource for systems biology research in Drosophila Kc167 cells. <b>2007</b> , 3, 139	160
939	Proteomic analysis of human cervico-vaginal fluid. <b>2007</b> , 6, 2859-65	119
938	Biosynthesis of sulfur-34 labelled yeast and its characterisation by multicollector-ICP-MS. <b>2007</b> , 22, 1105	21
937	Advancing mammalian cell culture engineering using genome-scale technologies. <b>2007</b> , 25, 401-8	64
936	Multiplexed ion mobility spectrometry-orthogonal time-of-flight mass spectrometry. <b>2007</b> , 79, 2451-62	61
935	Selective Fluorogenic Derivatization with Isotopic Coding of Catechols and 2-Amino Phenols with Benzylamine: A Chemical Basis for the Relative Determination of 3-Hydroxy-tyrosine and 3-Nitro-tyrosine Peptides. <b>2007</b> , 66, 649-659	10
934	Probing the urinary proteome of severe acute pancreatitis. <b>2007</b> , 9, 447-55	9
933	Current role of LC-MS(/MS) in doping control. 2007, 388, 1351-8	71
932	Identification of human hepatocellular carcinoma-related proteins by proteomic approaches. <b>2007</b> , 388, 637-43	23
931	Co-immunoprecipitations revisited: an update on experimental concepts and their implementation for sensitive interactome investigations of endogenous proteins. <b>2007</b> , 389, 461-73	59
930	Quantitative mass spectrometry in proteomics: a critical review. <b>2007</b> , 389, 1017-31	1252
929	A low perfusion rate microreactor for continuous monitoring of enzyme characteristics: application to glucose oxidase. <b>2007</b> , 389, 2029-33	5

928	Key clinical issues in renal cancer: a challenge for proteomics. <b>2007</b> , 25, 537-56	25
927	Molecular defense mechanisms of Barrett's metaplasia estimated by an integrative genomics. <b>2007</b> , 85, 733-43	38
926	Platelets from genome to proteome and beyond. 2007, 23, 245-8	1
925	Protein pE120R of African swine fever virus is post-translationally acetylated as revealed by post-source decay MALDI mass spectrometry. <b>2007</b> , 35, 81-5	5
924	Using cell engineering and omic tools for the improvement of cell culture processes. <b>2007</b> , 53, 3-22	38
923	Applications and current challenges of proteomic approaches, focusing on two-dimensional electrophoresis. <b>2007</b> , 33, 405-14	35
922	A Fast and Simple Algorithm for the Money Changing Problem. <b>2007</b> , 48, 413-432	42
921	Peptidomic analysis of human peripheral monocytes persistently infected by Chlamydia trachomatis. <b>2007</b> , 196, 103-14	3
920	Gaseous- versus solution-phase recognition of some aromatic amino esters by 2,8,14,20-tetrakis(L-valinamido)[4]resorcinarene. <b>2007</b> , 267, 24-29	6
919	Imaging of peptides in the rat brain using MALDI-FTICR mass spectrometry. <b>2007</b> , 18, 145-51	135
919	Imaging of peptides in the rat brain using MALDI-FTICR mass spectrometry. <b>2007</b> , 18, 145-51  Advances in proteomic workflows for systems biology. <b>2007</b> , 18, 378-84	135
		86
918	Advances in proteomic workflows for systems biology. <b>2007</b> , 18, 378-84	86
918	Advances in proteomic workflows for systems biology. <b>2007</b> , 18, 378-84  Gold nanoparticle-enhanced secondary ion mass spectrometry and its bio-applications. <b>2008</b> , 255, 1064-1067  Fragmentation of phosphorylated and singly charged peptide ions via interaction with metastable	86
918 917 916	Advances in proteomic workflows for systems biology. <b>2007</b> , 18, 378-84  Gold nanoparticle-enhanced secondary ion mass spectrometry and its bio-applications. <b>2008</b> , 255, 1064-1067  Fragmentation of phosphorylated and singly charged peptide ions via interaction with metastable atoms. <b>2008</b> , 278, 150-157  Multiple ion/ion reactions in the 3D ion trap: Selective reagent anion production for ETD and PTR	86 10 25
918 917 916 915	Advances in proteomic workflows for systems biology. 2007, 18, 378-84  Gold nanoparticle-enhanced secondary ion mass spectrometry and its bio-applications. 2008, 255, 1064-1067  Fragmentation of phosphorylated and singly charged peptide ions via interaction with metastable atoms. 2008, 278, 150-157  Multiple ion/ion reactions in the 3D ion trap: Selective reagent anion production for ETD and PTR from a single compound. 2008, 276, 82-90  Protein quantification by selective isolation and fragmentation of isotopic pairs using FT-ICR MS.	86 10 25 32
918 917 916 915 914	Advances in proteomic workflows for systems biology. 2007, 18, 378-84  Gold nanoparticle-enhanced secondary ion mass spectrometry and its bio-applications. 2008, 255, 1064-1067  Fragmentation of phosphorylated and singly charged peptide ions via interaction with metastable atoms. 2008, 278, 150-157  Multiple ion/ion reactions in the 3D ion trap: Selective reagent anion production for ETD and PTR from a single compound. 2008, 276, 82-90  Protein quantification by selective isolation and fragmentation of isotopic pairs using FT-ICR MS. 2008, 19, 973-7  Towards liquid chromatography time-scale peptide sequencing and characterization of post-translational modifications in the negative-ion mode using electron detachment dissociation	86 10 25 32 7

910	Differential liquid phase proteomic analysis of the effect of selenium supplementation in LNCaP cells. <b>2008</b> , 865, 63-73	4
909	Quantitative atlas of membrane transporter proteins: development and application of a highly sensitive simultaneous LC/MS/MS method combined with novel in-silico peptide selection criteria. <b>2008</b> , 25, 1469-83	400
908	Metallomics and metalloproteomics. 2008, 65, 3040-8	111
907	Elemental mass spectrometry for quantitative proteomics. <b>2008</b> , 390, 3-16	115
906	IIC coupled to ICP-SFMS with post-column isotope dilution analysis of sulfur for absolute protein quantification. <b>2008</b> , 391, 537-43	46
905	Mass spectrometry for monitoring protease reactions. <b>2008</b> , 392, 783-92	10
904	Challenges of using mass spectrometry as a bladder cancer biomarker discovery platform. <b>2008</b> , 26, 67-74	18
903	Genetic approaches towards overcoming water deficit in plants - special emphasis on LEAs. <b>2008</b> , 14, 277-98	20
902	Potential applications of global protein expression analysis (proteomics) in morbid obesity and bariatric surgery. <b>2008</b> , 18, 905-10	7
901	Modeling in biological chemistry. From biochemical kinetics to systems biology. <b>2008</b> , 139, 427-446	4
900	The tear proteomics analysis of conjunctivochalasis. <b>2008</b> , 22, 288-294	1
899	A flax-retting endopolygalacturonase-encoding gene from Rhizopus oryzae. <b>2008</b> , 94, 563-71	8
898	Evaluating the compatibility of three colorimetric protein assays for two-dimensional electrophoresis experiments. <b>2008</b> , 8, 2178-84	22
897	Application of proteomics technology for analyzing the interactions between host cells and intracellular infectious agents. <b>2008</b> , 8, 852-73	27
896	Alignment of LC-MS images, with applications to biomarker discovery and protein identification. <b>2008</b> , 8, 650-72	80
895	Protein Information Crawler (PIC): extensive spidering of multiple protein information resources for large protein sets. <b>2008</b> , 8, 42-4	3
894	Proteomic analysis for inhibitory effect of chitosan oligosaccharides on 3T3-L1 adipocyte differentiation. <b>2008</b> , 8, 569-81	46
893	Proteomics and phosphoproteomics for the mapping of cellular signalling networks. <b>2008</b> , 8, 4402-15	33

## (2008-2008)

892	A practical guide for the identification of membrane and plasma membrane proteins in human embryonic stem cells and human embryonal carcinoma cells. <b>2008</b> , 8, 4036-53	44
891	Quantitative proteomics and phosphoproteomics reveal novel insights into complexity and dynamics of the EGFR signaling network. <b>2008</b> , 8, 4383-401	86
890	Gel-based proteomics of Gram-positive bacteria: a powerful tool to address physiological questions. <b>2008</b> , 8, 4958-75	49
889	A novel workflow control system for Fourier transform ion cyclotron resonance mass spectrometry allows for unique on-the-fly data-dependent decisions. <b>2008</b> , 22, 1245-56	12
888	Highly efficient enrichment of phosphopeptides by magnetic nanoparticles coated with zirconium phosphonate for phosphoproteome analysis. <b>2008</b> , 22, 1069-80	49
887	PeakSelect: preprocessing tandem mass spectra for better peptide identification. <b>2008</b> , 22, 1203-12	22
886	An improved method for de novo sequencing of arginine-containing, Nalpha-tris(2,4,6-trimethoxyphenyl)phosphonium-acetylated peptides. <b>2008</b> , 22, 2063-72	13
885	Exploration of the normal human bronchoalveolar lavage fluid proteome. <b>2008</b> , 2, 585-95	41
884	Proteomics-based investigations of animal models of disease. <b>2008</b> , 2, 638-53	7
883	SEREX, Proteomex, AMIDA, and beyond: Serological screening technologies for target identification. <b>2008</b> , 2, 355-71	12
882	Neuroproteomics and systems biology-based discovery of protein biomarkers for traumatic brain injury and clinical validation. <b>2008</b> , 2, 1467-83	44
881	High-resolution biomarker discovery: Moving from large-scale proteome profiling to quantitative validation of lead candidates. <b>2008</b> , 2, 1422-34	5
880	Proteomic identification of proteins in the human brain: Towards a more comprehensive understanding of neurodegenerative disease. <b>2008</b> , 2, 1484-97	17
879	Proteomic profiles of bronchoalveolar lavage fluid from patients with ventilator-associated pneumonia by gel-assisted digestion and 2-D-LC/MS/MS. <b>2008</b> , 2, 1208-22	12
878	Probing peptide libraries from Conus achatinus using mass spectrometry and cDNA sequencing: identification of delta and omega-conotoxins. <b>2008</b> , 43, 791-805	21
877	Clinical perspectives of high-resolution mass spectrometry-based proteomics in neuroscience: exemplified in amyotrophic lateral sclerosis biomarker discovery research. <b>2008</b> , 43, 559-71	36
876	Live single-cell video-mass spectrometry for cellular and subcellular molecular detection and cell classification. <b>2008</b> , 43, 1692-700	134
875	Proteome analysis of non-model plants: a challenging but powerful approach. <b>2008</b> , 27, 354-77	168

874	Proteomics in gram-negative bacterial outer membrane vesicles. <b>2008</b> , 27, 535-55	222
873	Orbitrap mass spectrometry: instrumentation, ion motion and applications. <b>2008</b> , 27, 661-99	342
872	Proteomics of brain extracellular fluid (ECF) and cerebrospinal fluid (CSF). 2010, 29, 17-28	55
871	Optimizing protein extraction from plant tissues for enhanced proteomics analysis. <b>2008</b> , 31, 2032-9	115
870	Improvement of performance in label-free quantitative proteome analysis with monolithic electrospray ionization emitter. <b>2008</b> , 31, 2589-97	12
869	Proteome analysis of human dorsolateral prefrontal cortex using shotgun mass spectrometry. <b>2008</b> , 31, 3122-6	12
868	Infrared multiple-photon dissociation mechanisms of peptides of glycine. 2008, 14, 7765-70	12
867	Targeting tumor vascular endothelium: an emerging concept for cancer therapy. <b>2008</b> , 69, 340-351	1
866	LC/MS identification of 12 intracellular cytoskeletal and inflammatory proteins from monocytes adherent on surface-adsorbed fibronectin-derived peptides. <b>2008</b> , 85, 513-29	5
865	Antioxidant Pathways and One-Electron Oxidation of Dopamine and Cysteine in Electrospray and On-Line Electrochemistry Electrospray Ionization Mass Spectrometry. <b>2008</b> , 20, 1959-1967	32
864	Biomarker discovery in psychiatric disorders. <b>2008</b> , 29, 2884-90	27
863	Immunoaffinity capillary electrophoresis as a powerful strategy for the quantification of low-abundance biomarkers, drugs, and metabolites in biological matrices. <b>2008</b> , 29, 3259-78	80
862	MALDI in-source photooxidation reactions for online peptide tagging. <b>2008</b> , 47, 2646-8	35
861	MALDI In-Source Photooxidation Reactions for Online Peptide Tagging. <b>2008</b> , 120, 2686-2688	3
860	Exploring the Full Power of Combining High Throughput RNAi with High Content Readouts: From Target Discovery Screens to Drug Modifier Studies. <b>2008</b> , 145-168	3
859	Evidence for structural variants of a- and b-type peptide fragment ions using combined ion mobility/mass spectrometry. <b>2008</b> , 19, 609-13	79
858	Trapped-ion cell with improved DC potential harmonicity for FT-ICR MS. 2008, 19, 586-97	98
857	Top-down identification and characterization of biomolecules by mass spectrometry. <b>2008</b> , 19, 1045-53	99

856	How much peptide sequence information is contained in ion trap tandem mass spectra?. <b>2008</b> , 19, 1813-20	26
855	A hierarchical algorithm for calculating the isotopic fine structures of molecules. <b>2008</b> , 19, 1867-74	21
854	Mapping preferred sites for fluorescent labeling by combining fluorescence and MS analysis of tryptic CNA35 protein digests. <b>2008</b> , 863, 293-7	4
853	Quantitative analysis of backbone-cyclised peptides in plants. <b>2008</b> , 872, 107-14	19
852	Experimental and computational approaches to quantitative proteomics: status quo and outlook. <b>2008</b> , 71, 19-33	99
851	Assessing CMT cell line stability by two dimensional polyacrylamide gel electrophoresis and mass spectrometry based proteome analysis. <b>2008</b> , 71, 160-7	9
850	Evaluation of a standardized method of protein purification and identification after discovery by mass spectrometry. <b>2008</b> , 71, 368-78	9
849	High confidence determination of specific protein-protein interactions using quantitative mass spectrometry. <b>2008</b> , 19, 331-7	139
848	Electrospray ionization mass spectroscopic analysis of peptides modified with N-ethylmaleimide or iodoacetanilide. <b>2008</b> , 18, 4891-5	17
847	Peptide enrichment by microfluidic electrocapture for online analysis by electrospray mass spectrometry. <b>2008</b> , 374, 154-62	11
846	Toward Systme International d'Unit <sup>e</sup> traceable protein quantification: from amino acids to proteins. <b>2008</b> , 376, 242-51	71
845	Sodium-deoxycholate-assisted tryptic digestion and identification of proteolytically resistant proteins. <b>2008</b> , 377, 259-66	92
844	An overview of analytical methods for determining the geographical origin of food products. <b>2008</b> , 107, 897-911	393
843	Real-time monitoring of protein complexes reveals their quaternary organization and dynamics. <b>2008</b> , 15, 246-53	64
842	Development of an integrated chromatographic system for on-line digestion and characterization of phosphorylated proteins. <b>2008</b> , 1183, 65-75	23
841	Improving off-line accelerated tryptic digestion. Towards fast-lane proteolysis of complex biological samples. <b>2008</b> , 1195, 34-43	4
840	Simultaneous analysis by capillary electrophoresis of five amyloid peptides as potential biomarkers of Alzheimer's disease. <b>2008</b> , 1214, 157-64	33
839	Dynamic proteomics of individual cancer cells in response to a drug. <b>2008</b> , 322, 1511-6	467

