
Index

- A**
Amino acid residue masses, 91
Antibodies,
 immobilized, 157
 immunoprecipitation, 152,
 156–158
 Western blot analysis, 152, 168
Automation,
 acquisition of MS-MS spectra,
 74–75
 sample preparation, 86,
 189–190
- B,C**
Biotin,
 component of ICAT reagents,
 145–146
 oligonucleotide derivatives as
 “bait”, 162
Capillary electrophoresis, 46
Codon bias, 22–23, 40
Collision induced dissociation,
 68–69, 72
Cyanogen bromide, 53
- D,E**
Databases,
 BLAST searching, 99
 errors and uncertainties,
 86, 129
 genome sequence, 3, 9
Edman degradation, 98
Electrophoretic mobility shift
 assay (EMSA),
 see Oligonucleotide–protein
 binding
Electrospray ionization (ESI),
 analysis of multiply charged
 protein and peptide ions, 64
 description of ESI source,
 64, 68
- F,G**
Flicker, 140
Fourier–transform ion cyclotron
 resonance (FT-ICR, FT-MS),
 76, 187
- Genomes,
 human, 3, 19, 22
 other organisms, 21–22
- H,I**
High performance liquid
 chromatography (HPLC),
 ion exchange, 43–44, 132–133
 reverse phase, 43, 130–132
 stop flow control (peak
 parking), 132
 tandem LC (LC-LC), 43–45,
 132–133, 148, 156
ICAT reagents,
 analytical approach, 145–147
 application to yeast proteome
 changes, 148
 chemical structures, 146
 limitations, 149
Imaging,

- application of MALDI-TOF MS, 188–189
- of 2D gels, 138
- In-gel digestion, 53–54, 128
- Ion trap mass analyzer, 71–74
 - features of MS–MS spectra, 73–74
- MS_n , 73
- resolution, 74
- Isoelectric focusing (*see also* 2D-SDS-PAGE),
 - solution phase, 41, 134
- Isotope tags, 143–145
- L, M**
- Laser capture microdissection, 126
- MALDI-TOF MS (matrix-assisted laser desorption-time of flight mass spectrometry),
 - advantages and limitations, 61–63
 - description of MALDI source, 57–59
 - interfering substances, 62
 - matrix chemicals, 57
 - post-source decay (PSD), 61
 - resolution, 59–61
 - TOF mass analyzer, 59–61
- MALDI-Q-TOF MS, 188
- Mass spectrometers,
 - essential components, 55–56
- Melanie™, 139–140
 - annotation of 2D gel images, 139
 - multiple image comparisons, 140
- Microarrays,
 - DNA, 4–6
 - protein, 191–192
- Microscale instrumentation,
 - 190–191
- MS–MS spectra,
 - de novo* interpretation of peptide sequence from, 93–96
 - effects of amino acid sequence on fragmentation, 96–98
 - peptide fragmentation nomenclature, 92–93
- Multiprotein complexes,
 - analysis by tandem LC-MS-MS, 156,
 - capture with antibodies, 156–158
 - use of biotinylated oligonucleotides as “bait”, 162
 - use of immobilized proteins as “bait”, 158–160
- N, O**
- Nano electrospray, 186–187
- Oligonucleotide–protein binding,
 - analysis by electrophoretic mobility shift assay (EMSA), 160–161
 - analysis by MS, 162–163
- P**
- Peptide mass fingerprinting,
 - advantages and limitations, 83, 86–87
 - definition, 77
 - importance of mass accuracy, 81–82
 - use of specific proteases in, 79–80
 - software, 85–86
- Phosphopeptides,
 - analysis by MALDI-TOF MS, 170–171
 - fragmentation characteristics

- in MS-MS, 171-173
- immobilized metal affinity chromatography, 174
- Proteases (*see* Protein digestion)
- Protein,
 - domains, 18-19
 - life cycle, 16-18
 - paralogs, 22
 - sequence motifs, 19, 113-121
- Protein chemistry, 6-7
- Protein digestion,
 - glu-C, 51-52
 - nonspecific proteases, 52-53
 - overview, 60-61
 - rationale, 49-50
 - trypsin, 51-52
- Protein expression,
 - correlation with mRNA abundance, 23, 40
- Protein extraction, 32-33
- Protein modification mapping,
 - advantages of MS-MS data for, 171-173
 - importance of sequence coverage, 168-170
 - LC-MS-MS data mining with SALSAs, 175-182
 - non-MS approaches, 167-168
 - with MALDI-TOF MS, 170-171
- Protein-protein interactions (*see* Multiprotein complexes)
- Proteomes,
 - diversity of, 125-126
- Proteome mining,
 - selection of samples, 126-127
 - with 2D-SDS-PAGE, 127-130
 - with LC-MS-MS, 130-134
- Proteomics,
 - definition, 3
- Q-S
- Quadrupole-time of flight (Q-TOF) mass analyzer, 75-76, 187-188
- SALSAs,
 - combined use with Sequest, 182-184
 - detection of modified and variant peptides, 117-119, 175-182
 - primary and secondary search characteristics, 112-113
 - sequence motif searching, 113-117
 - spectral characteristics detected with, 110-112
- 1D-SDS-PAGE, 34-36, 47, 154
- disadvantages and limitations, 36
- 2D-SDS-PAGE, 36-38, 46
- disadvantages and limitations, 38-40
- use in proteome mining, 127-130, 134
- use in proteome profiling, 138-142
- Sequence coverage,
 - definition, 168
 - importance in mapping protein modifications, 168-170
- Sequest,
 - algorithm description, 100-103
 - combined use with SALSAs, 182-184
 - detection of modified peptide forms, 107, 175-176
 - evaluation of results, 103-105
 - limitations, 104-107

- use in proteome mining,
130–131
- Software for protein identification
(*see also* Sequest)
 - from MALDI-TOF data, 85–86
 - from MS-MS data, 107–108
- T–Y**
- Tandem MS spectra (*see* MS-MS
spectra)
- TOF–TOF mass analyzer, 188
- Triple quadrupole mass analyzer,
description, 69–71
 - features of MS–MS spectra, 71
 - resolution, 71
- Yeast two-hybrid assay, 153–154