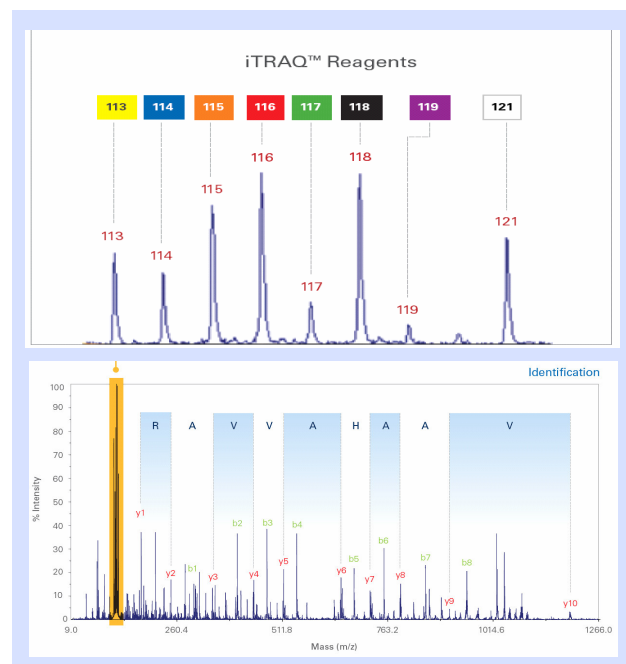


Biomarker Discovery: iTRAQ Analysis

OBS offers 8 label iTRAQ (8plex) as a biomarker discovery tool in order to ascertain differentially expressed proteins. This technique involves labelling the proteins in different samples with different reporter ions. The different reporter ions tags are not visible in MS mode however in MS/MS mode, it is possible to detect the reporter ions. Therefore, by comparing the relative abundance of each reporter ion, it is possible to determine proteins that either up or down regulated while preserving post-translational modification information.

The use of 8 plex iTRAQ along with specialised fractionation techniques enables OBS to explore low abundance proteins in crude biological samples. Prefractionation tools include the use of immunodepletion columns to remove high abundance proteins, bead-based combinatorial peptide libraries to enhance the relative concentration of low abundance proteins in crude samples and the enrichment of specific proteins such as glycoproteins or phosphoproteins.

The recent introduction of 8 iTRAQ reporter ions greatly increases the versatility of these N-terminal isobaric labels in discovery experiments. This technique is very powerful in that enables the simultaneous identification and quantitation whilst preserving post-translational modification information.



Standard iTRAQ Workflow

- 1 Deplete high abundance proteins or enrich low abundance proteins in crude samples
- 2 Digest depleted samples with trypsin
- 3 Label with iTRAQ reporter ions
- 4 Separate peptides using LC and perform MS/MS
- 5 Statistically analyse data (univariate and multivariate analysis) for differentially expressed proteins
- 6 Prioritize specific biomarkers using our proprietary database, DECIDER

For further information on our services please contact:

Oxford Biomarker Services
94A Milton Park
Abingdon, OX14 4RY
United Kingdom
T: +44 (0) 1235 861 770
F: +44 (0) 1235 861 771

Email: info@biomarkerservices.com
www.BiomarkerServices.com