838	One-step procedure for peptide extraction from in-gel digestion sample for mass spectrometric analysis. <b>2008</b> , 80, 9797-805	15
837	Immonium ion scanning for the discovery of post-translational modifications and its application to histones. <b>2008</b> , 7, 2632-41	32
836	Statistical validation of peptide identifications in large-scale proteomics using the target-decoy database search strategy and flexible mixture modeling. <b>2008</b> , 7, 286-92	98
835	Semisupervised model-based validation of peptide identifications in mass spectrometry-based proteomics. <b>2008</b> , 7, 254-65	114
834	Synthesis, characterization, and application of iodoacetamide derivatives utilized for the ALiPHAT strategy. <b>2008</b> , 130, 2122-3	42
833	Analysis of mass spectrometry data in proteomics. <b>2008</b> , 453, 105-22	8
832	Organic mass spectrometry at the beginning of the 21st century. <b>2008</b> , 63, 1128-1154	5
831	Numerical simulation of the evolution of ion clouds in a mass spectrometer by the particle-in-cell method. <b>2008</b> , 32, 125-134	
830	Discrimination analysis of mass spectrometry proteomics for ovarian cancer detection. <b>2008</b> , 29, 1240-6	11
829	Clinical proteomics in neurodegenerative disorders. <b>2008</b> , 118, 1-11	51
828	MALDI-TOF mass spectrometry as a tool for differentiation of invasive and noninvasive Streptococcus pyogenes isolates. <b>2008</b> , 53, 333-42	67
827	Comprehensive mass-spectrometry-based proteome quantification of haploid versus diploid yeast.  Nature, 2008, 455, 1251-4	745
826	MaxQuant enables high peptide identification rates, individualized p.p.brange mass accuracies and proteome-wide protein quantification. <b>2008</b> , 26, 1367-72	9012
825	Recent problems and advances in mass spectrometry (Review). 2008, 44, 1482-1490	2
825 824	Recent problems and advances in mass spectrometry (Review). 2008, 44, 1482-1490  Chip-NMR biosensor for detection and molecular analysis of cells. 2008, 14, 869-74	502
·		
824	Chip-NMR biosensor for detection and molecular analysis of cells. <b>2008</b> , 14, 869-74	502

# (2008-2008)

820	A database of mass spectrometric assays for the yeast proteome. <b>2008</b> , 5, 913-4	188
819	Methods for analyzing peptides and proteins on a chromatographic timescale by electron-transfer dissociation mass spectrometry. <b>2008</b> , 3, 1709-17	77
818	Application of proteomics to ecology and population biology. 2008, 100, 200-6	62
817	Proteolysis of multiple myelin basic protein isoforms after neurotrauma: characterization by mass spectrometry. <b>2008</b> , 104, 1404-14	52
816	Comprehensive proteomic analysis of protein changes during platelet storage requires complementary proteomic approaches. <b>2008</b> , 48, 425-35	72
815	Integration of metabolomics and proteomics in molecular plant physiologycoping with the complexity by data-dimensionality reduction. <b>2008</b> , 132, 176-89	78
814	Antigen analysis of Mycobacterium tuberculosis H37Rv culture filtrate proteins. 2008, 67, 245-52	57
813	. <b>2008</b> , 96, 1292-1309	6
812	Computational prediction models for early detection of risk of cardiovascular events using mass spectrometry data. <b>2008</b> , 12, 636-43	9
811	A nonparametric model for quality control of database search results in shotgun proteomics. <b>2008</b> , 9, 29	10
810	A robust linear regression based algorithm for automated evaluation of peptide identifications from shotgun proteomics by use of reversed-phase liquid chromatography retention time. <b>2008</b> , 9, 347	43
809	A probabilistic framework to predict protein function from interaction data integrated with semantic knowledge. <b>2008</b> , 9, 382	15
808	LC-MSsima simulation software for liquid chromatography mass spectrometry data. <b>2008</b> , 9, 423	40
807	The APEX Quantitative Proteomics Tool: generating protein quantitation estimates from LC-MS/MS proteomics results. <b>2008</b> , 9, 529	131
806	Corra: Computational framework and tools for LC-MS discovery and targeted mass spectrometry-based proteomics. <b>2008</b> , 9, 542	58
805	Quality assessment of peptide tandem mass spectra. <b>2008</b> , 9 Suppl 6, S13	15
804	High accuracy mass spectrometry analysis as a tool to verify and improve gene annotation using Mycobacterium tuberculosis as an example. <b>2008</b> , 9, 316	59
803	Evidence for insertional RNA editing in humans. <b>2008</b> , 18, 1760-5	12

802	Proteomics studies reveal important information on small molecule therapeutics: a case study on plasma proteins. <b>2008</b> , 13, 1042-51	20
801	Differential proteome of bone marrow mesenchymal stem cells from osteoarthritis patients. <b>2008</b> , 16, 929-35	20
800	Proteomics: methodologies and applications in oncology. <b>2008</b> , 18, 115-25	23
799	Nanobiocatalysis and its potential applications. <b>2008</b> , 26, 639-46	356
798	Candida albicans-macrophage interactions: genomic and proteomic insights. 2008, 3, 661-81	11
797	Proteome Analysis of the Ubiquitin Pathway. 443-453	1
796	Quantitative protein profiling by mass spectrometry using label-free proteomics. 2008, 439, 241-56	62
795	Quantitative protein profiling by mass spectrometry using isotope-coded affinity tags. 2008, 439, 225-40	30
794	An Introduction to Proteomics: Applications to Plant Biology. 1-7	3
793	The Arabidopsis Localizome: Subcellular Protein Localization and Interactions in ARABIDOPSIS. 61-81	
79 <sup>2</sup>	Proteomics in the study of the sperm cell composition, differentiation and function. 2008, 54, 23-36	63
791	Integrating Prediction of Structure, Function, and Interactions. 2008, 259-279	1
790	Molecular Recognition Using Amphiphilic Macromolecules. 9-36	1
789	A single lysis solution for the analysis of tissue samples by different proteomic technologies. <b>2008</b> , 2, 368-79	30
788	Carbonic anhydrase as a model for biophysical and physical-organic studies of proteins and protein-ligand binding. <b>2008</b> , 108, 946-1051	541
787	[Clinical proteomics and new biomarkers in biological fluids]. 2008, 131, 426-34	1
786	Detection of co-eluted peptides using database search methods. <b>2008</b> , 3, 27	19
785	Proteomics with a pinch of salt: a cyanobacterial perspective. <b>2008</b> , 4, 1	102

## (2008-2008)

784	mouse tissues. <b>2008</b> , 7, 3114-26	41
783	Biogenesis of and activities at the Toxoplasma gondii parasitophorous vacuole membrane. <b>2008</b> , 47, 155-64	21
782	An assessment of software solutions for the analysis of mass spectrometry based quantitative proteomics data. <b>2008</b> , 7, 51-61	387
781	Mass Spectrometry of Biological Molecules. 2008,	2
780	Psychiatric research: psychoproteomics, degradomics and systems biology. <b>2008</b> , 5, 293-314	31
779	Solid tumor proteome and phosphoproteome analysis by high resolution mass spectrometry. <b>2008</b> , 7, 5314-26	119
778	Blue Native PAGE and Mass Spectrometry Analysis of Ephrin Stimulation-Dependent Protein-Protein Interactions in NG108-EphB2 Cells. <b>2008</b> , 3-22	13
777	Applications of mass spectrometry in oncology. <b>2008</b> , 379-406	
776	Spectral index for assessment of differential protein expression in shotgun proteomics. 2008, 7, 845-54	92
775	Does trypsin cut before proline?. <b>2008</b> , 7, 300-5	180
775 774	Does trypsin cut before proline?. 2008, 7, 300-5  Improving sensitivity by probabilistically combining results from multiple MS/MS search methodologies. 2008, 7, 245-53	138
	Improving sensitivity by probabilistically combining results from multiple MS/MS search	
	Improving sensitivity by probabilistically combining results from multiple MS/MS search methodologies. <b>2008</b> , 7, 245-53	138
774 773	Improving sensitivity by probabilistically combining results from multiple MS/MS search methodologies. <b>2008</b> , 7, 245-53  Coimmunoprecipitation and proteomic analyses. <b>2008</b> , 439, 291-308	138
774 773 772	Improving sensitivity by probabilistically combining results from multiple MS/MS search methodologies. 2008, 7, 245-53  Coimmunoprecipitation and proteomic analyses. 2008, 439, 291-308  Drug Targets in Kinetoplastid Parasites. 2008,	138 1 3
774 773 772 771	Improving sensitivity by probabilistically combining results from multiple MS/MS search methodologies. 2008, 7, 245-53  Coimmunoprecipitation and proteomic analyses. 2008, 439, 291-308  Drug Targets in Kinetoplastid Parasites. 2008,  Antibody suspension bead arrays within serum proteomics. 2008, 7, 3168-79	138 1 3
774 773 772 771 770	Improving sensitivity by probabilistically combining results from multiple MS/MS search methodologies. 2008, 7, 245-53  Coimmunoprecipitation and proteomic analyses. 2008, 439, 291-308  Drug Targets in Kinetoplastid Parasites. 2008,  Antibody suspension bead arrays within serum proteomics. 2008, 7, 3168-79  Clinical Proteomics. 2008,  Proteomics and its Application to the Human-Pathogenic Fungi Aspergillus fumigatus and Candida	138 1 3 92 1

766	Human and Animal Relationships. 2008,	2
765	Clean substrates prepared by chemical adsorption of iodide followed by electrochemical oxidation for surface-enhanced Raman spectroscopic study of cell membrane. <b>2008</b> , 80, 5118-25	58
764	Functional proteomics. Preface. <b>2008</b> , 484, v-vii	5
763	EGFR Signaling Networks in Cancer Therapy. 2008,	7
762	Informatics Tools for Glycomics: Assisted Interpretation and Annotation of Mass Spectra. <b>2008</b> , 2219-2240	1
761	Experimental Methods for Protein Interaction Identification and Characterization. 2008, 1-32	1
760	Integrative Structure Determination of Protein Assemblies by Satisfaction of Spatial Restraints. <b>2008</b> , 99-114	6
759	Multidimensional LC separations in shotgun proteomics. <b>2008</b> , 80, 7187-93	185
758	Biomolecule analysis by ion mobility spectrometry. <b>2008</b> , 1, 293-327	396
757	Molecular Mechanisms in Spermatogenesis. 2008,	11
756	Protein kinases: starting a molecular systems view of endocytosis. <b>2008</b> , 24, 501-23	31
755	Practical Bioinformatics. 2008,	
754	Advances in the analysis of protein phosphorylation. 2008, 7, 1809-18	140
753	Genomics Protocols. 2008,	4
75 <sup>2</sup>	Key Technologies and Tools for Functional Glycobiology: Introduction. <b>2008</b> , 2115-2119	
751	Applications of Mass Spectrometry in Life Safety. 2008,	1
750	Progress in ecotoxicogenomics for environmental monitoring, mode of action, and toxicant identification. <b>2008</b> , 2, 21-323	13
749	Organelle proteomics. Preface. <b>2008</b> , 432, v-viii	

748	Protease proteomics: revealing protease in vivo functions using systems biology approaches. <b>2008</b> , 29, 339-58	75
747	Capillary liquid chromatography combined with tandem mass spectrometry for the study of neurosteroids and oxysterols in brain. <b>2008</b> , 52, 506-21	19
746	Integrated approaches to uncovering transcription regulatory networks in mammalian cells. <b>2008</b> , 91, 219-31	36
745	Proteomic methodological recommendations for studies involving human plasma, platelets, and peripheral blood mononuclear cells. <b>2008</b> , 7, 2280-90	69
744	Predicting tumor outcomes in urothelial bladder carcinoma: turning pathways into clinical biomarkers of prognosis. <b>2008</b> , 8, 1103-10	12
743	Phosphoproteomics in bacteria: towards a systemic understanding of bacterial phosphorylation networks. <b>2008</b> , 5, 619-27	56
742	MSPtool: A Versatile Tool for Mass Spectrometry Data Preprocessing. 2008,	O
741	Identifying Protein Complexes With Clear Module Structure Using Pairwise Constraints in Protein Interaction Networks. <b>2021</b> , 12, 664786	3
740	Deep Convolutional Neural Networks Help Scoring Tandem Mass Spectrometry Data in Database-Searching Approaches. <b>2021</b> , 20, 4708-4717	2
739	Characterization of the Primary Human Trophoblast Cell Secretome Using Stable Isotope Labeling With Amino Acids in Cell Culture. <b>2021</b> , 9, 704781	3
738	Application of Proteomics in Cancer: Recent Trends and Approaches for Biomarkers Discovery. <b>2021</b> , 8, 747333	19
737	AlphaMap: an open-source python package for the visual annotation of proteomics data with sequence specific knowledge. <b>2021</b> ,	3
736	Targeted proteomics analysis of plasma proteins using recombinant protein standards for addition only workflows. <b>2021</b> , 71, 473-483	2
735	MicroRNA Interactome Multiomics Characterization for Cancer Research and Personalized Medicine: An Expert Review. <b>2021</b> , 25, 545-566	1
734	StatsPro: Systematic integration and evaluation of statistical approaches for detecting differential expression in label-free quantitative proteomics. <b>2022</b> , 250, 104386	1
733	ProtView: A versatile tool for in silico protease evaluation and selection in a proteomic and proteogenomic context.	
732	High-throughput proteomics and AI for cancer biomarker discovery. <b>2021</b> , 176, 113844	7
731	Biomolecular Corona Associated with Nanostructures: The Potentially Disruptive Role of Raman Microscopy. 2100660	1

