INDEX

18S pre-rRNA, 206
30S pre-rRNA, 206
40S subunit synthesis, 205
60S biogenesis factors, 205
90S preribosomal complex, 204
90S preribosome particles, 205

Absolute quantification (AQUA), 148, 150
Acetylation, 17, 23
Achromobacter protease I, 89
Acid-cleavable linker, 136
Actinomycin D (inhibitor of RNA polymerase I), 170, 233, 234
Activity-based protein profiling (ABP), 16
Affinity purification, 177
Affinity purification-tags, 176
Affinity-tag-fused protein, 188
Affinity-tag purification, 174
All-in one capillary column, 73
All-in-one ESI column, 74
Aminoethylcysteine, 111, 114
Aminoethylcysteine modification, 113
Anaphase-promoting complex, 197
Anion exchange (AE), 72
Antibody-fixed beads, 180, 181
Antibody-fixed protein G-Sepharose beads, 185

Anti-FLAG antibody-fixed beads, 210
Arf, 208
ASAPRatio, 143
Assembly snapshot, 205
Assembly snapshot analysis, 171, 202
Automated multidimensional LC-MS/MS, 197
Automated quantification, 144
Avidin, 106

b series ion, 11, 12
B23, 219
B23-associated pre-rRNA complex, 224
B23-associated pre-rRNP complex, 231
B-cell lymphoma 6 (BCL6) transcription factor, 197
BEMAD, 22
Benchmark success rate, 198
Biomarker, 13
Biomarker discovery, 145
Biotinylated peptide, 106
Biphasic capillary column, 65
Bottom-up approach, 9, 70
Box C/D snoRNAs, 205
Box C/D snoRNPs, 218
5-Bromo-UTP (Br-UTP) incorporation, 233
C. elegans, 96, 98, 123
Capillary column, 74
¹³C4-succinic anhydride, 140
α-Casein, 116
β-Casein, 116
Cataloging proteomics, 15
CD4/lck receptor, 197
Cell-surface proteins, 102
Cellular localization, 204
Cellular machinery, 196
Chaperonin (GroEL), 15
Cleavable stable isotope-labeled synthetic peptide, 149
cMyc, 208
Coding sequence (CDS) identifier, 97
Codon adaptation index (CAI), 99, 100
Collision-induced dissociation (CID), 10, 11
Column packing, 76, 77
Complex-interaction proteomics, 16
Con-A agarose column, 121
Coomassie blue, 4
cprotein complex, 168
cullin-RING ubiquitin ligase complex, 197
Culture-derived isotope tag (CDIT), 134
α-Cyano-4-hydroxycinnamic acid, 7
Cytoplasm, 204

