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Identification of proteins in polyacrylamide gels by mass spectrometric peptide mapping combined with database search

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132	Progress with gene-product mapping of the Mollicutes: <i>Mycoplasma genitalium</i> . <b>1995</b> , 16, 1090-4		727
131	Matrix-assisted laser-desorption/ionization mass spectrometric approaches for the identification of gel-separated proteins in the 5-50 pmol range. <b>1995</b> , 16, 1104-14		79
130	Mass spectrometric approaches for the identification of gel-separated proteins. <b>1995</b> , 16, 1791-814		361
129	Cross-species identification of proteins separated by two-dimensional gel electrophoresis using matrix-assisted laser desorption ionisation/time-of-flight mass spectrometry and amino acid composition. <b>1995</b> , 16, 438-43		121
128	Sequencing electroblotted proteins by tandem mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , <b>1995</b> , 9, 1051-5	2.2	30
127	Evaluation of mass spectrometric techniques for characterization of engineered proteins. <b>1995</b> , 4, 1-12		14
126	Limited and defined truncation at the C terminus enhances receptor binding and degranulation activity of the neutrophil-activating peptide 2 (NAP-2). Comparison of native and recombinant NAP-2 variants. <b>1995</b> , 270, 6338-44		19
125	Matrix-assisted laser desorption/ionization mass spectrometry (MALDI-MS). <b>1995</b> , 5, 691-8		93
124	Mass spectrometry of proteins directly from polyacrylamide gels. <b>1996</b> , 68, 1910-7		86
123	Mass spectrometry. <b>1996</b> , 68, 599R-651R		162
122	Towards a Comprehensive Database of Proteins From the Urine of Patients With Bladder Cancer. <i>Journal of Urology</i> , <b>1996</b> , 155, 2113-2119	2.5	105
121	Sequence tag identification of intact proteins by matching tandem mass spectral data against sequence data bases. <b>1996</b> , 93, 8264-7		197
120	Interfacing polyacrylamide gel electrophoresis with mass spectrometry. <b>1996</b> , 305-313		4
119	Direct isolation of proteins from sodium dodecyl sulfate-polyacrylamide gel electrophoresis and analysis by electrospray-ionization mass spectrometry. <b>1996</b> , 17, 848-54		45
118	Mass spectrometric characterization of glycosylated interferon-gamma variants separated by gel electrophoresis. <b>1996</b> , 17, 925-31		68
117	9. Matrix-Assisted Laser Desorption and Ionization. <b>1997</b> , 30, 413-448		
116	Diffusive transfer to membranes as an effective interface between gel electrophoresis and mass spectrometry. <b>1997</b> , 169-170, 273-290		8

115	Identification of mouse liver proteins on two-dimensional electrophoresis gels by matrix-assisted laser desorption/ionization mass spectrometry of in situ enzymatic digests. <b>1997</b> , 18, 349-59	209
114	Sensitivity and mass accuracy for proteins analyzed directly from polyacrylamide gels: implications for proteome mapping. <b>1997</b> , 18, 382-90	64
113	Rapid mass spectrometric identification of proteins from two-dimensional polyacrylamide gels after in gel proteolytic digestion. <b>1997</b> , 18, 391-402	78
112	Identification of two-dimensional gel electrophoresis resolved yeast proteins by matrix-assisted laser desorption ionization mass spectrometry. <b>1997</b> , 18, 418-23	32
111	A two-dimensional gel database of human colon carcinoma proteins. <b>1997</b> , 18, 605-13	51
110	Proteome research: complementarity and limitations with respect to the RNA and DNA worlds. <b>1997</b> , 18, 1217-42	196
109	Proteome analysis of <i>Spiroplasma melliferum</i> (A56) and protein characterisation across species boundaries. <b>1997</b> , 18, 1335-46	46
108	Characterisation of basic proteins from <i>Spiroplasma melliferum</i> using novel immobilised pH gradients. <b>1997</b> , 18, 1393-8	34
107	Peptide-mass fingerprinting and the ideal covering set for protein characterisation. <b>1997</b> , 18, 1399-409	20
106	Evaluation of algorithms used for cross-species proteome characterisation. <b>1997</b> , 18, 1410-7	24
105	Protein identification from 2-DE gels by MALDI mass spectrometry. <b>1997</b> , 16, 145-62	136