730	Resistance to a nonselective 4-hydroxyphenylpyruvate dioxygenase-inhibiting herbicide via novel reduction-dehydration-glutathione conjugation in Amaranthus tuberculatus. <b>2021</b> , 232, 2089-2105	0
729	Deep neural network for detecting arbitrary precision peptide features through attention based segmentation. <b>2021</b> , 11, 18249	O
728	Mass Spectrometry-Based Techniques to Elucidate the Sugar Code. <b>2021</b> ,	8
727	SMAP: A pipeline for sample matching in proteogenomics.	
726	Pluripotent stem cells for skeletal tissue engineering. <b>2021</b> , 1-20	0
725	Mimicking LysC Proteolysis by 'Arginine-Modification-cum-Trypsin digestion': Comparison of Bottom-Up & Middle-Down Proteomic Approaches by ESI-QTOF-MS. <b>2021</b> ,	
724	NHS-Ester Tandem Labeling in One Pot Enables 48-Plex Quantitative Proteomics. <b>2021</b> , 93, 12827-12832	3
723	Long noncoding RNA and protein abundance in lncRNPs. <b>2021</b> , 27, 1427-1440	5
722	Analytical approaches to assess metabolic changes in psoriasis. <b>2021</b> , 205, 114359	1
721	Extraction of intrinsic column peak profiles of narrow-bore and microbore columns by peak deconvolution methods. <b>2021</b> , 1180, 338851	1
720	Industrial applications of immobilized nano-biocatalysts. <b>2021</b> , 1	5
719	Microfluidic protein analysis and applications. <b>2022</b> , 257-273	
718	Systems biology in diagnosis and treatment of kidney disease. <b>2022</b> , 465-479	
717	Functional Proteomics. <b>2022</b> ,	
716	Proteomic approaches to investigate gammaherpesvirus biology and associated tumorigenesis. <b>2021</b> , 109, 201-254	
715	Pathogenesis of Staphylococcus aureus and Proteomic Strategies for the Identification of Drug Targets. <b>2021</b> , 325-340	
714	Proteomics for food authentication. <b>2021</b> , 247-277	0
713	Computational Phosphorylation Network Reconstruction: An Update on Methods and Resources. <b>2021</b> , 2358, 203-219	

An Overview of Proteomics and Related Nanomaterials. **2021**, 1-35

711	In-depth and 3-dimensional exploration of the budding yeast phosphoproteome. <b>2021</b> , 22, e51121	30
710	IonQuant Enables Accurate and Sensitive Label-Free Quantification With FDR-Controlled Match-Between-Runs. <b>2021</b> , 20, 100077	21
709	Two-Dimensional Gel Electrophoresis: Basic Principles and Application to Platelet Signaling Studies. 87-110	1
708	Proteomic approaches to antibiotic drug discovery. <b>2005</b> , Chapter 1, Unit 1F.2	4
707	Comprehensive Two-Dimensional Liquid Chromatography Combined with Mass Spectrometry. 331-390	4
706	Proteomics and Cancer Risk Assessment. 207-217	1
705	Characterisation of proteins in scent marks: Proteomics meets semiochemistry. <b>2005</b> , 183-198	2
704	Proteomics Today, Proteomics Tomorrow. <b>2004</b> , 1-17	3
703	Managing Information Quality in e-Science: A Case Study in Proteomics. <b>2005</b> , 423-432	4
702	Efficient Model-Based Clustering for LC-MS Data. <b>2006</b> , 32-43	1
701	Testicular development and spermatogenesis: harvesting the postgenomics bounty. 2008, 636, 16-41	22
700	7.1 Proteomics. <b>2007</b> , 737-769	3
699	Genomics of Salmonella Species. <b>2011</b> , 171-235	1
698	Encyclopedia of Systems Biology. <b>2013</b> , 1775-1777	1
697	Fish Authentication. 2013, 205-222	4
696	Mass Spectrometry Applications. <b>2013</b> , 83-100	1
695	Blood <b>B</b> rain Barrier (BBB) Pharmacoproteomics: A New Research Field Opened Up by Quantitative Targeted Absolute Proteomics (QTAP). <b>2014</b> , 63-100	2

694	Lipid raft proteins and their identification in T lymphocytes. <b>2004</b> , 37, 121-52	17
693	RaptorX server: a resource for template-based protein structure modeling. 2014, 1137, 17-27	168
692	SILAC yeast: from labeling to comprehensive proteome quantification. <b>2014</b> , 1156, 81-109	8
691	See & Catch method for studying protein complexes in yeast cells: a technique unifying fluorescence microscopy and mass spectrometry. <b>2014</b> , 1163, 75-95	1
690	Omics Approaches to Macrophage Biology. <b>2014</b> , 587-615	1
689	Current status and future prospects of mass spectrometry imaging of small molecules. <b>2015</b> , 1203, 1-7	3
688	Quantitative protein analysis by mass spectrometry. <b>2015</b> , 1278, 281-305	26
687	Study of CPP Mechanisms by Mass Spectrometry. <b>2015</b> , 1324, 107-21	5
686	Identification of Direct Kinase Substrates via Kinase Assay-Linked Phosphoproteomics. <b>2016</b> , 1355, 263-73	5
685	Proteomic Analysis of Dental Tissue Microsamples. <b>2017</b> , 1537, 461-479	1
684	Protein Identification from Tandem Mass Spectra by Database Searching. 2017, 1558, 357-380	3
683	Mapping Biological Networks from Quantitative Data-Independent Acquisition Mass Spectrometry: Data to Knowledge Pipelines. <b>2017</b> , 1558, 395-413	5
682	Introduction to Mass Spectrometry-Based Proteomics. <b>2020</b> , 2051, 1-58	5
681	Targeted Proteomics as a Tool for Quantifying Urine-Based Biomarkers. <b>2020</b> , 2051, 277-295	3
680	New Insights and Future Advances in Cancer Diagnostics. <b>2004</b> , 15-26	2
679	Identifying bona fide components of an organelle by isotope-coded labeling of subcellular fractions : an example in peroxisomes. <b>2008</b> , 432, 357-71	4
678	Quantitative proteomic analysis to profile dynamic changes in the spatial distribution of cellular proteins. <b>2008</b> , 432, 389-401	27
677	Proteomic Strategies of Therapeutic Individualization and Target Discovery in Acute Myeloid Leukemia. <b>2008</b> , 161-187	3

# (2010-2009)

676	Identification of the Candida albicans immunome during systemic infection by mass spectrometry. <b>2009</b> , 470, 187-235	4
675	Using stable isotope tagging and mass spectrometry to characterize protein complexes and to detect changes in their composition. <b>2007</b> , 359, 17-35	10
674	The absolute quantification strategy: application to phosphorylation profiling of human separase serine 1126. <b>2007</b> , 359, 71-86	37
673	Temporal Dynamics of EGF Receptor Signaling by Quantitative Proteomics. 2008, 190-198	1
672	Proteomics in Defining Pathogenic Processes Involved in Glaucomatous Neurodegeneration. 2008, 425-441	1
671	Proteomic Strategies for Analyzing Body Fluids. <b>2007</b> , 3-30	2
670	The Human Plasma and Serum Proteome. <b>2007</b> , 195-224	6
669	The monitoring and affinity purification of proteins using dual tags with tetracysteine motifs. <b>2009</b> , 544, 421-38	5
668	Proteomic global profiling for cancer biomarker discovery. <b>2009</b> , 492, 309-20	7
667	Quantitative peptide and protein profiling by mass spectrometry. <b>2009</b> , 492, 21-38	8
666	Two-dimensional ion mobility analyses of proteins and peptides. <b>2009</b> , 492, 417-45	13
665	High accuracy mass spectrometry in large-scale analysis of protein phosphorylation. <b>2009</b> , 492, 131-42	43
664	Affinity Chromatography. <b>2008</b> , 1-23	2
663	Proteomic Analysis in Cancer Patients. 2008, 33-45	1
662	Introduction to omics. <b>2010</b> , 593, 1-23	2
661	Proteomics and metabolomics and their application to analgesia research. <b>2010</b> , 617, 457-73	1
660	Peptidome analysis of mouse liver tissue by size exclusion chromatography prefractionation. <b>2010</b> , 615, 207-16	1
659	Organelle proteomics by label-free and SILAC-based protein correlation profiling. 2010, 658, 255-65	9

658	A Protocol for top-down proteomics using HPLC and ETD/PTR-MS. <b>2010</b> , 658, 339-53	4
657	Modeling experimental design for proteomics. <b>2010</b> , 673, 223-30	5
656	Protein identification by spectral networks analysis. <b>2011</b> , 694, 151-68	7
655	Software pipeline and data analysis for MS/MS proteomics: the trans-proteomic pipeline. <b>2011</b> , 694, 169-89	35
654	High-throughput immunofluorescence microscopy using yeast spheroplast cell-based microarrays. <b>2011</b> , 706, 83-95	5
653	Biochemical purification of native immune protein complexes. <b>2011</b> , 712, 31-44	11
652	Whole cell proteome regulation by microRNAs captured in a pulsed SILAC mass spectrometry approach. <b>2011</b> , 725, 315-31	11
651	Profiling solid tumor heterogeneity by LCM and biological MS of fresh-frozen tissue sections. <b>2011</b> , 755, 95-106	14
650	Applications of nanoscale liquid chromatography coupled to Tandem mass spectrometry in quantitative studies of protein expression, protein-protein interaction, and protein phosphorylation. <b>2011</b> , 790, 99-113	4
649	High throughput profiling of serum phosphoproteins/peptides using the SELDI-TOF-MS platform. <b>2012</b> , 818, 199-216	7
648	Limited proteolysis in proteomics using protease-immobilized microreactors. 2012, 815, 187-98	3
647	Routine identity confirmation of recombinant proteins by MALDI-TOF mass spectrometry. <b>2012</b> , 824, 37-50	8
646	Shotgun proteomics of plant plasma membrane and microdomain proteins using nano-LC-MS/MS. <b>2014</b> , 1072, 481-98	12
645	Cross-Species Analysis of Protein-protein Interaction Networks. <b>2008</b> , 163-185	1
644	Waluation non invasive de la viabilit°de l⊞mbryon humain. <b>2011</b> , 507-510	2
643	Global Proteomics of Extremophilic Fungi: Mission Accomplished?. <b>2019</b> , 205-249	3
642	Deep Learning for Proteomics Data for Feature Selection and Classification. 2019, 301-316	0
641	Global Alignment of PPI Networks. <b>2021</b> , 3-25	O

640	Integration of Matrisome Omics: Towards System Biology of the Tumor Matrisome. 2020, 131-156	2
639	Comparison of Algorithms for Profile-Based Alignment of Low Resolution MALDI-ToF Spectra. <b>2014</b> , 193-201	2
638	Mass spectrometry-based biomarkers in drug development. <b>2014</b> , 806, 341-59	10
637	Rapid Profiling of Human Pathogenic Bacteria and Antibiotic Resistance Employing Specific Tryptic Peptides as Biomarkers. <b>2016</b> , 275-303	2
636	Transcriptomics and Proteomics of Foodborne Bacterial Pathogens. 2017, 167-200	1
635	Mass Spectrometry Analysis Using MALDIquant. <b>2017</b> , 101-124	8
634	Instrumentation. <b>2017</b> , 151-292	2
633	Use of Mass Spectrometry to Study the Centromere and Kinetochore. <b>2017</b> , 56, 3-27	3
632	Stochastic Context-Free Graph Grammars for Glycoprotein Modelling. 2005, 247-258	1
631	Chemical Methods for Mimicking Post-Translational Modifications. <b>2009</b> , 97-125	1
630	Robust Peak Detection and Alignment of nanoLC-FT Mass Spectrometry Data. 2007, 35-46	3
629	Alignment of Mass Spectrometry Data by Clique Finding and Optimization. 2006, 119-129	1
628	Structure Determination of Macromolecular Complexes by Experiment and Computation. 2008, 73-96	1
627	A Bayesian Approach to Protein Inference Problem in Shotgun Proteomics. <b>2008</b> , 167-180	10
626	Fast and Accurate Alignment of Multiple Protein Networks. 2008, 246-256	28
625	Support Vector Machines in Biomedical and Biometrical Applications. <b>2013</b> , 379-417	10
624	Kernel Methods and Applications in Bioinformatics. <b>2014</b> , 275-285	3
623	Understanding Information Processes at the Proteomics Level. <b>2014</b> , 57-72	2

622	Identification of Ultramodified Proteins Using Top-Down Spectra. 2013, 132-144	2
621	Current challenges and approaches for the synergistic use of systems biology data in the scientific community. <b>2007</b> , 97, 277-307	6
620	Omics Technology. <b>2010</b> , 11-31	7
619	Ultra-Fast Sample Preparation for High-Throughput Proteomics. <b>2011</b> , 125-139	2
618	Fibrinogen ⊞Chain as a Serum Marker of Liver Disease. <b>2017</b> , 493-511	О
617	Glycoconjugate Vaccines Used for Prevention from Biological Agents: Tandem Mass Spectrometric Analysis. <b>2014</b> , 233-274	1
616	Functional Genomics and System Biology Approach in Bioremediation of Soil and Water from Organic and Inorganic Pollutants. <b>2019</b> , 1-20	2
615	Target identification and validation of natural products with label-free methodology: A critical review from 2005 to 2020. <b>2020</b> , 216, 107690	12
614	Mitochondrial Protein Nitration Primes Neurodegeneration in Experimental Autoimmune Encephalomyelitis. <b>2006</b> , 281, 31950-31962	7
613	CHAPTER 1:Practical Considerations and Current Limitations in Quantitative Mass Spectrometry-based Proteomics. <b>2014</b> , 1-25	4
612	CHAPTER 2:High Resolution/Accurate Mass Targeted Proteomics. <b>2014</b> , 26-47	2
611	CHAPTER 4:Getting Absolute: Determining Absolute Protein Quantities via Selected Reaction Monitoring Mass Spectrometry. <b>2014</b> , 80-109	14
610	CHAPTER 13:Protein Quantification by MRM for Biomarker Validation. <b>2014</b> , 277-315	2
609	CHAPTER 1:Introduction: Biomarkers in Translational and Personalized Medicine. <b>2013</b> , 3-39	1
608	Higher-order structural characterisation of native proteins and complexes by top-down mass spectrometry. <b>2020</b> , 11, 12918-12936	30
607	Advances in environmental genomics: towards an integrated view of micro-organisms and ecosystems. <b>2008</b> , 154, 347-359	24
606	Mass-spectrometry of single mammalian cells quantifies proteome heterogeneity during cell differentiation.	19
605	A computational framework to explore cellular response mechanisms from multi-omics datasets.	1