DAT file, 88
Database search, 88
Data-dependent collision-induced dissociation MS/MS, 84
Data-dependent tandem MS, 66
DDX47-associated pre-rRNP complexes, 218, 232
Descriptive proteomics, 15
Diagnosis, 13
Diamond-Blackfan anemia, 208
5,6-Dichlorobenzimidazole riboside (DRB, inhibitor of RNA polymerase II), 234
Different LC-MS, 146
Dimethyl pimelimidate (DMP), 181
Direct analysis of large protein complexes (DALPC), 68
Direct delivery pump, 79
Direct nano LC (DNLC) system, 80, 83
Double-tagging approach, 177, 179
Double-tagging methodology, 196
Dynamic analysis, 224
Dynamic range of protein abundance, 14
Dyskeratosis congenital, 208
Edman sequencing, 5
EGF-receptor-MAP kinase, 197
Electrical switching valve, 81
Electrospray ionization (ESI), 6, 7
Electrospray ionization apparatus, 72
Electrospray ionization interface, 73
Electrospray ionization-MS/MS, 12
Electrospray ionization spray needle, 72
Electrospray ionization-ToF MS, 65
β-Elimination, 18, 110, 113
emPAI, 91, 152
Endopeptidase Lys-C, 8
Enhancer binding protein α (EBPα), 197
Epitope-tag, 174
Epitope-tagged ubiquitin, 127
Escherichia coli, 98
Estrogen receptor, 196
Exosome, 218
Exponentially modified version of PAI (emPAI), 152
Expression proteomics, 15
Extracted ion chromatograms (XICs), 140
Factor Xa recognition sequence, 188
Fast atom bombardment (FAB), 6
Fibrillarin, 208
Fibrillarin (FIB)-associated pre-rRNP complex, 223, 231
FLAG epitope, 196
FLAG-tag, 176, 179
Fluorescence loss in photobleaching (FLIP), 234
Fluorescence recovery after photobleaching (FRAT), 234
Fluorescent dye, 4
Focused proteomics, 16
Fourier transformed ion cyclotron resonance (FT-ICR), 6
Fraction-splitting phenomenon, 92
Fragment ion mass spectrum, 10
FT-ICR-MS, 70
Functional annotation, 236
Functional proteomics, 15, 101
Gas phase protein sequencer, 5
Gel-based technique, 10
Gel electrophoresis, 63
Gene ontology (GO) database, 108
Genome, 2
Global analysis of protein expression, 14
Global proteome machine, 71
Glucocorticoid receptor, 197
GluR6 kainate receptor, 197
Glutathione-S-transferase (GST)-tag, 176, 188
Glycosylation, 17, 21
Glycine–glycine (GG) modification, 125
Gradient device, 80
GST-fused hParvulin (GST-hParvulin), 192
GST-hParvulin, 189
GST-Sepharose, 189
H/ACA snoRNAs, 205
HA-tag, 176
High performance liquid chromatography (HPLC), 3
His-tag, 176
Histon H2AX-associating protein complex, 197
Histon H2B monoubiquitinating Rad6/Bre1, 197
Horizontally transferred gene, 100
hParvulin-associated complex, 194
HSA, 89
Human nucleolar proteome, 236
Human plasma, 5
Human pre-rRNP complexes, 211
Human ribosome biogenesis, 209
Human serum albumin (HAS), 86
Human trans-acting factors, 211
Human/mammalian ribosome biogenesis, 231
Hydrophilic interaction chromatography, 122
Hydropobicity, 90
ICAT, see Isotope-coded affinity tag
ICAT reagents, 134
IGOT, see Isotope-coded glycosylation-site specific tagging
IkB, 198
Image analyzing apparatus, 5
Immoobilized pH gradient, 5
Immobizized protein beads, 187
Immunooaffinity purification, 180, 184
Immunocytochemical analysis, 221
Immunoprecipitation, 208
In vitro labeling, 132
In vivo labeling, 132
In-gel protease digestion, 9
In-gel protease digestion (Protocol), 10
Integrated capillary column, 73
Interaction proteomics, 16
Interactome, 16
Internal standard, 148
Inward rectifier potassium channel
  (Kir2.x)-associated complex, 197
Ion-exchange column, 71, 78
Ion source, 6
Ion-trap (IT), 6
Ion trap FT-ICR, 234
Ionization, 6
Isobaric tag, 136
Isoelectric point (pI), 3, 99
Isolation of pre-rRNP complexes, 220
Isotope-coded affinity tag (ICAT), 69, 127, 170
Isotope-coded glycosylation-site specific tagging (IGOT), 21, 118, 123
Isotope labeled O-methylisourea, 226, 228
Isotope-labeled reagents, 224
iTRAQ, 138
iTRAQ reagents, 135
Keystone style arch, 75
Label-free quantification, 145, 146
Large scale identification technology (LSIT) with 2D-LC-MS/MS, 68
Large scale immunoprecipitation, 15
Laser-capture microdissection, 14
LC-FTICR MS/MS, 147
Lectin column, 124
Liquid chromatography, 63