104	Characterisation of bacterial proteomes by two-dimensional electrophoresis. <b>1998</b> , 372, 121-145	45
103	Protein identification using mass spectrometric information. <b>1998</b> , 19, 998-1005	186
102	One step microelectroelution concentration method for efficient coupling of sodium dodecylsulfate gel electrophoresis and matrix-assisted laser desorption time-of-flight mass spectrometry for protein analysis. <i>Journal of the American Society for Mass Spectrometry</i> , <b>1998</b> , 9, 88-91	3.5 29
101	On-line dual microdialysis with ESI-MS for direct analysis of complex biological samples and microorganism lysates. <b>1998</b> , 70, 1797-801	73
100	Identifying proteins using matrix-assisted laser desorption/ionization in-source fragmentation data combined with database searching. <b>1998</b> , 70, 673-83	96
99	Automation of data collection for matrix-assisted laser desorption/ionization mass spectrometry using a correlative analysis algorithm. <b>1998</b> , 70, 3213-9	17
98	Mass spectrometry. <b>1998</b> , 70, 647R-716R	185

97	Mass spectrometric mapping of ion channel proteins (porins) and identification of their supramolecular membrane assembly. <b>1998</b> , 33, 63-73		20
96	A novel protein modification pathway related to the ubiquitin system. <b>1998</b> , 17, 2208-14		286
95	Proteome in perspective. <b>1998</b> , 36, 825-36		59
94	Current Problems and Technical Solutions in Protein Biochemistry. <b>1998</b> , 3-120		6
93	Direct monitoring of protein-chemical reactions utilising nanoelectrospray mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , <b>1999</b> , 10, 112-8	3.5	31
92	Observation of gel-induced protein modifications in sodium dodecylsulfate [corrected] polyacrylamide gel electrophoresis and its implications for accurate molecular weight determination of gel-separated proteins by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , <b>1999</b> , 10, 512-20	3.5	36
91	Protein analysis using enzymes immobilized to paramagnetic beads. <b>1999</b> , 274, 153-62		76
90	Analysis of intact proteins from cerebrospinal fluid by matrix-assisted laser desorption/ionization mass spectrometry after two-dimensional liquid-phase electrophoresis. <i>Rapid Communications in Mass Spectrometry</i> , <b>1999</b> , 13, 2450-5	2.2	15
89	Identification of a heparin-binding region of rat thyroglobulin involved in megalin binding. <b>1999</b> , 274, 30377-86		29
88	A novel ubiquitination factor, E4, is involved in multiubiquitin chain assembly. <b>1999</b> , 96, 635-44		819
87	Characterization of proteins from human cerebrospinal fluid by a combination of preparative two-dimensional liquid-phase electrophoresis and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <b>1999</b> , 71, 642-7		49
86	Direct profiling of proteins in biological tissue sections by MALDI mass spectrometry. <b>1999</b> , 71, 5263-70		253
85	A method for application of samples to matrix-assisted laser desorption/ionization time-of-flight targets that enhances peptide detection. <b>2000</b> , 279, 1-8		77
84	Two-dimensional electrophoresis and mass spectrometry identification of proteins bound by a murine monoclonal anti-cardiolipin antibody: a powerful technique to characterize the cross-reactivity of a single autoantibody. <b>2000</b> , 21, 2531-9		9
83	Identification of proteins from human cerebrospinal fluid, separated by two-dimensional polyacrylamide gel electrophoresis. <b>2000</b> , 21, 2721-8		88
82	Use of non-porous reversed-phase high-performance liquid chromatography for protein profiling and isolation of proteins induced by temperature variations for Siberian permafrost bacteria with identification by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry and capillary electrophoresis-electrospray ionization mass spectrometry. <b>2000</b> , 748, 167-77		21
81	Identifying the proteome: software tools. <b>2000</b> , 11, 391-5		123
80	Database searching with mass-spectrometric information. <b>2000</b> , 18, 22-27		4

79	Cardiac phospholipase D2 localizes to sarcolemmal membranes and is inhibited by alpha-actinin in an ADP-ribosylation factor-reversible manner. <b>2000</b> , 275, 21295-301	99
