

## Index

### **a**

absolute quantification (AQUA) 13, 111  
 abundance 12  
 abundant 6  
 accurate mass and time (AMT) 442  
 affinity chromatography 251  
 affinity purification 364  
 albumin 6  
 algorithms 435  
 alkylation 136  
 amino acid composition 438, 439  
 amount 14  
 ampholytes 135  
 antibodies 6  
 ASB14 135  
 average peak intensity 427

### **b**

background electrolyte (BGE) 171  
 bacteria 358  
 bacterial 148  
 baseline reduction 424  
 bead-based immunoassays 391  
 biased 382  
 biodiscovery 9  
 biological variance 11  
 biomarker 9  
 bioorthogonal non-canonical amino acid tagging (BONCAT) 107  
 biotin 372  
 blue native (BN)-PAGE 304  
 blue-native electrophoresis (BNE) 144  
 body fluids 382  
 boronic acid 333  
 bottom-up approach 148  
 bronchoalveolar lavage (BL) 388

### **c**

<sup>13</sup>C 108  
 capillary electrophoresis (CE) 171  
 capillary gel electrophoresis (CGE) 172  
 capillary isoelectric focusing (CIFF) 172  
 capillary isotachophoresis (CITP) 172  
 capillary zone electrophoresis (CZE) 172  
 carbonate washing 123  
 carrier ampholytes 137  
 cation-exchange chromatography 321  
 cell disruption 130  
 cell walls 344  
 cellulases 132  
 cerebrospinal fluid (CSF) 388  
 chaotropes 135  
 chaotropic agents 135  
 CHAPS 135  
 chemical isotopic labeling 108  
 chemical shift perturbation (CSP) 274  
 chemical tags 106  
 chromolith CapRod 259  
 chromolith guard 259  
 circulating microparticles 394  
 citrated blood 389  
 clear-native electrophoresis (CNE) 144  
 clustering 428  
 collision-induced dissociation (CID) 46, 111  
 column 253  
 combined fractional diagonal chromatography (COFRADIC) 323  
 comparative analysis 16  
 confidence level 60  
 coomassie blue G-250 144  
 crushed crystal method 81  
 crystallography 281  
 culture-derived isotope tag (CDIT) 108

$\alpha$ -cyano-4-hydroxy-cinnamic acid 74  
cyanogen bromide 362  
cyomics 389

**d**

DAPI 239  
DDM 146  
deconvolution 53  
decoy-database 59  
deglycosylation 335  
dendritic cells 394  
depletion 11  
detection limits 13  
detector 172  
detergent lysis 132  
detergents 135  
dialysis 288  
difference gel electrophoresis (DIGE)  
    105, 140  
differential in gel electrophoresis 13  
differential display 140  
digitonin 146  
dihydroxybenzoic acid (DHB) 74, 320  
dissociation constants ( $K_D$ ) 273  
disulfide bonds 136  
dithiothreitol (DTT) 136  
dodecyl maltoside 135  
dodecyl- $\beta$ -D-maltoside (DDM) 146  
dried droplet method 80  
dried droplet preparation 90  
drop dialysis 83, 90  
dye-ligand chromatography 251  
dynamic range 6, 346

**e**

EDTA-blood 389  
effective length (L) 178  
electro-endosmosis 158  
electron transfer dissociation 46  
electrospray ionization 43  
 $\beta$ -elimination 322  
enrichment 11, 265  
equilibrium density gradient  
    centrifugation 119, 122  
erythrocytes and reticulocytes 393  
experiment 23

**f**

false-discovery rates 59  
field-amplified injection (FAI) 175  
filter 427  
flow cytometric immunophenotyping  
    (FC) 399  
flow cytometry 234

flow sorting 235  
fluorescence lifetime imaging microscopy  
    (FLIM) 209  
fluorescence resonance energy transfer  
    (FRET) 208  
fluorescence-activated cell sorting  
    (FACS) 140, 391  
fluorescent difference gel electrophoresis  
    (DIGE) 137  
free-flow electrophoresis (FFE) 155  
freeze/thawing 132  
Fungi 371

**g**

gel-based approach 60  
global internal standard technology (GIST)  
    110  
1,3-glucanases 132  
glycosylation 12, 328  
glycosylphosphatidylinositol-(GPI)-  
    anchor 371  
GRAVY (grand average of hydrophobicity)  
    304, 363  
GST pull-down method 296

