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An approach to correlate tandem mass spectral data of peptides with amino acid sequences in a protein database

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2050	Proteomic analysis of the human colon carcinoma cell line (LIM 1215): development of a membrane protein database. <b>2000</b> , 21, 1707-32	209
2049	Alteration of protein composition in mouse thymocytes by signals through T-cell receptor. <b>2000</b> , 21, 1846-52	12
2048	The role of nucleophileelectrophile interactions in the unimolecular and bimolecular gas-phase ion chemistry of peptides and related systems. <b>2000</b> , 35, 1377-81	96
2047	Mobile and localized protons: a framework for understanding peptide dissociation. <b>2000</b> , 35, 1399-406	849

2046	Proteome profiling-pitfalls and progress. <b>2000</b> , 17, 81-7		58
2045	Phosphopeptide sequencing by in-source decay spectrum in delayed extraction matrix-assisted laser desorption ionization time-of-flight mass spectrometry. <b>2000</b> , 277, 177-86		28
2044	Proteins of rat serum V: adjuvant arthritis and its modulation by nonsteroidal anti-inflammatory drugs. <b>2000</b> , 21, 2170-9		31
2043	A comprehensive characterization of the T-cell antigen receptor complex composition by microcapillary liquid chromatography-tandem mass spectrometry. <b>2000</b> , 21, 2180-95		19
2042	Tandem mass spectrometry methods for definitive protein identification in proteomics research. <b>2000</b> , 21, 2252-65		43
2041	Identification of platelet proteins separated by two-dimensional gel electrophoresis and analyzed by matrix assisted laser desorption/ionization-time of flight-mass spectrometry and detection of tyrosine-phosphorylated proteins. <b>2000</b> , 21, 2622-36		166
2040	Identification of proteins from human cerebrospinal fluid, separated by two-dimensional polyacrylamide gel electrophoresis. <b>2000</b> , 21, 2721-8		88
2039	Identification of differentially expressed proteins between human hepatoma and normal liver cell lines by two-dimensional electrophoresis and liquid chromatography-ion trap mass spectrometry. <b>2000</b> , 21, 3058-68		136
2038	Towards the proteome of the rhodopsin-bearing post-Golgi compartment of retinal photoreceptor cells. <b>2000</b> , 21, 3460-9		17
2037	Towards a two-dimensional proteome map of Mycoplasma pneumoniae. <b>2000</b> , 21, 3765-80		89
2036	Mass-selective ion accumulation and fragmentation in a linear octopole ion trap external to a fourier transform ion cyclotron resonance mass spectrometer. <b>2000</b> , 198, 113-120		42
2035	Refining the model for selective cleavage at acidic residues in arginine-containing protonated peptides. <b>2000</b> , 195-196, 467-479		108
2034	Mass spectrometry and proteomics. <b>2000</b> , 4, 489-94		262
2033	Method for screening peptide fragment ion mass spectra prior to database searching. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2000</b> , 11, 422-6	3.5	48
2032	Bacterial and host-derived cationic proteins bind alpha2-laminins and enhance Mycobacterium leprae attachment to human Schwann cells. <b>2000</b> , 2, 1407-17		36
2031	Advances in mass spectrometry for proteome analysis. <b>2000</b> , 11, 384-90		105
2030	Proteomics: the industrialization of protein chemistry. <b>2000</b> , 11, 413-8		62
2029	Proteomics to study genes and genomes. <b>2000</b> , 405, 837-46		1907

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2028	Identifying the proteome: software tools. <b>2000</b> , 11, 391-5	123
2027	Measuring gene expression by quantitative proteome analysis. <b>2000</b> , 11, 396-401	145
2026	Characterisation of bacteria by matrix-assisted laser desorption/ionisation and electrospray mass spectrometry. <b>2000</b> , 24, 193-219	133
2025	Studying heart disease using the proteomic approach. <b>2000</b> , 5, 76-84	53
2024	Characterisation of bacteria by matrix-assisted laser desorption/ionisation and electrospray mass spectrometry. <b>2000</b> , 24, 193-219	144