78	Purification and molecular cloning of a novel essential component of the apolipoprotein B mRNA editing enzyme-complex. <b>2000</b> , 275, 19848-56	136
77	A statistical basis for testing the significance of mass spectrometric protein identification results. <b>2000</b> , 72, 999-1005	110
76	Probing the stoichiometry and oxidation states of metal centers in iron-sulfur proteins using electrospray FTICR mass spectrometry. <b>2000</b> , 72, 1410-8	64
75	THE CHARACTERIZATION OF CONOTOXINS. <b>2000</b> , 19, 53-93	22
74	Towards functional proteomics of membrane protein complexes: analysis of thylakoid membranes from <i>Chlamydomonas reinhardtii</i> . <b>2001</b> , 28, 595-606	136
73	Proteome analysis of a human hepatocellular carcinoma cell line, HCC-M: an update. <b>2001</b> , 22, 2804-11	30
72	Proteomics based on selecting and quantifying cysteine containing peptides by covalent chromatography. <b>2001</b> , 924, 345-57	102
71	Application of a novel protein biochip technology for detection and identification of rheumatoid arthritis biomarkers in synovial fluid. <b>2002</b> , 1, 495-9	90
70	Combined in-gel tryptic digestion and CNBr cleavage for the generation of peptide maps of an integral membrane protein with MALDI-TOF mass spectrometry. <b>2002</b> , 1555, 111-5	44
69	Sub-proteome differential display: single gel comparison by 2D electrophoresis and mass spectrometry. <b>2002</b> , 318, 21-31	19
68	Proteomics in experimental gerontology. <b>2002</b> , 37, 721-34	25
67	Direct profiling and imaging of peptides and proteins from mammalian cells and tissue sections by mass spectrometry. <b>2002</b> , 23, 3125-35	194
66	Precalibration of matrix-assisted laser desorption/ionization-time of flight spectra for peptide mass fingerprinting. <i>Proteomics</i> , <b>2002</b> , 2, 1365-73	4.8 38
65	Identification and sequencing analysis of intact proteins via collision-induced dissociation and quadrupole time-of-flight mass spectrometry. <b>2002</b> , 37, 270-82	48
64	Improved in-gel approaches to generate peptide maps of integral membrane proteins with matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <b>2002</b> , 37, 322-30	69
63	Structure and functional characterization of the periplasmic N-terminal polypeptide domain of the sugar-specific ion channel protein (ScrY porin). <b>2002</b> , 11, 1565-74	12
62	Interpretation of mass spectrometry data for high-throughput proteomics. <b>2003</b> , 376, 1014-22	59

61	Determination of the protein composition of the occlusion-derived virus of <i>Autographa californica</i> nucleopolyhedrovirus. <b>2003</b> , 100, 9797-802		162
60	Mass spectrometric approaches for characterizing bacterial proteomes. <b>2004</b> , 1, 433-47		11
59	Protein profiling of microdissected prostate tissue links growth differentiation factor 15 to prostate carcinogenesis. <b>2004</b> , 64, 5929-33		83
58	Subunit composition of NDH-1 complexes of <i>Synechocystis</i> sp. PCC 6803: identification of two new <i>ndh</i> gene products with nuclear-encoded homologues in the chloroplast Ndh complex. <b>2004</b> , 279, 28165-73		101
57	Proteomics and mass spectrometry in nutrition research. <b>2004</b> , 20, 155-65		30
56	Regulation of phospholipase D2 by GTP-dependent interaction with dynamin. <b>2004</b> , 44, 249-64		6
55	"Affinity-proteomics": direct protein identification from biological material using mass spectrometric epitope mapping. <b>2004</b> , 378, 1102-11		30
54	An automated high performance capillary liquid chromatography-Fourier transform ion cyclotron resonance mass spectrometer for high-throughput proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2004</b> , 15, 212-32	3.5	65
53	Characterization of N-terminal processing of group VIA phospholipase A2 and of potential cleavage sites of amyloid precursor protein constructs by automated identification of signature peptides in LC/MS/MS analyses of proteolytic digests. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2004</b> , 15, 1780-93	3.5	15
52	Direct from polyacrylamide gel infrared laser desorption/ionization. <b>2004</b> , 76, 1078-82		17
51	Probiy: a protein identification algorithm with accurate assignment of the statistical significance of the results. <b>2004</b> , 3, 32-6		43