Loading capacity, 91
LSU knob, 211
Machinery proteomics, 16
MALDI-ToF, 8
MALDI-ToF mass spectrometer, 183
Malignant progeression, 208
Mammalian ribosome biogenesis, 209
Mascot, 12, 66, 68, 88, 143
Mass analyzer, 6
Mass spectrometry (MS), 6
Mass-to-charge ratio (m/z), 6
Mass-coded abundance tagging (MCAT), 139
MassLynx, 88
Mataborome, 2
α-Mating factor, 172
Matrix molecule, 7
Matrix-assisted laser desorption (MALDI), 6, 7
Metabolic labeling, 234
Metabotropic glutamate receptor 5 protein, 197
β-Methylaminooethylcysteine, 114
Methylation, 17, 22
N-methyl-D-aspartate (NMDA) receptor-adhesion protein, 197
MG132 (proteasome inhibitor), 234
Michael addition, 120
Micropipette puller, 75
Mitochondria proteome, 233
Modification specific proteomics, 16, 17, 109
Molecular weight (mass) (M), 3, 9, 99
Moment-by-moment mass analysis, 224
Monoclonal IgG1-fixed protein-G beads, 184
Monolith column, 79
Mouse embryonic stem (ES) cell, 104
MS/MS instrument, 10
MS/MS ion search, 12
MS2Ratio, 144
MS-based quantification, 131
MS-Fit, 9, 186
MSQuant, 152
Multidimensional LC-MS/MS, 64
Multidimensional liquid chromatography (multi-LC), 64
Multidimensional protein identification technology (MudPIT), 68
Multidimensional separation, 92
Multi-protein complexes, 167, 196
myc-tag, 176
mzXML, 71
Nanoflow LC system, 80
Nanoflow pump, 83
Natural isotope abundance, 229
Natural isotope abundance ratio, 141
Natural isotopes, 141
NCBInr, 88
NF-E2p18/MafK, 173
NF-κB, 198
N-glycosylation site, 118
N-glycosylation site mapping, 117
Nitrification, 28
2-Nitrobenzenesulfenyl (NBS)-ClC6, 138
2-Nitrobenzenesulfenyl (NBS) reagents, 135
S-Nitrosylation, 27
Nop56-associated pre-rRNP complex, 232
Northern blot analysis, 201
Nuclear pore complex, 169, 197
Nucleolar proteome, 234
Nucleolin, 208
Nucleolin (NCL)-associated pre-rRNP complex, 223, 230
Nucleolus, 170, 233
Nucleophosmin (B23), 208
Nucleophosmin 3 (NPM3), 219
Nucleoplasm, 204
Nucleus/cytoplasm, 205
One-dimensional (1D)-RPLC-MS/MS, 84
\(^{18}\)O-labeled peptide, 123
\(^{18}\)O-labeling, 138
\(^{18}\)O-water, 138
\(\alpha\)-glycosylation, 120
\(\alpha\)-methylisourea, 135, 139, 225
Organellar proteomics, 16, 101
Outline pathway of ribosome synthesis in yeast, 204
Packaging materials, 78
Parl4-associated pre-rRNP complexes, 218, 232
Particle size, 78
Peptide mass fingerprinting (PMF), 8, 186
Peptide sequence tag, 11, 12
Peptide-N-glycosidase (PNGase), 120
Peptidyl prolyl cis-trans isomerase, 188, 195
Perl language, 144
Phosphopeptide, 110
Phosphoproteomics, 110
Phosphorylation, 17, 18
Phosphorylation site, 116
Phosphorylation site mapping, 109, 114, 115
Phosphoserine, 114
Phosphospecific proteolysis, 115
Phosphothreonine, 114
pf, see Isoelectric point
Pin1, 189
Plasma membrane, 102
Playing hands style arch, 75
PMF method, see Peptide mass fingerprinting
Polyubiquitin, 124
Porosity, 78
Post-transcriptional modification, 206
Post-translational modification (PTM), 17, 109, 168, 206
Pre-40S particles, 206
Pre-60 particles, 201
Pre-60S processing factors, 218
Pre-90S processing factors, 218
Precursor ion scanning, 18
Preparation of nuclear extract, 194
Preribosomal ribonucleoprotein (pre-rRNP) complex, 196, 199, 201, 209
Preribosomal RNA (pre-rRNA), 198
Pre-rRNA processing machinery, 219
PreSession recognition sequence, 188
Presynaptic MALS-CASK-liprin-\(\alpha\), 197
Processing pathway of the primary 35S pre-rRNA, 203
Processome, 206
Protease digestion, 222
Protease digestion in solution, 186
Proteasome, 125
Protein abundance index (PAI), 151
Protein chemistry, 2
Protein cleavage-isotope dilution mass spectrometry (PC-IDMS), 149
Protein content, 152
Protein glycosylation, 117
Protein identification, 107
Protein phosphorylation, 109
Protein profiling, 65
Protein-A, 180
Protein-G, 180
ProteinProspector, 141
Protein-protein interaction, 168
Proteome, 1
Proteome analysis, 1
Proteome-browsing technology, 150
Proteomics, 1
PTMs, see Post-translational modification
Pull-down purification, 187
Pulse chase, 201
Pulse chase monitored by quantitative MS (PC/QMS), 207

