

# SUBJECT INDEX

- A**  
 Acylation ..... 80  
 Affinity capture ..... 300  
 Affinity chromatography ..... 11–12, 81, 105, 111, 188–189, 244, 291–292, 294–295, 300, 311, 313  
 Amidation ..... 81–85, 87–89, 305, 307–308  
 Azidohomoalanine (azhal) ..... 169–180
- B**  
 Bioinformatics  
 automated protein quantification ..... 58  
 census ..... 374–376, 378  
 ICPLQuant ..... 57–58, 60  
 Mascot Distiller ..... 374–375, 377, 379–384, 386–396  
 MaxQuant ..... 374–381, 383–384, 388–392, 396  
 MsQuant ..... 374–376, 379–381, 383–384, 388–396  
 peptide identification ..... 17–20, 35, 48, 51, 55, 145–146, 193–194, 200, 248, 363, 365, 367, 377, 379–380, 382–384, 392–394, 396  
 peptide quantification ..... 373–396  
 protein identification ..... 10, 17, 30, 38, 40, 66, 71–74, 79, 139, 145, 158, 179, 192, 195, 230–231, 244, 366, 374  
 protein quantification ..... 15, 63, 94–96, 108, 113, 126, 276, 285, 366–368, 379, 392, 396  
 protein sequence databases ..... 3, 17–20, 146, 165, 185, 202, 361, 363  
 Rover ..... 367–368, 381–382, 391–392, 396  
 Biotinylation ..... 237, 239–240, 265, 267
- C**  
*Caenorhabditis elegans* ..... 30–31, 33–34, 36–37, 39  
 Carbohydrate specificity ..... 290  
 Cell fractionation ..... 118  
 Cell-free protein expression ..... 103–104  
 Cell signaling ..... 184  
 Chemical protein deglycosylation ..... 323–332  
 Combined fractional diagonal chromatography (COFRADIC) ..... 11–12, 172–173, 176, 179, 233, 276, 374
- D**  
*Drosophila melanogaster* ..... 34, 40, 188, 194
- E**  
 Electron transfer dissociation (ETD) ..... 8, 83, 158–160, 165, 198–200, 302, 326  
 Endocytosis ..... 120
- Endoproteinase Lys-N ..... 200  
*Escherichia coli* ..... 30–31, 33–34, 36, 39, 97, 99–100, 102–104, 170, 172–173, 177, 237–238, 244, 246, 254
- F**  
 Fourier transform mass spectrometry (FTMS) ..... 6, 79, 82–84, 224, 226
- G**  
 GeLCMS ..... 10, 143–154
- I**  
 Immobilized metal ion affinity chromatography (IMAC) ..... 12, 81, 105–107, 111, 113, 119, 126, 186–189, 191–196, 198, 203–204
- L**  
 Lectin chromatography ..... 12, 291–292, 294–295  
 Lipid-based protein immobilization (LPI) ..... 129–141
- M**  
 Membrane proteins ..... 127, 129–141, 158, 170, 188–189, 203, 294, 311–314, 318, 320
- N**  
 N-terminal peptide isolation ..... 231–232  
 N-terminomics ..... 243–254, 276
- P**  
 Peptide library ..... 258–259, 263, 265, 268  
 Phagocytosis ..... 118–120  
 Phosphopeptide sequencing ..... 198, 200  
 Platelets ..... 274, 300–305, 310  
 Positional proteomics ..... 229–240  
 Protease  
 active site specificity ..... 257  
 cleavage site ..... 258–259, 268  
 degradomics ..... 276  
 protease-mediated cellular signaling ..... 184  
 protein processing ..... 274  
 specificity ..... 257–271  
 subsite cooperativity ..... 258, 269, 271  
 substrate profiling ..... 257–271  
 Protein digestion  
 protein in-gel digestion ..... 135–136  
 protein in-solution digestion ..... 135  
 sequential protein digestion ..... 130  
 Protein modification  
 protein acetylation ..... 71

- protein degradation . . . . . 108, 131, 294, 332
  - protein glycosylation . . . . . 309
  - protein O-glycosylation . . . . . 299–300
  - protein phosphorylation . . . . . 12, 95–96, 183, 196, 203, 215
  - protein processing . . . . . 10, 12, 274
  - protein sialylation . . . . . 310
  - protein ubiquitination . . . . . 336
  - Protein quantification
    - absolute quantification . . . . . 15, 95, 108–110, 204, 367
    - chemical labeling . . . . . 65, 204
    - dimethylation . . . . . 81, 258–259, 268, 275–276, 278, 283–285
    - enzymatic labeling . . . . . 15, 373
    - ICPLQuant . . . . . 57–58, 60, 62
    - Isobaric peptide termini labeling (IPTL) . . . . . 65–75
    - Isobaric tag for relative and absolute quantitation (iTRAQ) . . . . . 15, 30, 56, 65, 80, 171–172, 174–179, 180, 201, 204, 319
    - IsobariQ . . . . . 67, 71–75
    - Isotope coded protein labels (ICPL) . . . . . 55–63, 80, 319
    - Nitrogen-15 labeling . . . . . 13–14
    - post-metabolic oxygen-18 labeling . . . . . 15
    - Protein standard absolute quantification (PSAQ) . . . . . 95–96, 99, 104, 108–111
    - quantitative proteomics . . . . . 9, 13–16, 29, 37, 43–53, 56, 79, 81, 93–113, 368, 373
    - stable isotope labeling . . . . . 13, 43, 56, 95, 104, 111, 144, 204
    - Tandem mass tags (TMT) . . . . . 65, 319
  - Proteome simplification . . . . . 229–240
  - Pulse-chase labeling . . . . . 340–341, 348–349
- R**
- Reticulocyte lysate . . . . . 337–339, 341–342, 344, 350–353
- S**
- Strong cation exchange chromatography (SCX) . . . . . 4, 10, 12, 158–166, 171, 175, 179, 186–187, 193–196, 299–308
- T**
- Titanium dioxide . . . . . 12, 215–227, 300, 309–320
  - Translational regulation . . . . . 169
  - Two-dimensional chromatography . . . . . 224
- U**
- Ubiquitin . . . . . 80, 335–336, 339, 344–347, 350–355
  - Ubiquitin aldehyde . . . . . 339, 354