50	Functional proteomics of circadian expressed proteins from <i>Chlamydomonas reinhardtii</i> . <b>2004</b> , 559, 129-35		47
49	Protein expression profiling of CLL B cells using replicate off-line strong cation exchange chromatography and LC-MS/MS. <b>2005</b> , 819, 33-9		13
48	Comparison of different search engines using validated MS/MS test datasets. <b>2005</b> , 534, 11-20		35
47	Denaturation of metalloproteins with EDTA to facilitate enzymatic digestion and mass fingerprinting. <i>Rapid Communications in Mass Spectrometry</i> , <b>2005</b> , 19, 1268-72	2.2	11
46	Peptide de novo sequencing facilitated by a dual-labeling strategy. <b>2005</b> , 77, 6300-9		46
45	Protein identification in complex mixtures. <b>2005</b> , 4, 387-93		23
44	Crosstalk between Src and major vault protein in epidermal growth factor-dependent cell signalling. <b>2006</b> , 273, 793-804		48

43	Characterization of proteinase-adhesin complexes of <i>Porphyromonas gingivalis</i> . <b>2006</b> , 152, 2381-2394		57
42	The RgpB C-terminal domain has a role in attachment of RgpB to the outer membrane and belongs to a novel C-terminal-domain family found in <i>Porphyromonas gingivalis</i> . <b>2006</b> , 188, 6376-86		115
41	Archaeal and bacterial SecD and SecF homologs exhibit striking structural and functional conservation. <b>2006</b> , 188, 1251-9		28
40	Methods, algorithms and tools in computational proteomics: a practical point of view. <i>Proteomics</i> , <b>2007</b> , 7, 2815-32	4.8	80
39	Immunoproteomics: From biomarker discovery to diagnostic applications. <b>2008</b> , 2, 167-80		39
38	Online microwave D-cleavage LC-ESI-MS/MS of intact proteins: site-specific cleavages at aspartic acid residues and disulfide bonds. <b>2008</b> , 7, 1012-26		28
37	Immunoproteomic identification and serological responses to novel <i>Chlamydia pneumoniae</i> antigens that are associated with persistent <i>C. pneumoniae</i> infections. <b>2008</b> , 180, 5490-8		43
36	The cytoplasmic peptidase DPP9 is rate-limiting for degradation of proline-containing peptides. <b>2009</b> , 284, 27211-9		69
35	"Unknown genome" proteomics: a new NADP-dependent epimerase/dehydratase revealed by N-terminal sequencing, inverted PCR, and high resolution mass spectrometry. <b>2009</b> , 8, 122-31		5
34	A lectin from the rhizomes of turmeric ( <i>Curcuma longa</i> L.) and its antifungal, antibacterial, and Eglucosidase inhibitory activities. <b>2010</b> , 19, 907-916		23
33	Antifungal and antiproliferative activities of lectin from the rhizomes of <i>Curcuma amarissima</i> Roscoe. <i>Applied Biochemistry and Biotechnology</i> , <b>2010</b> , 162, 912-25	3.2	28
32	A novel Eglucosidase inhibitor protein from the rhizomes of <i>Zingiber ottensii</i> valeton. <i>Applied Biochemistry and Biotechnology</i> , <b>2010</b> , 162, 1938-51	3.2	7
31	A thermostable lectin from the rhizomes of <i>Kaempferia parviflora</i> . <i>Journal of the Science of Food and Agriculture</i> , <b>2010</b> , 90, 1920-5	4.3	7
30	Analysis of oligomeric protein complexes in the chloroplast sub-proteome of nucleic acid-binding proteins from mustard reveals potential redox regulators of plastid gene expression. <i>Proteomics</i> , <b>2010</b> , 10, 2191-204	4.8	80
29	Combinatorial optimization of multiple MALDI matrices on a single tissue sample using inkjet printing. <i>ACS Combinatorial Science</i> , <b>2011</b> , 13, 218-22	3.9	12
28	Identification of essential subunits in the plastid-encoded RNA polymerase complex reveals building blocks for proper plastid development. <i>Plant Physiology</i> , <b>2011</b> , 157, 1043-55	6.6	108
27	An extracellular glucoamylase produced by endophytic fungus EF6. <i>Applied Biochemistry and Microbiology</i> , <b>2011</b> , 47, 412-418	1.1	3
26	Degradation and oxidation postmortem of myofibrillar proteins in porcine skeleton muscle revealed by high resolution mass spectrometric proteome analysis. <i>International Journal of Mass Spectrometry</i> , <b>2011</b> , 305, 217-227	1.9	35

25	Biomarker candidates of <i>Chlamydomonas pneumoniae</i> proteins and protein fragments identified by affinity-proteomics using FTICR-MS and LC-MS/MS. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2011</b> , 22, 784-8	3.5	2