QTAX, see Quantitative analysis of tandem affinity-purified in vivo cross-linked protein complexes
Quantitative analysis, 224
Quantitative analysis of tandem affinity-purified in vivo cross-linked protein complexes (QTAX), 173, 207
Quantitative proteomics, 131, 140, 170

RCA120, 124
rDNA, 219
rDNA transcription, 219
RecQ5-specific antibody-fixed protein-G beads, 183
Reference peptides, 150
RelEx, 143
ReNCon device, 81
ReNCon system, 80
Retention time, 90
Reversed-phase (RP) column, 71, 72
Reverse-tagging, 171
Reverse-tagging analysis, 210, 220
Reverse-tagging approach, 211
Reverse-tagging methodology, 174
Reverse-tagging strategy, 201
Ribosomal protein, 131
Ribosome biogenesis, 169, 198
Ribosome RNA (rRNA), 200
RNA interference, 179
RNA polymerase (RNAP) II, 170
RNA polymerase II preinitiation complex, 172, 197
RNase treatment, 222, 230

Sedimentation profile, 203
Semi-quantitative mass spectrometric analysis, 226
SEQUEST, 12, 66, 68, 143
Shotgun, 102
Shotgun analysis, 68, 220
Shotgun approach, 130

Shotgun method, 186, 210
SILAC, see Stable isotope labeling by amino acids in cell culture
Silver staining, 4
Sin3-histon deacetylase (HDAC), 197
Size exclusion (SE), 72
Size of pre-rRNAs, 201
Small nucleolar RNA ( snoRNA), 200
Small subunit (SSU) processome, 211
Small ubiquitin-like modifier (SUMO), 126
Snapshot analysis, 201, 211
Sodium dodecyl sulfate (SDS), 3
Sonar, 143
SpecArray, 147
Spliceosome, 197
Split flow system, 79
Splitter, 79
Stable isotope-labeled reference peptide, 148
Stable isotope labeling, 224
Stable isotope labeling by amino acids in cell culture (SILAC), 133, 134, 168, 233
Stable isotope tagging, 122
Stable-isotope dilution, 132
Stage-specific protein association, 173
STEM, 13, 69, 88, 143, 225, 229
Strong cation exchange (SCX), 72
Strong cation-exchange (SCX) column, 91
Subcellular proteomics, 16, 101
Sulfo-N-hydroxysuccinimide (NHS)-LC-biotin, 98, 102, 108
Sumoylation, 17, 24
System biology, 168

Tabacco etch virus (TEV)-protease, 175
Tandem affinity purification (TAP)-tag, 177
Tandem MS (MS/MS), 10, 11
TAP strategy, 197
TAP-MS approach, 198
TAP-tag, 175, 176, 179
TAP-tagged trans-acting factors, 201
TATA-binding protein, 171
Taylor cone, 74
Thrombin, 193
Thrombin cleavage, 188, 189
Time of flight (ToF), 6
TNF-α/NF-κB pathway, 197
TNF-α/NF-κB signal transduction pathway, 199
ToF-ToF, 8
Top-down approach, 10, 70
Trans-acting factor, 200
Trans-acting factors involved in human/mammalian ribosome biogenesis, 213
Transcription, 169
Transcription machinery, 197
Transcriptome, 2
Translation, 169
Treacher Collins syndrome, 208, 218
Treacle, 218
Triple-stage quadrupole (TSQ), 6
Trypsin, 8
Tumor suppressor Arf, 232, 219
2D-LC system, 90
2D-PAGE, 17, 64
Two-dimensional differential image gel electrophoresis (2D-DIGE), 4, 131
Two-dimensional electrophoresis (2DE), 3, 5
Two-dimensional electrophoresis (2DE) catalog database, 13
Two-dimensional electrophoresis (2DE) gel-based protein profiling, 13
Two-dimensional image-converted analysis of liquid chromatography and mass spectrometry (2D-ICAL), 147
Two-step affinity purification (TAP), 175
U3 snoRNA, 201
U3-snoRNA-associated processing machinery, 206
U3 snoRNP, 205
U3 snoRNP complex, 179
UBF1, 219
Ubiquitin E3 ligase, 125
Ubiquitinated protein, 129
Ubiquitination, 17, 23, 124
Ubiquitin-proteasome system, 232
Ubiquitin-protein conjugate, 130
Ubiquitin-related protein, 129
Ubiquitin-ubiquitin linkage, 126
Ultracentrifugation of pre-rRNP complexes, 221
Universal signal response factor, 153
Wnt signaling complex, 197
XIC, 233
xPAI, 233
XPRESS, 143
y series ion, 11, 12
Yeast cell fusion library, 14
Yeast transcription factor STE12, 172
Yellow fluorescent protein (YFP), 235