604	DeepLC can predict retention times for peptides that carry as-yet unseen modifications.	14
603	Training a neural network to learn other dimensionality reduction removes data size restrictions in bioinformatics and provides a new route to exploring data representations.	1
602	IonQuant enables accurate and sensitive label-free quantification with FDR-controlled match-between-runs.	3
601	A Community Challenge for Pancancer Drug Mechanism of Action Inference from Perturbational Profile Data.	3
600	Systematic detection of functional proteoform groups from bottom-up proteomic datasets.	1
599	Ultra-high sensitivity mass spectrometry quantifies single-cell proteome changes upon perturbation.	46
598	Multi Bmics comparison reveals metabolome biochemistry, not microbiome composition or gene expression, corresponds to elevated biogeochemical function in the hyporheic zone.	2
597	Genomic, Proteomic and Phenotypic Heterogeneity in HeLa Cells across Laboratories: Implications for Reproducibility of Research Results.	4
596	MS-PyCloud: An open-source, cloud computing-based pipeline for LC-MS/MS data analysis.	5
595	Online parallel accumulation Berial fragmentation (PASEF) with a novel trapped ion mobility mass spectrometer.	7
594	Uncovering hidden members and functions of the soil microbiome using de novo metaproteomics.	3
593	Plasma proteome profiling to detect and avoid sample-related biases in biomarker studies.	4
592	Molecular Phenotyping of Oxidative Stress in Diabetes Mellitus with Point-of-care NMR system.	5
591	Proteomics Standards Initiative Extended FASTA Format (PEFF).	1
590	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens.	7
589	In-depth and 3-Dimensional Exploration of the Budding Yeast Phosphoproteome.	2
588	Multiplexed Single Ion Mass Spectrometry Improves Measurement of Proteoforms and Their Complexes.	1
587	Tailor: non-parametric and rapid score calibration method for database search-based peptide identification in shotgun proteomics.	1

586	Harvesting the genome's bounty: integrative genomics. 2003, 68, 431-43	8
585	Exploiting proteomics in the discovery of drugs that target mitochondrial oxidative damage. <b>2004</b> , 2004, pe12	7
584	Computational Prediction of Protein Complexes from Protein Interaction Networks. 2017,	11
583	Constructing Reliable Protein-Protein Interaction (PPI) Networks. <b>2017</b> , 15	1
582	Protein Biochips and Array-Based Proteomics. <b>2003</b> , 1-80	3
581	Fishing for Pharmaceutically Relevant Phosphoinositide-Binding Proteins Using Chemical Proteomics. <b>2005</b> , 211-242	2
580	An Examination of the Physics of the High-Capacity Trap (HCT). 2010, 593-617	1
579	Chemical Derivatization and Multistage Tandem Mass Spectrometry for Protein Structural Characterization. <b>2009</b> , 83-119	1
578	- Epigenomics: Basics and Applications. <b>2013</b> , 96-117	1
577	Proteomics and Metabolomics. <b>2010</b> , 211-246	2
576	The beauty of being (label)-free: sample preparation methods for SWATH-MS and next-generation targeted proteomics. 2, 272	38
575	The beauty of being (label)-free: sample preparation methods for SWATH-MS and next-generation targeted proteomics. <b>2013</b> , 2, 272	49
574	Proteomic changes resulting from gene copy number variations in cancer cells. <b>2010</b> , 6, e1001090	97
	"Omic" investigations of protozoa and worms for a deeper understanding of the human gut	
573	"parasitome". <b>2017</b> , 11, e0005916	22
573 572		84
	"parasitome". <b>2017</b> , 11, e0005916	
572	"parasitome". <b>2017</b> , 11, e0005916  A topological map of the compartmentalized Arabidopsis thaliana leaf metabolome. <b>2011</b> , 6, e17806	84

## (2009-2013)

568	Completion of proteomic data sets by Kd measurement using cell-free synthesis of site-specifically labeled proteins. <b>2013</b> , 8, e82352	8
567	Detection of viral proteins in human cells lines by xeno-proteomics: elimination of the last valid excuse for not testing every cellular proteome dataset for viral proteins. <b>2014</b> , 9, e91433	3
566	GASOLINE: a Greedy And Stochastic algorithm for optimal Local multiple alignment of Interaction NEtworks. <b>2014</b> , 9, e98750	21
565	Optimization of plasma sample pretreatment for quantitative analysis using iTRAQ labeling and LC-MALDI-TOF/TOF. <b>2014</b> , 9, e101694	13
564	Design and validation of DNA libraries for multiplexing proximity ligation assays. <b>2014</b> , 9, e112629	1
563	Fast and Efficient XML Data Access for Next-Generation Mass Spectrometry. <b>2015</b> , 10, e0125108	10
562	Prediction of adjuvant chemotherapy response in triple negative breast cancer with discovery and targeted proteomics. <b>2017</b> , 12, e0178296	16
561	Laser capture microdissection: Big data from small samples. <b>2015</b> , 30, 1255-69	131
560	Successful Application of Whole Cell Panning for Isolation of Phage Antibody Fragments Specific to Differentiated Gastric Cancer Cells. <b>2019</b> , 9, 624-631	4
559	Chronic venous ulcers: a review on treatment with fibrin sealant and prognostic advances using proteomic strategies. <b>2020</b> , 26, e20190101	11
558	Proteomic profiling of high risk medulloblastoma reveals functional biology. <b>2015</b> , 6, 14584-95	17
557	Integrated quantitative proteomic and transcriptomic analysis of lung tumor and control tissue: a lung cancer showcase. <b>2016</b> , 7, 14857-70	12
556	Polymer - Nanoparticle Assemblies for Array Based Sensing. <b>2015</b> , 109, 1054-1062	7
555	Exploring the Potential of Neuroproteomics in Alzheimer's Disease. <b>2020</b> , 20, 2263-2278	7
554	Bioinformatics Tools for Mass Spectrometry-Based High-Throughput Quantitative Proteomics Platforms. <b>2011</b> , 8, 125-137	5
553	An iTRAQ Based Comparative Proteomic Profiling of Thermotolerant Saccharomyces cerevisiae JRC6 in Response to High Temperature Fermentation. <b>2019</b> , 16, 289-296	3
552	Mass Spectrometry for Proteomics and Recent Developments in ESI, MALDI and other Ionization Methodologies. <b>2019</b> , 16, 267-276	2
551	[Not Available]. <b>2009</b> , 3, 74-9	20

550	Japan Astrobiology Mars Project (JAMP): Search for Microbes on The Mars Surface with Special Interest in Methane-Oxidizing Bacteria. <b>2010</b> , 24, 67-82	7
549	Protein recycling in Bering Sea algal incubations. <b>2014</b> , 515, 45-59	8
548	[Prediction of peptide retention time in reversed-phase liquid chromatography and its application in protein identification]. <b>2010</b> , 28, 529-34	1
547	[Application of online two-dimensional separation system using monolithic columns for proteome analysis of human cartilage]. <b>2010</b> , 28, 140-5	2
546	[Optimization of two-dimensional high performance liquid chromatographic columns for highly efficient separation of intact proteins]. <b>2010</b> , 28, 158-62	3
545	Progress of Protein Quality Control Methods in Shotgun Proteomics*. <b>2009</b> , 2009, 668-675	2
544	Algorithm Development of de novo Peptide Sequencing Via Tandem Mass Spectrometry. <b>2011</b> , 37, 1278-1288	2
543	Development of Algorithms for Mass Spectrometry-based Label-free Quantitative Proteomics*. <b>2011</b> , 38, 506-518	2
542	Characterization of Interaction Proteins for Gastric Cancer Related Novel Protein RKIP*. 2012, 39, 68-77	1
541	Circulating biomarkers in malignant pleural mesothelioma. <b>2020</b> , 1,	Ο
540	Identification of proteins of human colorectal carcinoma cell line SW480 by two-dimensional electrophoresis and MALDI-TOF mass spectrometry. <b>2005</b> , 11, 4679-84	7
539	Moving forward in colorectal cancer research, what proteomics has to tell. <b>2007</b> , 13, 5813-21	16
538	Proteomic landscape of human coronary artery atherosclerosis. <b>2020</b> , 46, 371-383	3
537	Application of Genomics and Proteomics in Bioremediation. <b>2016</b> , 97-112	7
536	Informatics and Data Analytics to Support Exposome-Based Discovery. 2018, 145-187	3
535	Current Omics Technologies in Biomarker Discovery. <b>2011</b> , 79-111	1
534	Molecular markers in transitional cell carcinoma of the bladder: New insights into mechanisms and prognosis. <b>2008</b> , 24, 61-7	4
533	decoction extract regulates differentially expressed proteins in the hippocampus after chronic cerebral hypoperfusion. <b>2019</b> , 14, 470-479	11

# (2021-2015)

532	Systematic Analysis of Yeast Proteome Reveals Peptide Detectability Factors for Mass Spectrometry. <b>2015</b> , 8, 231-239	2
531	Plant Cell Wall, a Challenge for Its Characterisation. <b>2016</b> , 06, 70-105	13
530	MFC: Mining Maximal Frequent Dense Subgraphs without Candidate Maintenance in Imbalanced PPI Networks. <b>2011</b> , 6,	2
529	Statistical Methods for Proteomic Biomarker Discovery based on Feature Extraction or Functional Modeling Approaches. <b>2012</b> , 5, 117-135	10
528	A Comprehensive Identification of Synaptic Vesicle Proteins in Rat Brains by cRPLC/MS-MS and 2DE/MALDI-TOF-MS. <b>2007</b> , 28, 1499-1509	O
527	Protein Analysis Using a Combination of an Online Monolithic Trypsin Immobilized Enzyme Reactor and Collisionally-Activated Dissociation/Electron Transfer Dissociation Dual Tandem Mass Spectrometry. <b>2012</b> , 33, 3233-3240	3
526	Proteomics: applications to the study of rheumatoid arthritis and osteoarthritis. 2006, 14, 325-32	9
525	Quantitative analysis of nucleic acidsthe last few years of progress. <b>2004</b> , 37, 1-10	73
524	Proteomic studies in plants. 2004, 37, 133-8	43
523	Evaluation of proteomic strategies for analyzing ubiquitinated proteins. <b>2008</b> , 41, 177-83	39
522	Proteome analysis of chloroplast proteins in stage albinism line of winter wheat (triticum aestivum) FA85. <b>2009</b> , 42, 450-5	26
521	Small-molecule probes elucidate global enzyme activity in a proteomic context. <b>2014</b> , 47, 149-57	8
520	Optimization of Nano-Liquid Chromatography Coupled with Mass Spectrometry Systems for Proteomics. <b>2007</b> , 55, 157-164	1
519	Sample Preparation for the Systematic Analysis of a Protein-Protein Interaction Network. <b>2007</b> , 55, 165-171	O
518	Utility of Application of Liquid Chromatography/Triple Stage Mass Spectrometry (LC/MS3) for Proteome Analysis. <b>2009</b> , 57, 317-325	O
5 <sup>1</sup> 7	Insights from the molecular characterization of mercury stress proteins identified by proteomics in E.coli nissle 1917. <b>2013</b> , 9, 485-90	3
516	Mass Spectrometry-Based Methods for Immunoglobulin G N-Glycosylation Analysis. <b>2021</b> , 112, 73-135	
515	Protein-protein interaction prediction based on ordinal regression and recurrent convolutional neural networks. <b>2021</b> , 22, 485	3

514	Communication-avoiding micro-architecture to compute Xcorr scores for peptide identification <b>2021</b> , 2021, 99-103	1
513	Metabolic modulation of tumours with engineered bacteria for immunotherapy. <i>Nature</i> , <b>2021</b> , 598, 662- <u>6</u> 64	30
512	Proteomics with Enhanced In-Source Fragmentation/Annotation: Applying XCMS-EISA Informatics and Q-MRM High-Sensitivity Quantification. <b>2021</b> , 32, 2644-2654	1
511	Proteomic Analysis of the Functional Inward Rectifier Potassium Channel (Kir) 2.1 Reveals Several Novel Phosphorylation Sites. <b>2021</b> , 60, 3292-3301	O
510	Propargylic -adenosyl-l-selenomethionine: A Chemical Tool for Methylome Analysis. <b>2021</b> , 54, 3818-3827	1
509	The stereospecific interaction sites and target specificity of cGMP analogs in mouse cortex. 2021,	1
508	Single-molecule mechanical fingerprinting with DNA nanoswitch calipers. 2021,	3
507	Protein identification by nanopore peptide profiling. <b>2021</b> , 12, 5795	15
506	Qualitative lysine crotonylome analysis in the ovarian tissue of Harmonia axyridis (Pallas). <b>2021</b> , 16, e0258371	
505	Preface: Mass spectrometry in Alzheimer disease: This is the Preface for the special issue "Mass Spectrometry in Alzheimer Disease". <b>2021</b> , 159, 207-210	
504	Defining NASH from a Multi-Omics Systems Biology Perspective. <b>2021</b> , 10,	1
503	In-depth proteomic profiling captures subtype-specific features of craniopharyngiomas. <b>2021</b> , 11, 21206	О
502	Protein Interaction Mapping by Coprecipitation and Mass Spectrometric Identification. 2003, 295-300	
501	PROTEOMICS. <b>2004</b> , 1102-1109	
500	A Kernel-Based Case Retrieval Algorithm with Application to Bioinformatics. <b>2004</b> , 544-553	
499	An Automata Approach to Match Gapped Sequence Tags Against Protein Database. <b>2005</b> , 167-177	
498	Multi-Dimensional Protein Profiling Using LC/MS-Toward Clinical Proteomics 2005, 53, 108-116	1
497	Genomics, Proteomics, and Neurology. <b>2005</b> , 217-236	