24	Antifungal and antibacterial activities of lectin from the seeds of <i>Archidendron jiringa</i> Nielsen. <i>Food Chemistry</i> , <b>2011</b> , 126, 1025-1032	8.5	61
23	Mass spectrometric protein identification from two-dimensional gel separation with stain-free detection and visualization using native fluorescence. <i>International Journal of Mass Spectrometry</i> , <b>2011</b> , 301, 22-28	1.9	6
22	Liquid chromatography and mass spectrometry in food allergen detection. <i>Journal of Food Protection</i> , <b>2011</b> , 74, 316-45	2.5	60
21	An improved calibration method for the matrix-assisted laser desorption/ionization-Fourier transform ion cyclotron resonance analysis of <sup>15</sup> N-metabolically- labeled proteome digests using a mass difference approach. <i>European Journal of Mass Spectrometry</i> , <b>2012</b> , 18, 269-77	1.1	5
20	A Chitinase-Like Protein with α-Amylase Inhibitory Activity from Kluai Hom Thong Banana Fruit: Musa (AAA group). <i>Food Biotechnology</i> , <b>2012</b> , 26, 218-238	2.2	1
19	Application of MALDI-TOF-mass spectrometry to proteome analysis using stain-free gel electrophoresis. <i>Topics in Current Chemistry</i> , <b>2013</b> , 331, 37-54		18
18	Equal ratio of graphite carbon to activated charcoal for enrichment of N-glycopeptides prior to matrix-assisted laser desorption/ionization time-of-flight mass spectrometric identification. <i>Rapid Communications in Mass Spectrometry</i> , <b>2012</b> , 26, 269-74	2.2	13
17	Angiotensin I-converting enzyme inhibitory proteins and peptides from the rhizomes of Zingiberaceae plants. <i>Applied Biochemistry and Biotechnology</i> , <b>2012</b> , 166, 2037-50	3.2	8
16	Zingipain, a ginger protease with acetylcholinesterase inhibitory activity. <i>Applied Biochemistry and Biotechnology</i> , <b>2013</b> , 170, 934-50	3.2	5
15	Inhibition of nitric oxide production in the macrophage-like RAW 264.7 cell line by protein from the rhizomes of Zingiberaceae plants. <i>Preparative Biochemistry and Biotechnology</i> , <b>2013</b> , 43, 60-78	2.4	9
14	A purification strategy for analysis of the DNA/RNA-associated sub-proteome from chloroplasts of mustard cotyledons. <i>Frontiers in Plant Science</i> , <b>2014</b> , 5, 557	6.2	3
13	A superoxide dismutase purified from the roots from <i>Stemona tuberosa</i> . <i>Preparative Biochemistry and Biotechnology</i> , <b>2014</b> , 44, 663-79	2.4	3
12	A personal account of the early stages of proteomics at Aarhus University. <i>Journal of Proteomics</i> , <b>2014</b> , 107, 31-8	3.9	2
11	Identification of Electroblooded Proteins by Peptide Mass Searching of a Sequence Database. <b>1996</b> , 151-170		3
10	Probing circadian rhythms in <i>Chlamydomonas reinhardtii</i> by functional proteomics. <i>Methods in Molecular Biology</i> , <b>2009</b> , 479, 173-88	1.4	13
9	Towards a Comprehensive Database of Proteins From the Urine of Patients With Bladder Cancer. <i>Journal of Urology</i> , <b>1996</b> , 2113-2119	2.5	6
8	Identification of novel target proteins of cyclic GMP signaling pathways using chemical proteomics. <i>BMB Reports</i> , <b>2003</b> , 36, 299-304	5.5	13



7	Nutriproteomics: identifying the molecular targets of nutritive and non-nutritive components of the diet. <i>BMB Reports</i> , <b>2004</b> , 37, 59-74	5.5	16
6	Proteome.		
5	Proteomics: examining the effects of processing on food proteins. <b>2004</b> , 483-516		
4	Identification of the molecular composition of the 20S proteasome of mouse intestine by high-resolution mass spectrometric proteome analysis. <i>Methods in Molecular Biology</i> , <b>2009</b> , 564, 173-86 <sup>1.4</sup>		
3	Mass spectrometry in protein structural analysis. <i>Pharmaceutical Biotechnology</i> , <b>1995</b> , 7, 145-77		
2	Online Effective Identification of Glycopeptide Using Liquid Chromatography Combined with Fourier Transform Ion Cyclotron Resonance Mass Spectrometry (FTICR-MS)*. <i>Advances in Bioscience and Biotechnology (Print)</i> , <b>2015</b> , 06, 624-628	0.9	0
1	Pattern Recognition for Mass-Spectrometry-Based Proteomics.		0