2023	Mass spectrometry. From genomics to proteomics. <b>2000</b> , 16, 5-8	305
2022	Malaria research in the post-genomic era. <b>2000</b> , 16, 434-8	6
2021	The Toxoplasma homolog of Plasmodium apical membrane antigen-1 (AMA-1) is a microneme protein secreted in response to elevated intracellular calcium levels. <b>2000</b> , 111, 15-30	96
2020	New methods of proteome analysis: multidimensional chromatography and mass spectrometry. <b>2000</b> , 18, 27-30	5
2019	Database searching with mass-spectrometric information. <b>2000</b> , 18, 22-27	4
2018	The integration of SPR biosensors with mass spectrometry: possible applications for proteome analysis. <b>2000</b> , 18, 45-8	104
2017	Isolation and rapid identification of an abundant self-peptide from class II HLA-DRB1*0401 alleles induced by measles vaccine virus infection. <b>2000</b> , 246, 1-12	13
2016	HuCHRAC, a human ISWI chromatin remodelling complex contains hACF1 and two novel histone-fold proteins. <b>2000</b> , 19, 3377-87	166
2015	Serum-stimulated, rapamycin-sensitive phosphorylation sites in the eukaryotic translation initiation factor 4GI. <b>2000</b> , 19, 434-44	225
2014	Mass spectrometry and proteomics. <b>2000</b> , 2, 59-65	34
2013	Identification of immunodominant antigens from Helicobacter pylori and evaluation of their reactivities with sera from patients with different gastroduodenal pathologies. <b>2000</b> , 68, 915-20	102
2012	Active recycling of yeast Golgi mannosyltransferase complexes through the endoplasmic reticulum. <b>2000</b> , 97, 13643-8	48
2011	A family of chromatin remodeling factors related to Williams syndrome transcription factor. <b>2000</b> , 97, 1038-43	137

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2006 Mutation-tolerant protein identification by mass-spectrometry. <b>2000</b> ,	6
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2004 Structure elucidation of gluten-derived peptides by tandem mass spectrometry. <b>2000</b> , 41, 75-88	
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Searching sequence databases via de novo peptide sequencing by tandem mass spectrometry. <b>2001 2000</b> , 146, 41-61	12
2000 Use of mass spectrometry to study signaling pathways. <b>2000</b> , 2000, pl1	72
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Molecular cloning and expression of a gene encoding Cryptosporidium parvum glycoproteins gp40 and gp15. <b>2000</b> , 68, 4108-16	143
1994 Mass spectrometric analysis of proteins. <b>2000</b> , 54, 1-30	20
1993 Identification of Proteins by Mass Spectrometry. <b>2000</b> , 197-231	26

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1992	Secretion of an acid phosphatase (SapM) by Mycobacterium tuberculosis that is similar to eukaryotic acid phosphatases. <b>2000</b> , 182, 6850-3	85
1991	The surface conformation of Sindbis virus glycoproteins E1 and E2 at neutral and low pH, as determined by mass spectrometry-based mapping. <b>2000</b> , 74, 5667-78	24
1990	Evaluation of two-dimensional gel electrophoresis-based proteome analysis technology. <b>2000</b> , 97, 9390-5	1131
1989	Breakdown of cytoskeletal proteins during meiosis of starfish oocytes and proteolysis induced by calpain. <b>2000</b> , 259, 117-26	25
1988	Colon cancer cells adhesion and spreading on autocrine laminin-10 is mediated by multiple integrin receptors and modulated by EGF receptor stimulation. <b>2000</b> , 261, 360-71	44
1987	MALDI-TOF mass spectrometry in protein chemistry. <b>2000</b> , 88, 81-97	30
1986	Identification of novel MAP kinase pathway signaling targets by functional proteomics and mass spectrometry. <b>2000</b> , 6, 1343-54	224
1985	BRCA1 is associated with a human SWI/SNF-related complex: linking chromatin remodeling to breast cancer. <b>2000</b> , 102, 257-65	441
1984	Functional genomics by mass spectrometry. <b>2000</b> , 480, 25-31	91