MASS SPECTROMETRY | Multidimensional. 2005, 430-438 496 BloodBrain Barrier Genomics and Proteomics. 2005, 27-46 495 Proteomic Approaches to the Study of Rheumatoid Arthritis. 2005, 219-233 494 The Future of Cancer Diagnostics: Proteomics, Immunoproteomics, and Beyond. 2006, 1183-1192 493 Managing Data in High Throughput Laboratories: An Experience Report from Proteomics. 2006, 569-580 492 Protein microarrays for diagnosis and research of allergic diseases. 2006, 25, 221-225 491 Toxicogenomics and Toxicoproteomics. 2006, 849-868 490 A Grid Service Based on Suffix Trees for Pattern Extraction from Mass Spectrometry Proteomics 489 Data. 2006, 658-667 Genomic and Proteomic Medicine in Critical Care. 2006, 1434-1443 488 New Tricks for an Old Dog. 2006, 37-55 487 Informatics For Protein Identification by Tandem Mass Spectrometry; Focused on Two Most-widely 486 Applied Algorithms, Mascot and SEQUEST. 2006, 1, 88-93 Expression, Prediction and Function of the Thylakoid Proteome in Higher Plants and Green Algae. 485 **2007**, 125-143 Mass Spectrometry for Studying Protein Modifications and for Discovery of Protein Interactions. 484 2007, 143-167 Nanoprobe-Based Affinity Mass Spectrometry for Cancer Marker Protein Profiling. 483 Toxicogenomics in Ecological Risk Assessments: Regulatory Context, Technical Background, and 482 Workshop Overview. 2007, 29-40 481 Application of Genomics to Tiered Testing. 2007, 61-90 Application of Genomic, Proteomic, and Metabolomic Technologies to the Development of 480 Countermeasures against Chemical Warfare Agents. 2007, 149-170 Application of Genomic, Proteomic, and Metabolomic Technologies to the Development of Countermeasures against Chemical Warfare Agents. 2007,

Web-based resources for clinical bioinformatics. 2008, 141, 309-29 478 Capturing biotinylated proteins and peptides by avidin functional affinity electrophoresis. 2008, 418, 51-62 Regulation of Gene Expression. 2008, 149-190 476 Classification of Proteomic Signals by Block Kriging Error Matching. 2008, 281-288 475 Antibody-Based Proteomics Analysis of Tumor Cell Signaling Pathways. 2008, 117-134 474 Exploiting Provenance to Make Sense of Automated Decisions in Scientific Workflows. 2008, 174-185 473 Fundamentals of Cancer Genomics and Proteomics. 2008, 1925-1932 472 Biomarkers for Renal Disease and Uremic Toxins. 435-452 471 Quantitative Proteomics Using Nano-LC with High Accuracy Mass Spectrometry. 89-100 470 HPLC in Protein Discovery. 53-60 469 Applications of Stable Isotope Tagging Based Quantitative Proteomics in Cancer Research. 121-143 468 Pulmonary Proteomics. 323-347 467 466 Computer Aided Knowledge Discovery in Biomedicine. 2009, 126-141 Optimization-Based Peptide Mass Fingerprinting for Protein Mixture Identification. 2009, 16-30 465 Management and Analysis of Mass Spectrometry Proteomics Data on the Grid. 2009, 206-227 464 463 Functional Genomic of Arbuscular Mycorrhizal Symbiosis: Why and How Using Proteomics. 2009, 243-274 Computational Models for the Analysis of Modern Biological Data. 2009, 117-125 462 Biochips. 2009, 179-202 461

## (2011-2009)

460	Lab on a Chip. <b>2009</b> , 999-1016	
459	Eye: Proteomics.	
458	Multidimensional Techniques in Protein Separations for Neuroproteomics. <b>2009</b> , 25-49	
457	Methods for Multi-Stage Ion Processing Involving Ion/Ion Chemistry in a Quadrupole Linear Ion Trap. <b>2009</b> , 59-79	
456	Toxicogenomics in Risk Assessment.	
455	Introduction and Overview of Technological Advances and Predictive Assays. <b>2010</b> , 623-640	
454	Development of Dual Stable Isotope Labeling by Amino Acids in Cell Culture and Application to Quantitative Proteomics. <b>2010</b> , 58, 81-87	
453	Omics Technologies and Their Input for the Comprehension of Metabolic Systems Particularly Pertaining to Yeast Organisms. <b>2010</b> , 105-122	
452	Proteomics and Related Applications in Oral Cancer and Sjgren's Syndrome. <b>2010</b> , 17-28	
451	Indexing and Searching a Mass Spectrometry Database. <b>2010</b> , 62-76	1
450	Difference gel electrophoresis as a tool to discover stress-regulated proteins. <b>2010</b> , 639, 207-18	
449	Applications of Proteomics in Prostate Cancer. <b>2010</b> , 407-417	
448	Optic neuritis. <b>2010</b> , 278-288	
447	Mixture Model on Graphs: A Probabilistic Model for Network-Based Analysis of Proteomic Data. <b>2010</b> , 371-397	O
446	Capillary Separation Techniques. 1	
445	Peptidomics for Bioactive Peptide Analysis. 305-324	
444	Cryoelectron Tomography: Visualizing the Molecular Architecture of Cells.	
443	High Throughput Molecular Profiling Approaches for the Identifications of Genomic Alterations and Therapeutic Targets in Oral Cancer. <b>2011</b> , 431-452	

442	Proteomic and Biochemical Profiling of Aged Skeletal Muscle. <b>2011</b> , 259-287	О
441	Statistical Analysis of Spectral Count Data Generated by Label-Free Tandem Mass Spectrometry-Based Proteomics. <b>2011</b> , 297-309	
440	Proteomic Profiling of Hepatic Metastases: Paving the Way to Individualized Therapy. <b>2011</b> , 401-416	
439	. <b>2011</b> , 31, 99	4
438	Cancer Signaling Network Analysis by Quantitative Mass Spectrometry. <b>2011</b> , 55-75	
437	Introduction. <b>2011</b> , 285-287	
436	Data management in mass spectrometry-based proteomics. <b>2011</b> , 728, 321-32	1
435	[Application of mass spectrometry-based chromatographic technologies in the diagnosis of Alzheimer's disease]. <b>2011</b> , 29, 293-7	
434	Systems Biology <b>&amp;</b> n Overview. <b>2011</b> , 11-25	
433	Platelet Proteomics in Transfusion Medicine. 321-340	
432	Types of Sample and Experimental Planning. 11-39	
431	Methods and Approaches to Mass Spectroscopy-Based Protein Identification. 77-101	
430	Mass Spectrometry-Based Proteomics in Systems Toxicology.	1
429	Antibody Microarrays in Proteome Profiling. 219-243	
428	Proteomics in the Vitreous of Diabetic Retinopathy Patients. <b>2012</b> , 173-188	
427	Acoustic technology-assisted rapid proteolysis for high-throughput proteome analysis. <b>2011</b> , 24, 510-518	
426	Meat Science and Proteomics. <b>2012</b> , 330-355	
425	Computer Aided Knowledge Discovery in Biomedicine. <b>2012</b> , 1389-1403	_

Analytical Methodologies of Chitosan in Functional Foods. 2012, 513-544 424 Enhanced Ion Evaporation by Fast Gas Flow in Nano-Sonic Spray Ionization (nano-SSI). 2012, 60, 43-46 423 Comparative Analysis of Patenting Biotechnology Inventions in the U.S., Europe, Japan and China. 422 Neural Network-Based Method for Peptide Identification in Proteomics. 2012, 437-444 421 PROTEOMICS OF TEAR FLUID IN THYROID-ASSOCIATED ORBITOPATHY. 120605080134005 420 Challenges and Applications of Proteomics for Analysis of Changes in Early Postmortem Meat. 2013 419 , 103-109 418 Principles of Proteomic Approaches to the Cytoskeleton. 2013, 85-116 Methods and Progress of Mass Spectrometry-based Selected Reaction Monitoring\*. 2012, 39, 1118-1127 417 Clinical Translation of Protein Biomarkers Integrated with Bioinformatics. 2013, 295-308 416 Proteomics and Islet Research. 2013, 1-31 415 Proteomics and Metabolomics. 2013, 443-467 414 CHAPTER 11. Discovery and Validation Case Studies, Recommendations: Discovery and Development of Multimarker Panels for Improved Prediction of Near-Term Myocardial Infarction. 413 2013, 315-333 Peptidome analysis: tools and technologies. 2013, 172-202 412 Encyclopedia of Systems Biology. 2013, 220-231 411 INDIVIDUALIZATION OF CANCER TREATMENT: CONTRIBUTION OF OMICS TECHNOLOGIES TO 410 CANCER DIAGNOSTIC. 2013, 6, 105-117 Sensing via Quenching of Conjugated Polyelectrolyte Fluorescence. 169-200 409 References. 2013, 239-262 408 2DE analysis of forest tree proteins using fluorescent labels and multiplexing. 2014, 1072, 141-54 407

406	Proteomic Approaches to Toxicity Assessment. <b>2013</b> , 42-76
405	Proteomics in the Systems-Level Study of the Metabolic Syndrome. <b>2014</b> , 185-212
404	The Application of Omics Techniques for Cancers That Metastasise to Bone: From Biological Mechanism to Biomarkers. <b>2014</b> , 125-153
403	Introduction. <b>2014</b> , 1-6
402	Large-Scale Proteome and Phosphoproteome Quantification by Using Dimethylation Isotope Labeling. <b>2014</b> , 67-94
401	Chapter 11:Probe Electrospray Ionization. <b>2014</b> , 267-306
400	Encyclopedia of Psychopharmacology. <b>2014</b> , 1-8
399	CHAPTER 6:Overview and Implementation of Mass Spectrometry-Based Label-Free Quantitative Proteomics. <b>2014</b> , 129-153
398	Lecture 1 Introduction: Computer Science Meets Life Science. <b>2014</b> , 1-56
397	Systems-Wide Analysis of Protein Ubiquitylation: We Finally Have the Tiger by the Tail. <b>2014</b> , 367-391
396	Path Finding in Biological Networks. <b>2014</b> , 289-309
395	The Proteomics Toolbox Applied to Peroxisomes. <b>2014</b> , 275-301
394	MRCQuant: An Accurate LC-MS Relative Isotopic Quantifi cation Algorithm on TOF Instruments. <b>2014</b> , 365-394
393	Learning Genetic Epistasis Using Bayesian Network Scoring Criteria. <b>2014</b> , 263-292
392	Proteomics and Islet Research. 2015, 1131-1163
391	Recombinant Protein Techniques. <b>1996</b> , 385-430
390	Principles and Practice of DNA Microarray Technology. 978-994
389	A Simple Carbamidomethylation-Based Isotope Labeling Method for Quantitative Shotgun Proteomics. <b>2014</b> , 5, 63-69

388	Early Biomarkers in Breast Cancer. <b>2015</b> , 61-142
387	Fibrinogen Æhain as a Serum Marker of Liver Disease. <b>2015</b> , 1-20
386	Dual-Polarity Linear Ion Trap Femtosecond Laser-Induced Ionisation/Dissociation Mass Spectroscopy for Proteomics. <b>2015</b> ,
385	Novel Fish-derived Peptides Which Induce Vasorelaxation of Porcine Coronary Arteries. <b>2015</b> , 64, 101-107
384	An Approach for Matching Mixture MS/MS Spectra with a Pair of Peptide Sequences in a Protein Database. <b>2015</b> , 223-234
383	Verification of GM2 Activator Protein for Potential Application as Lung Cancer Biomarker. <b>2015</b> , 4, 280-287 1
382	Proteomics and Metaproteomics for Studying Probiotic Activity. 296-303
381	Chapter 10:Data Analysis for Data Independent Acquisition. <b>2016</b> , 200-228
380	An Effective Numerical Calculation Method for Multi-Time-Scale Mathematical Models in Systems Biology. <b>2016</b> , 07, 2241-2268
379	Proteomics and Metabolomics. <b>2016</b> , 400-433
378	Proteomics: Principles and Application in Microbiology of Prokaryotes. <b>2016</b> , 243-261
377	Towards comprehensive and quantitative proteomics for diagnosis and therapy of human disease. 2
376	Signalling maps in cancer research: construction and data analysis.
375	Matrix-Assisted Laser Desorption/Ionization. <b>2017</b> , 651-720
374	Development of Selected Reaction Monitoring Methods to Systematically Quantify Kinase Abundance and Phosphorylation Stoichiometry in Human Samples. <b>2017</b> , 1636, 353-369
373	Real-World Cases of Network Structure Analytics. <b>2017</b> , 229-280
372	Existence of Unprocessed a Mitochondrial Enzyme: YDL178wp in the Membrane Fraction as an Oligomeric Formation with a Protein-Unfolding Activity. <b>2017</b> , 4,
371	Quantitative Protein Topography Measurements by High Resolution Hydroxyl Radical Protein Footprinting Enable Accurate Molecular Model Selection.

370	Proteomics Approaches to Uncover the Drug Resistance Mechanisms of Microbial Biofilms. <b>2017</b> , 129-162
369	Evaluating Protein Complex Prediction Methods. <b>2017</b> , 91
368	Identifying Evolutionarily Conserved Protein Complexes. 2017, 165
367	Identifying Dynamic Protein Complexes. <b>2017</b> , 145
366	Introduction to Protein Complex Prediction. 2017, 1
365	Open Challenges in Protein Complex Prediction. <b>2017</b> , 107
364	Preface. <b>2017</b> , xi
363	References. <b>2017</b> , 233
362	Computational Methods for Protein Complex Prediction from PPI Networks. 2017, 59
361	Protein Complex Prediction in the Era of Systems Biology. <b>2017</b> , 185
360	Conclusion. <b>2017</b> , 225
359	Magnetoresistive biosensors for quantitative proteomics. 2017,
358	Eye: Proteomics. 1-13
357	ProteomeGenerator: A framework for comprehensive proteomics based on de novo transcriptome assembly and high-accuracy peptide mass spectral matching.
356	MALDI- <del>IIIII[C</del> 60] <del>IIIII   1</del> <del>IIII-</del> <b>2018</b> , 1105-1110
355	OBSOLETE: Proteomics. 2018,
354	Protein and Post Translational Modification in Asthma. <b>2018</b> , 103-121
353	Understanding the limit of open search in the identification of peptides with post-translational modifications 🖪 simulation-based study.