**h**

heparinized blood 389  
heteronuclear single quantum correlation  
    (HSQC) 274  
high resolution two-dimensional  
    electrophoresis 171  
highly abundant proteins 134  
high-performance liquid chromatography  
    (HPLC) 171, 245  
high-resolution, clear native electrophoresis  
    (hrCNE) 152  
Human Proteome Organisation (HUPO)  
    174, 386  
hydrolytic enzymes 132  
hydrophilic interaction liquid chromatography  
    (HILIC) 333  
hydrophobic protein domains 135  
hydroxyethyl disulfide 136  
hydroxypropyl methyl cellulose (HPC) 158

**i**

immobilized metal-affinity chromatography  
    (IMAC) 12, 251, 319  
immobilized pH gradients 129  
immunophenotyping 399  
immunoprecipitation 266, 319  
in-gel digestion 51  
*in-silico* 11  
insoluble material 134

in-solution digestion 51  
 interferometric quadrature 189  
 interferometry 189  
 iodixanol (Optiprep) 120  
 iodixanol cushion 122  
 iodoacetamide 136  
 ion suppression 48  
 ion trapping 45  
 ion-exchange chromatography 436  
 isoelectric focusing (IEF) 130, 158, 438  
 isoelectric point (*pI*) 156, 434  
 isotachophoresis (ITP) 175  
 isotope tags for relative and absolute quantitation (iTRAQ) 110, 119, 364  
 isotope-coded affinity tags (ICAT) 108  
 isotope-coded protein label (ICPL) 111

***I***

laser capture microdissection 140  
 laser microdissection and pressure catapulting (LMPC) 219  
 leading electrolyte (LE) 176  
 lectin affinity chromatography 332  
 lectins 12  
 lignins 345  
 limit of detection (LOD) 175  
 lipid rafts 397  
 lipidomic 380  
 lipids 134  
 liquid chromatography 46  
 liquid chromatography Fourier transform ion cyclotron resonance (LC-FT-ICR) 95  
 liquid chromatography/mass spectrometry (LC/MS) 245  
 liquid-based homogenization 131  
 liquid-liquid extraction 249  
 liquid-phase transfection (LPT) 209  
 localization 118  
 localization of organelle proteins by isotope tagging (LOPIT) 118f.  
 lower limit of detection 14  
 low-molecular-weight (LMW) 379  
 lymphocytes 394  
 LysC 362  
 lysozyme 132

***m***

magnetic bead-based separation 392  
 magnetic beads 234  
 MALDI matrix 75  
 mammalian 148  
 mannitol 158  
 mass accuracy 46, 442  
 mass calibration ladder 151

mass measurement accuracy (MMA) 443  
 mass spectrometry 43  
 matrix-assisted laser desorption/ionization mass spectrometry (MALDI MS) 73  
 mechanical cell disruption 130  
 membrane protein 361  
 membrane proteomes 303  
 membrane-protein complexes 303  
 metabolomic 380  
 micellar electrokinetic chromatography (MEKC) 172  
 micro-batch 288  
 microdissection 393  
 6-1minohexanoic acid 148  
 molecular imprinted polymer (MIP) 176  
 monocytes 394  
 mononuclear cells 394  
 multidimensional protein identification technology (MudPIT) 50, 56, 245, 353, 358  
 multidimensional-nano-LC/MS 56  
 multiple-reaction monitoring (MRM) 111

***n***

<sup>15</sup>N 108  
 nano-ESI 45  
 nano-HPLC 46  
 native electrophoresis 144  
 native isoelectric focusing (native IEF) 144  
*n*-butyl (C4) 56  
 N-hydroxysuccinimide (NHS)-ester 372  
 N-linked glycopeptide 330  
*n*-octadecyl (C18) 56  
*n*-octyl (C8) 56  
 noise filter 424  
 NP-40 135  
 nuclear magnetic resonance (NMR) 273  
 nucleic acids 134  
 nucleolus/nucleosome 398

***o***

<sup>16</sup>O/<sup>18</sup>OExchange 110  
 octyl- $\beta$ -glycoside 135  
 O-linked glycopeptide 330  
 open reading frames (ORFs) 295  
 organelles 396  
 orthogonal separations 259  
 osmolysis 131

***p***

peak lists 424  
 peak-based statistics 426  
 pectins 345  
 peptide fragment analysis 75