1983	Serpins identified as cell growth inhibitors in human plasma. <b>2000</b> , 3, 76-81	7
1982	Functional genomics with protein-protein interactions. <b>2000</b> , 5, 45-86	7
1981	Celiac Disease. 2000,	1
1980	Mutation-tolerant protein identification by mass spectrometry. <b>2000</b> , 7, 777-87	107
1979	Identification of peptide oxidation by tandem mass spectrometry. <b>2000</b> , 33, 299-306	77
1978	De novo peptide sequencing by two-dimensional fragment correlation mass spectrometry. <b>2000</b> , 72, 2337-50	57
1977	Mobility labeling for parallel CID of ion mixtures. <b>2000</b> , 72, 2737-40	103
1976	Protein identification using a quadrupole ion trap mass spectrometer and SEQUEST database matching. <b>2001</b> , Chapter 16, Unit 16.10	6
1975	Identification of major tyrosine phosphorylation sites in the human insulin receptor substrate Gab-1 by insulin receptor kinase in vitro. <b>2000</b> , 39, 10898-907	50

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1973	Integrated microfluidic system enabling protein digestion, peptide separation, and protein identification. <b>2001</b> , 73, 2648-55	235
1972	An automated multidimensional protein identification technology for shotgun proteomics. <b>2001</b> , 73, 5683-90	1674
1971	Quantitative proteomic analysis using a MALDI quadrupole time-of-flight mass spectrometer. <b>2001</b> , 73, 978-86	171
1970	Characterization of peptides formed during fermentation of cocoa bean. <b>2001</b> , 49, 5822-7	35
1969	Mycobacterium tuberculosis Protocols. 2001,	19
1968	Sensitive and High Resolution CE/MS/MS for Protein Identification in Complex Mixtures. 2001, 90-99	
1967	GDF-8 propeptide binds to GDF-8 and antagonizes biological activity by inhibiting GDF-8 receptor binding. <b>2001</b> , 18, 251-9	207
1966	A new approach to decoding life: systems biology. <b>2001</b> , 2, 343-72	1187
1965	Mass spectrometry in proteomics. <b>2001</b> , 101, 269-95	1057
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1955	Phosphorylation of the cohesin subunit Scc1 by Polo/Cdc5 kinase regulates sister chromatid separation in yeast. <b>2001</b> , 105, 459-72	326
1954	Dual inhibition of sister chromatid separation at metaphase. <b>2001</b> , 107, 715-26	389
1953	Heterophile antibodies indicate progression of autoimmunity in human type 1 diabetes mellitus before clinical onset. <b>2001</b> , 34, 247-64	2
1952	Identification of the target of monoclonal antibody A6H as dipeptidyl peptidase IV/CD26 by LC MSMS. <b>2001</b> , 20, 231-6	2
1951	Ion trap/ion mobility/quadrupole/time-of-flight mass spectrometry for peptide mixture analysis. <b>2001</b> , 73, 177-84	77
1950	Human monomethylarsonic acid (MMA(V)) reductase is a member of the glutathione-S-transferase superfamily. <b>2001</b> , 14, 1051-7	189
1949	Erythrocyte spectrin is an E2 ubiquitin conjugating enzyme. <b>2001</b> , 40, 11630-42	15
1948	Chemical and biochemical issues related to X-ray crystallography of the ligand-binding domain of estrogen receptor alpha. <b>2001</b> , 12, 406-13	10
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1937	Functional genomic technologies applied to the control of the human malaria parasite, Plasmodium falciparum. <b>2001</b> , 2, 137-42		8
1936	Specific lectin binding to beta1 integrin and fibronectin on the apical membrane of madin-darby canine kidney cells. <b>2001</b> , 184, 273-81		11
1935	Automated LC-LC-MS-MS platform using binary ion-exchange and gradient reversed-phase chromatography for improved proteomic analyses. <b>2001</b> , 752, 281-91		121
1934	Do all b2 ions have oxazolone structures? Multistage mass spectrometry and ab initio studies on protonated N-acyl amino acid methyl ester model systems. <b>2001</b> , 210-211, 71-87		89
1933	Gaseous apomyoglobin ion dissociation in a quadrupole ion trap: $[M + 2H]2+-[M + 21H]21+$ . <b>2001</b> , 212, 359-376		48