352	Unbiased Precision Estimation under Separate Sampling.	
351	Improving peptide-spectrum matching by fragmentation prediction using Hidden Markov Models.	
350	METHODOLOGICAL ASPECTS OF IDENTIFICATION OF TISSUE-SPECIFIC PROTEINS AND PEPTIDES FORMING THE CORRECTIVE PROPERTIES OF INNOVATIVE MEAT PRODUCTS. <b>2018</b> , 3, 36-55	2
349	Transcriptomics within the Exposome Paradigm. <b>2019</b> , 183-214	1
348	Screening a Resource of Recombinant Protein Fragments for Targeted Proteomics.	1
347	Rapid Proteomic Screen of CRISPR Experiment Outcome by Data Independent Acquisition Mass Spectrometry: A Case Study for HMGN1.	
346	Proteomics for Cancer: Approaches and Challenges. <b>2019</b> , 343-368	
345	Quantitative Analysis of Mass Spectrometry-Based Proteomics Data. <b>2019</b> , 129-142	O
344	Proteomics Approaches Applied to Regenerative Medicine: Perspectives in Stem Cell Proteomics. <b>2019</b> , 107-121	
343	Encyclopedia of Big Data Technologies. <b>2019</b> , 161-180	1
342	Informatics and Data Analytics to Support Exposome-Based Discovery. 2019, 744-787	
341	Parallel and Distributed Computing Methodologies in Bioinformatics. <b>2019</b> , 498-507	
340	Genomics, Proteomics, and Metabolomics for Stem Cells Monitoring in Regenerative Medicine. <b>2019</b> , 51-66	1
339	Application of Genomic, Proteomic, and Metabolomic Technologies to the Development of Countermeasures against Chemical Warfare Agents. <b>2019</b> , 523-537	
338	Transcription Regulatory Networks Analysis Using CAGE. <b>2019</b> , 153-168	
337	Selected Reaction Monitoring of Kinase Activity-Targeted Phosphopeptides. <b>2019</b> , 40, 39-47	2
336	SECAT: Quantifying differential protein-protein interaction states by network-centric analysis.	
335	An Accelerated Computational Approach in Proteomics. <b>2020</b> , 389-432	O

334 Detection and Evaluation of Biofilms. **2020**, 111-154

333	Human chorionic gonadotropin determination using mass spectrometry. <b>2020</b> , 123-138	
332	The scaffold protein IQGAP1 links heat-induced stress signals to alternative splicing regulation in gastric cancer cells.	0
331	Current Status and Future Prospects of Biomarker Strategy for Drug Development. <b>2020</b> , 51, 151-160	
330	Discovery of protein modifications using high resolution differential mass spectrometry proteomics.	
329	A Simple Optimization Workflow to Enable Precise and Accurate Imputation of Missing Values in Proteomic Datasets.	1
328	DeepLC can predict retention times for peptides that carry as-yet unseen modifications. <b>2021</b> , 18, 1363-1369	18
327	Proteomics and enriched biological processes in Antiphospholipid syndrome: A systematic review. <b>2021</b> , 20, 102982	1
326	Serum integrative omics reveals the landscape of human diabetic kidney disease. <b>2021</b> , 54, 101367	3
325	Meta-analysis of peptides to detect protein significance. <b>2020</b> , 13, 465-474	
324	Chapter 15:Canonical Phosphoproteomics: Phosphoserine, Phosphothreonine, and Phosphotyrosine. <b>2020</b> , 452-489	
323	New mixture models for decoy-free false discovery rate estimation in mass spectrometry proteomics. <b>2020</b> , 36, i745-i753	2
322	Proteomic Analysis of Pre-Invasive Serous Lesions of the Endometrium and Fallopian Tube Reveals Their Metastatic Potential. <b>2020</b> , 10, 523989	1
321	Accurate Prediction of Formylation PTM Site using Multiple Feature Fusion with LightGBM Resolving Data Imbalance Issue. <b>2020</b> ,	
320	Leveraging well-annotated databases for deep learning in biomedical research 2020, 9, 7682-7684	1
319	Mass spectrometry for human kinome analysis. <b>2022</b> , 191-216	O
318	An iterative and automated computational pipeline for untargeted strain-level identification using MS/MS spectra from pathogenic samples.	
317	Shotgun Proteomics of Plant Plasma Membrane and Microdomain Proteins Using Nano-LC-MS/MS. <b>2020</b> , 2139, 89-106	0

316	Selected Reaction Monitoring Mass Spectrometry. <b>2020</b> , 53-88	1
315	The Mass Spectrometer and Its Components. <b>2020</b> , 17-52	
314	Applications of mass spectrometry-based proteomics in archaeology and palaeoanthropology. <b>2020</b> , 128, 1-19	
313	Emerging biotechnological approaches with respect to tissue regeneration: from improving biomaterial incorporation to comprehensive omics monitoring. <b>2020</b> , 83-112	1
312	Defense Against Biological Terrorism: Vaccines and Their Characterizations. <b>2020</b> , 175-208	
311	Omics (Genomics, Proteomics, Metabolomics, Etc.) Tools to Study the Environmental Microbiome and Bioremediation. <b>2020</b> , 235-260	1
310	Mass spectrometry imaging in lipid and proteomic profiling: an emerging tool for cancer diagnosis. <b>2020</b> , 259-295	Ο
309	A regulatory interface on RIPK2 is required for XIAP binding and NOD signaling activity.	
308	Bayesian Network Marker Selection via the Thresholded Graph Laplacian Gaussian Prior. <b>2020</b> , 15, 79-102	6
307	Depletion of Highly Abundant Protein Species from Biosamples by the Use of a Branched Silicon Nanopillar On-Chip Platform. <b>2021</b> , 93, 14527-14536	O
306	Novel insights about albumin in cardiovascular diseases: Focus on heart failure. <b>2021</b> , e21743	2
305	Proteomics analysis of the gut-brain axis in a gut microbiota-dysbiosis model of depression. <b>2021</b> , 11, 568	6
304	Advances in integrative African genomics. 2021,	2
303	Distinct lipid profile, low-level inflammation and increased antioxidant defense as a signature in HIV-1 elite control status.	
302	TopPIC Gateway: A Web Gateway for Top-Down Mass Spectrometry Data Interpretation. 2020,	
301	Proteoforms in Acute Leukemia: Evaluation of Age- and Disease-Specific Proteoform Patterns.	O
300	Mining Protein Interactome Networks to Measure Interaction Reliability and Select Hub Proteins. 222-238	
299	Current Omics Technologies in Biomarker Discovery. 465-497	

298	Proteomics of Tobacco Bright Yellow-2 (BY-2) Cell Culture Plastids. <b>2006</b> , 313-326	
297	Proteomics and applications within the drug development pipeline. <b>2005</b> , 213-227	
296	Proteomics in the Investigation of Diabetic Nephropathy. <b>2006</b> , 255-275	
295	Differential Protein Expression, Protein Profiles of Human Gliomas, and Clinical Implications. <b>2007</b> , 149-173	
294	Methods for Protein-Protein Interaction Analysis. <b>2007</b> , 160-182	
293	Classification of Mass Spectrometry Based Protein Markers by Kriging Error Matching. <b>2008</b> , 82-94	Ο
292	Markov Additive Chains and Applications to Fragment Statistics for Peptide Mass Fingerprinting. <b>2006</b> , 29-41	1
291	A High-Throughput Bioinformatics Platform for Mass Spectrometry-Based Proteomics. <b>2007</b> , 71-88	
290	Services, Standards, and Technologies for High Performance Computational Proteomics. 2007, 404-413	
289	Mass Spectrometry Based Cancer Classification Using Fuzzy Fractal Dimensions. <b>2007</b> , 614-623	
288	Ionization and dissociation of benzene and aniline under deep ultraviolet laser irradiation. <b>2020</b> , 33, 583-589	О
288	Ionization and dissociation of benzene and aniline under deep ultraviolet laser irradiation. <b>2020</b> , 33, 583-589  Antibody Arrays: Barcode Technology. <b>2021</b> , 2237, 93-102	0
287	Antibody Arrays: Barcode Technology. <b>2021</b> , 2237, 93-102  Formative evaluation of a prototype system for automated analysis of mass spectrometry data.	0
287	Antibody Arrays: Barcode Technology. 2021, 2237, 93-102  Formative evaluation of a prototype system for automated analysis of mass spectrometry data. 2005, 241-5	3
287 286 285	Antibody Arrays: Barcode Technology. 2021, 2237, 93-102  Formative evaluation of a prototype system for automated analysis of mass spectrometry data. 2005, 241-5  Clinical proteomics: present and future prospects. 2006, 27, 99-116	o 3 50
287 286 285 284	Antibody Arrays: Barcode Technology. 2021, 2237, 93-102  Formative evaluation of a prototype system for automated analysis of mass spectrometry data. 2005, 241-5  Clinical proteomics: present and future prospects. 2006, 27, 99-116  Investigation of the human tear film proteome using multiple proteomic approaches. 2008, 14, 456-70	o 3 50 114

280	Mass spectrometry-based proteomics and peptidomics for biomarker discovery in neurodegenerative diseases. <b>2009</b> , 2, 132-48	10
279	Biomarker discovery in animal health and disease: the application of post-genomic technologies. <b>2007</b> , 2, 185-96	16
278	Methodology and applications of disease biomarker identification in human serum. 2007, 2, 21-43	18
277	Application of mass spectrometry-based proteomics for biomarker discovery in neurological disorders. <b>2009</b> , 12, 3-11	9
276	Transfusion medicine and proteomics. Alliance or coexistence?. <b>2010</b> , 8 Suppl 3, s16-25	1
275	The Profile of Human Sperm Proteome; A Mini-review. <b>2011</b> , 12, 193-9	11
274	The spectra count label-free quantitation in cancer proteomics. <b>2012</b> , 9, 135-42	14
273	Proteomic approaches for studying alcoholism and alcohol-induced organ damage. <b>2008</b> , 31, 36-48	3
272	Beyond laser microdissection technology: follow the yellow brick road for cancer research. <b>2014</b> , 4, 1-28	17
271	Update on current applications of proteomic in the study of inflammatory bowel disease. <b>2012</b> , 25, 303-308	2
270	Computational methods and opportunities for phosphorylation network medicine. <b>2014</b> , 3, 266-278	6
269	Cancer metabolism: what we can learn from proteomic analysis by mass spectrometry. <b>2012</b> , 9, 373-81	9
268	Molecular Aspects of Wound Healing and the Rise of Venous Leg Ulceration: Omics Approaches to Enhance Knowledge and Aid Diagnostic Discovery. <b>2017</b> , 38, 35-55	11
267	The Challenge of Human Spermatozoa Proteome: A Systematic Review. <b>2017</b> , 18, 267-279	6
266	Novel predication of protein biomarkers in interferon-gamma-stimulated breast cancer cells. <b>2019</b> , 13, 35-43	1
265	Plasma CAMK2A predicts chemotherapy resistance in metastatic triple negative breast cancer. <b>2018</b> , 11, 650-663	3
264	Serum proteomics study reveals candidate biomarkers for systemic lupus erythematosus. <b>2017</b> , 10, 10681-106	694
263	Hyphenated Mass Spectrometry versus Real-Time Mass Spectrometry Techniques for the Detection of Volatile Compounds from the Human Body. <b>2021</b> , 26,	O

262	Sampling and Sample Preparation in Bioanalysis. <b>2022</b> , 53-82	1
261	Proteoforms and their expanding role in laboratory medicine <b>2022</b> , 28, e00260	2
260	Introduction to Bioanalytical Mass Spectrometry. <b>2022</b> , 431-465	
259	Automated Multidimensional Nanoscale Chromatography for Ultrasensitive Targeted Mass Spectrometry. <b>2022</b> , 2393, 207-224	
258	Single-sample proteome enrichment enables missing protein recovery and phenotype association.	
257	15N metabolic labeling quantification workflow in Arabidopsis using Protein Prospector.	1
256	Analysis of Peptide Photofragmentation for Single-Molecule Protein Sequencing.	
255	Integrated proteomic and metabolomic analyses of the mitochondrial neurodegenerative disease MELAS <b>2022</b> ,	1
254	Uncovering the impacts of alternative splicing on the proteome with current omics techniques <b>2022</b> , e1707	2
253	Protein Sequencing, One Molecule at a Time <b>2022</b> ,	1
252	Targeted proteomics for the analysis of cultural heritage: application of broadband collision-induced dissociation mass spectrometry <b>2022</b> , 414, 1723	О
251	Gene Ontology GAN (GOGAN): a novel architecture for protein function prediction. 1	o
250	Delineation of altered brain proteins associated with furious rabies virus infection in dogs by quantitative proteomics <b>2021</b> , 104463	
249	Amperometric detection of tumor suppressor protein p53 via pencil graphite electrode for fast cancer diagnosis <b>2021</b> , 639, 114528	2
248	Chapitre 3. Mthodes et techniques d <b>E</b> ude du mtabolisme hergtique ^lexercice. <b>2017</b> , 33-60	
247	Biomedical applications of SRS microscopy in functional genetics and genomics. <b>2022</b> , 475-485	
246	A community challenge for a pancancer drug mechanism of action inference from perturbational profile data <b>2022</b> , 3, 100492	5
245	Developments, advancements, and contributions of mass spectrometry in omics technologies. <b>2022</b> , 327-356	O

244	Label-free visual proteomics: Coupling MS- and EM-based approaches in structural biology <b>2022</b> , 82, 285-303	3
243	Proteomics as a tool to gain next level insights into photo-crosslinkable biopolymer modifications <b>2022</b> , 17, 204-220	O
242	High-throughput technologies in probiotics science. <b>2022</b> , 77-101	
241	Proteomics based markers of clinical pain severity in juvenile idiopathic arthritis 2022, 20, 3	O
240	MSLibrarian: Optimized Predicted Spectral Libraries for Data-Independent Acquisition Proteomics <b>2022</b> ,	О
239	Emerging techniques in biological sciences. <b>2022</b> , 3-18	
238	Quantification of human plasma metalloproteins in multiple sclerosis, ischemic stroke and healthy controls reveals an association of haptoglobin-hemoglobin complexes with age <b>2022</b> , 17, e0262160	1
237	Advances in Proteomic and Metabolomic Profiling of Neurodegenerative Diseases <b>2021</b> , 12, 792227	1
236	SPEQ: Quality Assessment of Peptide Tandem Mass Spectra with Deep Learning 2022,	О
235	Mega-High-Throughput Screening Platform for the Discovery of Biologically Relevant Sequence-Defined Non-Natural Polymers <b>2022</b> , 8, 86-101	1
234	A Photosensitized Singlet Oxygen (O) Toolbox for Bio-Organic Applications: Tailoring O Generation for DNA and Protein Labelling, Targeting and Biosensing <b>2022</b> , 27,	О
233	Nano liquid chromatography, an updated review <b>2022</b> , e5317	2
232	Common Decoy Distributions Simplify False Discovery Rate Estimation in Shotgun Proteomics <b>2022</b> ,	2
231	Organic Residues Analysis (ORA) in Archaeology. <b>2022</b> , 1075-1119	1
230	Inorganic Matrices Assisted Laser Desorption/Ionization Mass Spectrometry for Metabolic Analysis in Bio-fluids <b>2021</b> ,	1
229	Multiplexed nanomaterial-assisted laser desorption/ionization for pan-cancer diagnosis and classification <b>2022</b> , 13, 617	6
228	An Immunoproteomic Survey of the Antibody Landscape: Insights and Opportunities Revealed by Serological Repertoire Profiling <b>2022</b> , 13, 832533	Ο
227	Absolute quantification of proteins using element mass spectrometry and generic standards <b>2022</b> , 256, 104499	1