- peptide mass fingerprint (PMF) 75, 111  
 peptidome 386  
 phagosomes 398  
 phenol extraction 351  
 phenols 134  
 phosphatase inhibitors 137  
 phosphoamidates 322  
 phosphorylation 12, 317  
 physico-chemical properties 433  
 plant proteomics 343  
 plant tissue 345  
 plasma proteome 379  
 plasma proteome project (PPP) 386  
 plasma/serum 386  
 platelets 395  
 PNGase 335  
 polyaccharides 134  
 polyacrylamide gel electrophoresis 46  
 polyethylene glycol (PEG) 353  
 polyphenolics 345  
 Ponceau S 149  
 post-translation modifications (PTMs)  
     11f., 317, 328  
 pre-column technique 253  
 primary amine 124  
 prolytes 159  
 propidium iodide 239  
 proteases 133, 137  
 protein database (PDB) 282, 309  
 protein digestion 51  
 protein equalizer technology 252  
 protein localization 118  
 protein secretion 398  
 protein solubilization 135  
 proteinase K 333, 362  
 protein-ligand interaction 273  
 proteolytic digestion 333  
 proteome 21  
 purification (TAP) 295
- q**  
 quadrupole time-of-flight 45, 46  
 quality control 423  
 quantification 13  
 quantitative structure-retention  
     relationships (QSRRs) 439  
 Quantitative MudPIT 363
- r**  
 raft-associated proteins 397  
 RAM-SCX particulate column 253  
 raw mass spectra 424  
 recalcitrant 345  
 recovery 12  
 reducing agents 136  
 reproducibility 23  
 restricted access material (RAM) 255  
 retention coefficient 438  
 reverse transfection (RT) 209  
 reversed-phase (RP) 319, 359, 438  
 reversed-phase liquid chromatography  
     (RPLC) 157, 438  
 reverse-phase microcolumns 333  
 RPLC/ESI-MS/MS 50  
 rubisco 346
- s**  
 salt 133  
 sample clean-up 133  
 sample recovery 12  
 sample size 14  
 saturation transfer difference (STD) 276  
 scaling up 14  
 SCX-RPLC 365  
 SEC-RPLC 365  
 SELDI-TOF MS 224  
 selective multiple-reaction monitoring  
     (SRM) 111  
 separation 157  
 sequence coverage 110  
 sequence-specific retention calculator  
     (SSRCalc) 440  
 sequential extraction 140  
 serial extraction 351  
 shaving 307  
 shotgun approach 307  
 signal-to-noise 53  
 signal-to-noise ratio (SNR) 427  
 silicamonolithic 253  
 sinapinic acid 74  
 small interfering (si) RNA 211  
 solid-phase extraction (SPE) 163, 245  
 solid-phase micro-extraction (SPME) 175  
 sonication 131  
 SPADNS (2-(4-sulfophenylazo) 1,8-dihydroxy-  
     3,6-naphthalenedisulfonic acid) 159  
 spiking of labeled peptides 111  
 spinning disc interferometry (SDI) 187  
 spotter 213  
 stable isotope 106  
 stable isotope labeling (SILAC) 13, 107,  
     364  
 stable isotope tagging 118  
 standard operating procedure (SOP) 380  
 statistical validation 425  
 storage 12  
 strong cation-exchange (SCX) 359, 436  
 subcellular compartments 118

- subcellular fractionation 8  
subcellular localization 119  
subcellular protein extraction 17  
sucrose density gradient centrifugation 397  
sum of isotope peaks 427  
sum of satellite peaks 427  
surfactants 135
- t**  
tandem affinity 295  
tandem affinity purification (TAP) 308  
tandem mass spectrometry (MS/MS)  
    46, 157  
technical variance 11  
terminating buffer (TE) 176  
terpenes 345  
thin-layer chromatography 80, 265  
thin-layer peptide mapping electro-  
    phoresis 271  
thin-layer preparation 90  
three-dimensional (3-D) structure 273, 281  
thresholding 427  
time-of-flight 74  
tissue arrays 390  
titanium dioxide 12, 320, 333  
titanium oxide 251  
top-down approach 248  
total ion count (TIC) 427  
total length (TL) 178  
total number of peaks (TNP) 427
- transmembrane 362  
tributylphosphine (TBP) 137  
Tris-(2-carboxyethyl)phosphine (TCEP) 137  
Tris(carboxyethyl) phosphine 124  
Triton X-100 135, 146  
trypsin 51, 333  
two-dimensional (2-D) LC 47  
two-dimensional (2-D) phosphopeptide  
    mapping 265  
two-dimensional gel electrophoresis  
    (2-DGE) 129
- u**  
ubiquitination 12  
unbiased 382  
urine 387
- v**  
vapour diffusion, batch 288
- w**  
whole proteome 14
- y**  
yeast 148, 371  
yeast two-hybrid (Y-2-H) method 308
- z**  
ZIC-HILIC 333  
zirconium dioxide 320