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1931	Transformations in pharmaceutical research and development, driven by innovations in multidimensional mass spectrometry-based technologies. <b>2001</b> , 212, 135-196		37
1930	The role of mass spectrometry in proteome studies. <b>2001</b> , 18, 221-7		33
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1926	Direct interaction of a vancomycin derivative with bacterial enzymes involved in cell wall biosynthesis. <b>2001</b> , 8, 1095-106		29
1925	Differential stable isotope labeling of peptides for quantitation and de novo sequence derivation. <b>2001</b> , 15, 1214-21		258
1924	Automatic function switching and its usefulness in peptide and protein analysis using direct infusion microspray quadrupole time-of-flight mass spectrometry. <b>2001</b> , 15, 1802-6		4
1923	Automated molecular weight assignment of electrospray ionization mass spectra. <b>2001</b> , 15, 2446-55		15
1922	Advanced glycation end products: a highly complex set of biologically relevant compounds detected by mass spectrometry. <b>2001</b> , 36, 370-8		46
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1919	RNA fragmentation studied in a matrix-assisted laser desorption/ionisation tandem quadrupole/orthogonal time-of-flight mass spectrometer. <b>2001</b> , 15, 8-14	58
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1917	Proteome analysis of Corynebacterium glutamicum. <b>2001</b> , 22, 1712-23	94
1916	Investigation of charge variants of rViscumin by two-dimensional gel electrophoresis and mass spectrometry. <b>2001</b> , 22, 2888-97	36
1915	Identification of peroxisomal membrane proteins of Saccharomyces cerevisiae by mass spectrometry. <b>2001</b> , 22, 2955-68	88
1914	Proteome alterations in human hepatoma cells transfected with antisense epidermal growth factor receptor sequence. <b>2001</b> , 22, 3001-8	25
1913	Possibilities to improve automation, speed and precision of proteome analysis: a comparison of two-dimensional electrophoresis and alternatives. <b>2001</b> , 22, 4035-52	86
1912	The application of proteomics in defining the T cell antigens of Mycobacterium tuberculosis. <b>2001</b> , 1, 574-86	97
1911	Automated signature peptide approach for proteomics. <b>2001</b> , 924, 359-68	68
1910	Analysis of proteins and proteomes by mass spectrometry. <b>2001</b> , 70, 437-73	906
1909	Mass spectrometry for protein and peptide characterisation. <b>2001</b> , 58, 868-84	50
1908	Mass spectrometry innovations in drug discovery and development. <b>2001</b> , 18, 131-45	86
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1906	Transcription of chromosomal rRNA genes by both RNA polymerase I and II in yeast uaf30 mutants lacking the 30 kDa subunit of transcription factor UAF. <b>2001</b> , 20, 4512-21	43
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1898	Matching peptide mass spectra to EST and genomic DNA databases. <b>2001</b> , 19, S17-22	46
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1895	Smooth muscle cell phenotypic transition associated with calcification: upregulation of Cbfa1 and downregulation of smooth muscle lineage markers. <b>2001</b> , 89, 1147-54	648
1894	Identification and enzymatic characterization of two diverging murine counterparts of human interstitial collagenase (MMP-1) expressed at sites of embryo implantation. <b>2001</b> , 276, 10253-62	219
1893	Electrospray and tandem mass spectrometry in biochemistry. <b>2001</b> , 355, 545-61	144
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1891	Advances in proteome analysis by mass spectrometry. <b>2001</b> , 276, 45497-500	111
1890	The yeast NuA4 and Drosophila MSL complexes contain homologous subunits important for	112
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1889	The low density lipoprotein receptor-related protein/alpha2-macroglobulin receptor is a receptor for connective tissue growth factor. <b>2001</b> , 276, 40659-67	161
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