226	Unraveling virus-induced cellular signaling cascades by label-free quantitative phosphoproteomics <b>2022</b> , 3, 101089	
225	Inverse Drug Discovery identifies weak electrophiles affording protein conjugates 2022, 67, 102113	1
224	Mass spectrometry-based analysis of IgG glycosylation and its applications. <b>2022</b> , 474, 116799	
223	A novel tyrosine hyperoxidation enables selective peptide cleavage <b>2022</b> , 13, 2753-2763	Ο
222	Calibr improves spectral library search for spectrum-centric analysis of data independent acquisition proteomics <b>2022</b> , 12, 2045	2
221	Application of Proteomics in Apical Periodontitis. 2022, 3,	O
220	Proteome analysis of the circadian clock protein PERIOD2 2022,	2
219	OMICS Applications for Medicinal Plants in Gastrointestinal Cancers: Current Advancements and Future Perspectives <b>2022</b> , 13, 842203	O
218	Proteome-wide analysis reveals molecular pathways affected by AgNP in a ROS-dependent manner <b>2022</b> , 1-15	О
217	SMAP is a pipeline for sample matching in proteogenomics <b>2022</b> , 13, 744	
216	Cataloguing the proteome: Current developments in single-molecule protein sequencing. <b>2022</b> , 3, 011304	О
215	Multi-omics approach in tea polyphenol research regarding tea plant growth, development and tea processing: current technologies and perspectives. <b>2022</b> , 11, 524-536	2
214	Redox Proteomics Analysis of Atherosclerotic Aortas: Application of the "OxICAT" Method <b>2022</b> , 2419, 629-644	
213	Mass spectrometry-based proteomics in neurodegenerative lysosomal storage disorders 2022,	
212	A New Tag Index Scheme Enables Fast Peptide Retrieval for Protein Identification. 2022, 10, 14-23	
211	Personalized nutrition. 2022,	
210	In Situ and Operando Techniques in Bioelectrochemistry. <b>2022</b> , 115-135	
209	N Metabolic Labeling Quantification Workflow in Arabidopsis Using Protein Prospector <b>2022</b> , 13, 832562	4

208	Protein Lipidation Types: Current Strategies for Enrichment and Characterization 2022, 23,	1
207	mzMD: Visualization Oriented MS Data Storage and Retrieval <b>2022</b> ,	
206	Strawberry Proteome Responses to Controlled Hot and Cold Stress Partly Mimic Post-harvest Storage Temperature Effects on Fruit Quality <b>2021</b> , 8, 812666	1
205	The structural context of PTMs at a proteome wide scale.	1
204	Microfluidic Point-of-Care (POC) Devices in Early Diagnosis: A Review of Opportunities and Challenges <b>2022</b> , 22,	10
203	Prioritized single-cell proteomics reveals molecular and functional polarization across primary macrophages.	3
202	Identification of carcinogenesis and tumor progression processes in pancreatic ductal adenocarcinoma using high-throughput proteomics.	
201	Microalgae Bioactive Carbohydrates as a Novel Sustainable and Eco-Friendly Source of Prebiotics: Emerging Health Functionality and Recent Technologies for Extraction and Detection <b>2022</b> , 9, 806692	O
200	A Shaving Proteomic Approach to Unveil Surface Proteins Modulation of Multi-Drug Resistant Strains Isolated From Cystic Fibrosis Patients <b>2022</b> , 9, 818669	0
199	Effect of Dietary Betaine on Muscle Protein Deposition, Nucleic Acid and Amino Acid Contents, and Proteomes of Broilers <b>2022</b> , 12,	
198	ReviewBrogress in Electroanalysis of p53, CEA, and CA19B. <b>2022</b> , 169, 037518	
197	Comprehensive spectral libraries for various rabbit eye tissue proteomes <b>2022</b> , 9, 111	O
196	The Interleukin-1 (IL-1) Superfamily Cytokines and Their Single Nucleotide Polymorphisms (SNPs) <b>2022</b> , 2022, 2054431	4
195	PyFragMS-A Web Tool for the Investigation of the Collision-Induced Fragmentation Pathways <b>2022</b> , 7, 9710-9719	O
194	VIQoR: a web service for Visually supervised protein Inference and protein Quantification 2022,	
193	Barrel Nanopores with an Acidic-Aromatic Sensing Region Identify Proteinogenic Peptides at Low pH <b>2022</b> ,	O
192	Mass spectrometric studies of the variety of beta-amyloid proteoforms in Alzheimer's disease <b>2022</b> , e21775	0
191	Robust co-immunoprecipitation with mass spectrometry for using solid-phase enhanced sample preparation <b>2022</b> ,	Ο

190	Using Artificial Intelligence to Better Predict and Develop Biomarkers <b>2022</b> , 18, 275-285	0
189	Peptide purity assignment for antibody quantification by combining isotope dilution mass spectrometry and liquid chromatography.	
188	6-Glycosylaminoquinoline-assisted LDI MS for detection and imaging of small molecules with enhanced detection selectivity and sensitivity <b>2022</b> , 1201, 339620	0
187	Exploring protein-protein interactions at the proteome level 2022,	1
186	Retention Time Prediction for TMT-Labeled Peptides in Proteomic LC-MS Experiments 2022,	O
185	Cross-linking and mass spectrometry as a tool for studying the structural biology of ribonucleoproteins <b>2022</b> ,	2
184	Comparative Proteomic Profiling of Secreted Extracellular Vesicles from Breast Fibroadenoma and Malignant Lesions: A Pilot Study <b>2022</b> , 23,	1
183	Label-free plasma proteomics for the identification of the putative biomarkers of oral squamous cell carcinoma <b>2022</b> , 104541	3
182	Highly bioactive iridium metal-complex alleviates spinal cord injury via ROS scavenging and inflammation reduction <b>2022</b> , 284, 121481	2
181	Statistical and machine learning methods to study human CD4 T cell proteome profiles <b>2022</b> , 245, 8-17	О
180	Integrated Proteomic and Metabolomic Analyses of the Mitochondrial Neurodegenerative Disease MELAS.	O
179	Plasma Proteomics Characteristics of Subclinical Vitamin E Deficiency of Dairy Cows During Early Lactation <b>2021</b> , 8, 723898	
178	Mass Spectrometry as a Crucial Analytical Basis for Omics Sciences. <b>2021</b> , 76, 1567-1587	1
177	Advances in Multi-Omics Approaches for Molecular Breeding of Black Rot Resistance in L <b>2021</b> , 12, 742553	O
176	Ultrasensitive Trace Sample Proteomics Unraveled the Protein Remodeling during Mesenchymal-Amoeboid Transition <b>2021</b> ,	2
175	Deephos: Predicted spectral database search for TMT-labeled phosphopeptides and its false discovery rate estimation <b>2022</b> ,	
174	Mass Spectrometry-Based Proteomics for Biomarker Discovery <b>2022</b> , 2486, 3-17	
173	Obtaining Complete Human Proteomes 2022,	Ο

## (2022-2007)

Expression, Prediction and Function of the Thylakoid Proteome in Higher Plants and Green Algae. 172 2007, 125-143 Focusing Target Discovery and Validation Through Proteogenomics and Molecular Imaging. 2005, 151-163 171 Table\_1.docx. 2020, 170 169 Table\_2.xlsx. 2020, 168 Data\_Sheet\_1.docx. 2019, DataSheet\_1.xlsx. 2020, 167 166 DataSheet\_2.docx. 2020, Image\_1.jpeg. 2020, 165 Image\_2.jpeg. 2020, 164 163 Image\_3.jpeg. 2020, Image\_4.jpeg. **2020**, 162 Presentation\_1.pdf. 2018, 161 Tear Proteomics of Children and Young Adult Soft Contact Lens, Orthokeratology and Spectacle 160 Wearers - A Pilot Study.. 2022, 1-11 Hollow Cathode Discharge Ionization Mass Spectrometry: Detection, Quantification and Gas Phase 159 Ion-Molecule Reactions of Explosives and Related Compounds.. 2022, 1-27 Application of proteomics to the study of polycystic ovary syndrome. 2011, 34, 869-75 6 158 Advances in agricultural bioinformatics: an outlook of multi Bmics approaches. 2022, 3-21 157 OUP accepted manuscript. 156 Microalgae potentials as bioactive phytochemicals for human's health: Novel highlights on their 155 production, applications, and emerging analytical technologies. 2022, 377-408

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

153	Proteomics in thrombosis research <b>2022</b> , 6, e12706	
152	Proteomic Investigation of Molecular Mechanisms in Response to PEG-Induced Drought Stress in Soybean Roots <b>2022</b> , 11,	1
151	Proteomic Approaches to Unravel Mechanisms of Antibiotic Resistance and Immune Evasion of Bacterial Pathogens <b>2022</b> , 9, 850374	O
150	SPIN enables high throughput species identification of archaeological bone by proteomics <b>2022</b> , 13, 2458	1
149	Prosit-TMT: Deep Learning Boosts Identification of TMT-Labeled Peptides 2022,	1
148	Identification of Carcinogenesis and Tumor Progression Processes in Pancreatic Ductal Adenocarcinoma Using High-Throughput Proteomics. <b>2022</b> , 14, 2414	
147	Cancer-related micropeptides encoded by ncRNAs: Promising drug targets and prognostic biomarkers <b>2022</b> , 215723	O
146	The Integration of Proteomics and Metabolomics Data Paving the Way for a Better Understanding of the Mechanisms Underlying Microbial Acquired Drug Resistance. <b>2022</b> , 9,	1
145	Protein-protein interaction networks as miners of biological discovery <b>2022</b> , e2100190	2
144	Proteomic Analysis of Human Neural Stem Cell Differentiation by SWATH-MS 2022,	
143	The structural context of posttranslational modifications at a proteome-wide scale <b>2022</b> , 20, e3001636	8
142	Formation of Gaseous Peptide Ions from Electrospray Droplets: Competition between the Ion Evaporation Mechanism and Charged Residue Mechanism <b>2022</b> ,	1
141	Automating Assignment, Quantitation, and Biological Annotation of Redox Proteomics Datasets with ProteoSushi. <b>2022</b> , 61-84	
140	Xlink Mapping and AnalySis (XMAS) - Smooth Integrative Modeling in ChimeraX.	1
139	Mapping the O-GlcNAc Modified Proteome: Applications for Health and Disease. <b>2022</b> , 9,	1
138	A New Strategy for High-Efficient Tandem Enrichment and Simultaneous Profiling of N-Glycopeptides and Phosphopeptides in Lung Cancer Tissue. <b>2022</b> , 9,	
137	Trapped Ion Mobility Spectrometry, Ultraviolet Photodissociation, and Time-of-Flight Mass Spectrometry for Gas-Phase Peptide Isobars/Isomers/Conformers Discrimination.	1

136	Advances in high-resolution mass spectrometry techniques for analysis of high mass-to-charge ions.	1
135	Multiple and Single Reaction Monitoring Mass Spectrometry for Absolute Quantitation of Proteins.	
134	A streamlined platform for analyzing tera-scale DDA and DIA mass spectrometry data enables highly sensitive immunopeptidomics. <b>2022</b> , 13,	О
133	A perspective toward mass spectrometry-based de novo sequencing of endogenous antibodies. <b>2022</b> , 14,	1
132	Integrated multi-omics analyses reveals molecules governing sperm metabolism potentially influence bull fertility. <b>2022</b> , 12,	1
131	The Redox State of Serum Albumin as a Potential Protein Nutrition Biomarker. <b>2022</b> , 1-20	
130	Co-immunoprecipitation of Protein Complexes from Different Subcellular Compartments in Vasculogenic Mimicry Studies. <b>2022</b> , 61-72	
129	Omics Perspective: Molecular Blueprint for Agrochemical Bioremediation Process in the Environment. <b>2022</b> , 585-608	O
128	High sensitivity limited material proteomics empowered by data-independent acquisition on linear ion traps.	0
127	Peptidomic Approaches and Observations in Neurodegenerative Diseases. <b>2022</b> , 23, 7332	
126	Engineered Serum Markers for Noninvasive Monitoring of Gene Expression in the Brain.	
125	Rapid Multivariate Analysis Approach to Explore Differential Spatial Protein Profiles in Tissue.	O
124	A review of suspension trapping digestion method in bottom-up proteomics.	3
123	Consensus draft of the native mouse podocyte-ome.	O
122	Uncovering Hidden Members and Functions of the Soil Microbiome Using De Novo Metaproteomics.	О
121	Leveraging Systems Immunology to Optimize Diagnosis and Treatment of Inborn Errors of Immunity. 2,	
120	Seamlessly Integrated Miniaturized Filter-Aided Sample Preparation Method to Fractionation Techniques for Fast, Loss-Less, and In-Depth Proteomics Analysis of 1 g of Cell Lysates at Low Cost. <b>2022</b> , 94, 10135-10141	1
119	Protocol for establishing a protein-protein interaction network using tandem affinity purification followed by mass spectrometry in mammalian cells. <b>2022</b> , 3, 101569	0

118	Defining the Role of Mass Spectrometry in Cancer Diagnostics. <b>2004</b> , 13, 1555-1557	4
117	Application of quantitative proteomics to investigate fruit ripening and eating quality. <b>2022</b> , 153766	Ο
116	Locality-sensitive hashing enables efficient and scalable signal classification in high-throughput mass spectrometry raw data. <b>2022</b> , 23,	
115	Proteome-Based Clustering Approaches Reveal Phylogenetic Insights into Amphistegina.	
114	Plasma Protein Profiling by Mass Spectrometry for Cancer Diagnosis: Opportunities and Limitations. <b>2005</b> , 11, 963-965	22
113	Proteomic Discovery and Validation of Novel Fluid Biomarkers for Improved Patient Selection and Prediction of Clinical Outcomes in Alzheimer Disease Patient Cohorts. <b>2022</b> , 10, 26	Ο
112	High-throughput mass spectrometry maps the sepsis plasma proteome and differences in response.	1
111	Levels of IL-23/IL-17 Axis in Plasma and Gingival Tissue of Periodontitis Patients According to the New Classification. <b>2022</b> , 12, 8051	
110	Molecular formula discovery via bottom-up MS/MS interrogation.	
109	Integrative modeling of the cell. 2022,	
108	Spectral Library-Based Single-Cell Proteomics Resolves Cellular Heterogeneity. <b>2022</b> , 11, 2450	1
108	Spectral Library-Based Single-Cell Proteomics Resolves Cellular Heterogeneity. 2022, 11, 2450  Ultrafast analysis of peptides by laser diode thermal desorption per quadrupole mass spectrometry. 2022, 36,	1
	Ultrafast analysis of peptides by laser diode thermal desorption <b>E</b> riple quadrupole mass	1
107	Ultrafast analysis of peptides by laser diode thermal desorption <b>E</b> riple quadrupole mass spectrometry. <b>2022</b> , 36,	1 0
107	Ultrafast analysis of peptides by laser diode thermal desorption riple quadrupole mass spectrometry. 2022, 36,  Molecular formula discovery via bottom-up MS/MS interrogation.	
107 106 105	Ultrafast analysis of peptides by laser diode thermal desorption riple quadrupole mass spectrometry. 2022, 36,  Molecular formula discovery via bottom-up MS/MS interrogation.  Gene Ontology Capsule GAN: an improved architecture for protein function prediction. 8, e1014	
107 106 105	Ultrafast analysis of peptides by laser diode thermal desorptionEriple quadrupole mass spectrometry. 2022, 36,  Molecular formula discovery via bottom-up MS/MS interrogation.  Gene Ontology Capsule GAN: an improved architecture for protein function prediction. 8, e1014  Evaluation and minimization of over-alkylation in proteomic sample preparation. 2022, 481, 116919	

100	Challenges and opportunities in healthcare biotechnology. 2022, 321-342	О
99	Twins and omics: the role of twin studies in multi-omics. <b>2022</b> , 547-584	О
98	Quantitative Mass Spectrometry by SILAC in Haloferax volcanii. 2022, 255-266	O
97	Dissecting Lipopolysaccharide Composition and Structure by GC-MS and MALDI Spectrometry. <b>2022</b> , 181-209	1
96	Role of DmicsDpproaches in sustainable development and improvement of oil palm (Elaeis guineensis Jacq). <b>2022</b> , 205-214	0
95	Research Progress of Protein-Protein Interaction Based on Liquid Chromatography Mass Spectrometry?. <b>2022</b> , 80, 817	O
94	Useful methods to study epigenetic marks: DNA methylation, histone modifications, chromatin structure, and noncoding RNAs. <b>2022</b> , 283-310	0
93	Tear proteomic analysis of young glasses, orthokeratology, and soft contact lens wearers. <b>2023</b> , 270, 104738	O
92	Nanohydrophobic Interaction Chromatography Coupled to Ultraviolet Photodissociation Mass Spectrometry for the Analysis of Intact Proteins in Low Charge States. <b>2022</b> , 21, 2493-2503	1
91	Addressing the Protease Bias in Quantitative Proteomics. <b>2022</b> , 21, 2526-2534	O
90	Molecular biomarkers for gestational diabetes mellitus and postpartum diabetes. Publish Ahead of Print,	1
89	Chemoselective labeling and immobilization of phosphopeptides with phosphorimidazolide reagents.	O
88	Proteomics-based mass spectrometry profiling of SARS-CoV-2 infection from human nasopharyngeal samples.	О
87	CEMS Methods for the Characterization of Monoclonal Antibodies. <b>2022</b> , 281-312	O
86	The Redox State of Serum Albumin as a Potential Protein Nutrition Biomarker. 2022, 47-66	0
85	Genetic Engineering Strategies and Degradation of Pollutants Using Genetically Engineered Microorganisms (GEMs). <b>2022</b> , 209-232	O
84	On the potential of micro-flow LC-MS/MS in proteomics. <b>2022</b> , 19, 153-164	0
83	Quartet protein reference materials and datasets for multi-platform assessment of label-free proteomics.	O

82	Capillary Vibrating Sharp-Edge Spray Ionization Augments Field-Free Ionization Techniques to Promote Conformer Preservation in the Gas-Phase for Intractable Biomolecular Ions.	O
81	Radiation-Induced Intestinal Normal Tissue Toxicity: Implications for Altered Proteome Profile. <b>2022</b> , 13, 2006	O
80	Processes in DNA damage response from a whole-cell multi-omics perspective. <b>2022</b> , 25, 105341	O
79	Recent advances in the field of single-cell proteomics. <b>2023</b> , 27, 101556	1
78	Overview and considerations in bottom-up proteomics.	2
77	Integrated top-down and bottom-up proteomics mass spectrometry for the characterization of endogenous ribosomal protein heterogeneity. <b>2022</b> ,	O
76	Pattern Recognition for Mass-Spectrometry-Based Proteomics.	O
75	The utility of proteases in proteomics, from sequence profiling to structure and function analysis. 2200132	2
74	Using SILAC to Develop Quantitative Data-Independent Acquisition (DIA) Proteomic Methods. <b>2023</b> , 245-257	O
73	Free Radical-Based Sequencing for Native Top-Down Mass Spectrometry.	O
72	Mass Spectrometry-based Methodologies for Studying Proteolytic Networks and the Degradome. <b>2016</b> , 396-410	O
71	Cross-Linking Mass Spectrometry Data Analysis. <b>2022</b> , 339-370	O
70	Biological Sequence Classification: A Review on Data and General Methods. <b>2022</b> , 2022,	2
69	A DISTRIBUTED ALGORITHM FOR PROTEIN IDENTIFICATION FROM TANDEM MASS SPECTROMETRY DATA. <b>2022</b> , 18, 16-27	O
68	Exploring the cardiac ECM during fibrosis: A new era with next-gen proteomics. 9,	1
67	Identifying Protein Haplotypes by Mass Spectrometry.	O
66	Middle-Down Mass Spectrometry Reveals Activity-Modifying Phosphorylation Barcode in a Class C G Protein-Coupled Receptor. <b>2022</b> , 144, 23104-23114	1
65	Proteomic Comparison of Three Wild-Type Pseudorabies Virus Strains and the Attenuated Bartha Strain Reveals Reduced Incorporation of Several Tegument Proteins in Bartha Virions. <b>2022</b> , 96,	O

64	Challenges and opportunities for omics-based precision medicine in chronic low back pain.	O
63	Systematic comparison of modeling fidelity levels and parameter inference settings applied to negative feedback gene regulation. <b>2022</b> , 18, e1010683	0
62	A review of sensors for classification and subtype discrimination of cancer: Insights into circulating tumor cells and tumor-derived extracellular vesicles. <b>2022</b> , 340703	О
61	Interrogation of an ovine serum peptide spectral library to annotate ambiguous clinicopathological biomarkers using data-independent acquisition. 11, 1433	0
60	Proteomic Portrait of Human Lymphoma Reveals Protein Molecular Fingerprint of Disease Specific Subtypes and Progression.	0
59	Protein adsorption by nanomechanical mass spectrometry: Beyond the real-time molecular weighting. 9,	3
58	Achieving a deeper understanding of drug metabolism and responses using single cell technologies. DMD-MR-2022-001043	0
57	Top-Down Mass Spectrometry of Synthetic Single Guide Ribonucleic Acids Enabled by Facile Sample Clean-Up.	o
56	Bynuclein as a potential biomarker for developing diagnostic tools against neurodegenerative disorders. <b>2023</b> , 116922	0
55	The Need for Biomarkers in the ALSETD Spectrum: A Clinical Point of View on the Role of Proteomics. <b>2023</b> , 11, 1	o
54	Deep learning prediction boosts phosphoproteomics-based discoveries through improved phosphopeptide identification.	O
53	Differentiated extracts from freshwater and terrestrial mollusks inhibit virulence factor production in Cryptococcus neoformans.	o
52	High Sensitivity Top-down Proteomics Captures Single Muscle Cell Heterogeneity in Large Proteoforms.	0
51	Microbial Proteomics. <b>2019</b> , 103-138	o
50	Omics Approaches for Microalgal Applications in Wastewater Treatment. <b>2023</b> , 143-156	0
49	Characterization and Quantification of Mal d 1 Isoallergen Profiles and Contents in Traditional and Commercial Apple Varieties by Mass Spectrometry. <b>2023</b> , 71, 2554-2565	О
48	An Isobaric Labeling Approach to Enhance Detection and Quantification of Tissue-Derived Plasma Proteins as Potential Early Disease Biomarkers. <b>2023</b> , 13, 215	O
47	MS Ana: Improving Sensitivity in Peptide Identification with Spectral Library Search. <b>2023</b> , 22, 462-470	O

46	May Big Data Analysis be Used to Diagnose Early Autism?.	O
45	Charge-State-Dependent Collision-Induced Dissociation Behaviors of RNA Oligonucleotides via High-Resolution Mass Spectrometry.	o
44	Analysis of affinity purification-related proteomic data for studying proteinprotein interaction networks in cells.	0
43	Automating the design-build-test-learn cycle towards next-generation bacterial cell factories. <b>2023</b> , 74, 1-15	O
42	Proteoforms expand the world of microproteins and short open reading frame-encoded peptides. <b>2023</b> , 26, 106069	0
41	Absolute Quantitative Targeted Proteomics Assays for Plasma Proteins. 2023, 439-473	O
40	Prioritized mass spectrometry increases the depth, sensitivity and data completeness of single-cell proteomics.	0
39	Identification of a novel amphioxus leucine-rich repeat receptor involved in phagocytosis reveals a role for Slit2-N-type LRR in bacterial elimination. <b>2023</b> , 104689	o
38	NULISA: a novel proteomic liquid biopsy platform with attomolar sensitivity and high multiplexing.	O
37	Oleaginous Red Yeasts: Concomitant Producers of Triacylglycerides and Carotenoids. <b>2023</b> , 3, 490-500	o
36	Proteins and Proteomics. <b>2021</b> , 123-154	0
35	The isotope distribution: A rose with thorns.	1
34	Mass Spectrometry, Protein Interaction and Amalgamation of Bioinformatics. 2023, 77-93	0
33	Using Artificial Intelligence to Better Predict and Develop Biomarkers. <b>2023</b> , 43, 99-114	O
32	Bioinformatics Tools and Knowledgebases to Assist Generating Targeted Assays for Plasma Proteomics. <b>2023</b> , 557-577	0
31	Benchmarking Bioinformatics Pipelines in Data-Independent Acquisition Mass Spectrometry for Immunopeptidomics. <b>2023</b> , 22, 100515	O
30	Towards multiomic analysis of oral mucosal pathologies.	0
29	Network-based elucidation of colon cancer drug resistance by phosphoproteomic time-series analysis.	О

28	Contribution of Proteomics in Transplantation: Identification of Injury and Rejection Markers. Publish Ahead of Print,	1
27	P-Massive: A Real-Time Search Engine for a Multi-Terabyte Mass Spectrometry Database. <b>2022</b> ,	O
26	Challenges and Opportunities for Single-cell Computational Proteomics. 2023, 22, 100518	О
25	Proteomic profiling and its applications in cancer research. 2023, 121-153	O
24	Applications of mass spectroscopy in understanding cancer proteomics. <b>2023</b> , 179-204	0
23	Proteomics: Application of next-generation proteomics in cancer research. 2023, 55-76	O
22	Proteomics: A modern tool for identifying therapeutic targets in different types of carcinomas. <b>2023</b> , 333-362	О
21	Realization of Arithmetic Operations using a Combined Computational Unit in Ribosomal Computing. <b>2023</b> , 104, 461-473	O
20	Quality Control <b>A</b> Stepchild in Quantitative Proteomics: A Case Study for the Human CSF Proteome. <b>2023</b> , 13, 491	О
19	Mass spectrometry imaging in Alzheimer disease.	Ο
18	The GlycoPaSER prototype as a real-time N-glycopeptide identification tool based on the PaSER parallel computing platform.	O
17	PROSE: phenotype-specific network signatures from individual proteomic samples. <b>2023</b> , 24,	O
17 16	PROSE: phenotype-specific network signatures from individual proteomic samples. 2023, 24,  LC-MS/MS: A sensitive and selective analytical technique to detect COVID-19 protein biomarkers in the early disease stage. 1-14	0
	LC-MS/MS: A sensitive and selective analytical technique to detect COVID-19 protein biomarkers in	
16	LC-MS/MS: A sensitive and selective analytical technique to detect COVID-19 protein biomarkers in the early disease stage. 1-14	0
16 15	LC-MS/MS: A sensitive and selective analytical technique to detect COVID-19 protein biomarkers in the early disease stage. 1-14  ProInfer: An interpretable protein inference tool leveraging on biological networks. 2023, 19, e1010961	0
16 15 14	LC-MS/MS: A sensitive and selective analytical technique to detect COVID-19 protein biomarkers in the early disease stage. 1-14  ProInfer: An interpretable protein inference tool leveraging on biological networks. 2023, 19, e1010961  Biomarkers. 2013, 165-175.e3	0 0

10	Recent Advances in Top-Down Proteomics for Proteoform Analysis. 2023, 38, 12-20	О
9	Integrative proteomic and phosphoproteomic analysis in the female goat hypothalamus to study the onset of puberty.	O
8	An automated proximity proteomics pipeline for subcellular proteome and protein interaction mapping.	0
7	BUDDY: molecular formula discovery via bottom-up MS/MS interrogation.	O
6	Progress in Top-Down LC-MS Analysis of Antibodies: Review. <b>2023</b> , 28, 226-233	0
5	An overview of diagnostic evaluation of parasitic diseases of dogs and cats. <b>2023</b> , 297-332	0
4	The GlycoPaSER Prototype as a Real-Time N-Glycopeptide Identification Tool Based on the PaSER Parallel Computing Platform. <b>2023</b> , 24, 7869	O
3	Targeting Protein <b>P</b> rotein Interfaces with Peptides: The Contribution of Chemical Combinatorial Peptide Library Approaches. <b>2023</b> , 24, 7842	O
2	Ultra-High-Throughput and Low-Volume Analysis of Intact Proteins with LAP-MALDI MS.	0
1	Oxiforms: Unique cysteine residue- and chemotype-specified chemical combinations can produce functionally-distinct proteoforms.	O