The National Institute for Bioprocessing Research and Training (NIBRT) is a global centre of excellence for training and research in bioprocessing. Our world leading NIBRT Investigators including Prof. Pauline Rudd and Dr. Jonathan Bones continue to drive advancements in the field of bioprocessing analytics through pioneering and innovative peer reviewed research.

NIBRT provides unrivalled detailed bioanalytical characterisation of biologics including post-translational modifications with a specialist focus on glycosylation. Specialised consultancy and tailored client method development services are also available.

**WHY CHOOSE NIBRT?**

By choosing NIBRT Contract Bioanalytical Research you will be supported by a team of characterisation specialists with expertise in the analysis of monoclonal antibodies, erythropoietin, interferon, enzymes and many other biological products.

Clients gain direct access to leading NIBRT scientists throughout the project lifetime and access to best-in-class bioanalytical facilities. Our team provide extensive project reports to ensure full clarity and satisfaction of results.

**WHAT BIOANALYTICAL SERVICES DOES NIBRT PROVIDE?**

NIBRT Contract Bioanalytical Research provides a range of analytical services to support Clients with the physiochemical characterisation requirements of ICH-Q6B and Q5E including protein and peptide analysis, glycosylation and oligosaccharide analysis and protein aggregation.

**GLYCAN**

**Monosaccharide composition analysis**
- Relative quantification of released monosaccharides by HILIC UPLC-FLR, CE-LIF.

**Glycan profiling, antennary and linkage analysis**
- Relative quantification of N- and O-glycan populations by HILIC-UPLC-FLR, CE-LIF.
- Enzymatic digestion arrays with HILIC-UPLC-FLR, CE-LIF and WAX-HPLC to unveil antennary structures and monosaccharide linkage.
- Conformation of structures by orthogonal LC-MS analysis.

**Glycosylation site analysis**
- Glycan site occupancy analysis and percentage occupancy delivered through LC-MS/MS based peptide sequencing.

**PEPTIDE**

**Peptide Sequencing**
- Peptide sequence and N- and C- terminus sequence is determined by LC-MS/MS analysis.

**Post-translational modification (PTM) identification**
- PTM's including oxidation and deamidation are identified by LC-MS/MS analysis.

**AGGREGATES**

**Analytical Ultracentrifugation and Size Exclusion Chromatography**
- Molecular weight profiles and aggregate quantification.

**PROTEIN**

**Intact mass analysis**
- Un-treated, reduced and/or deglycosylated intact protein analysis by LC-MS.
- Charge variant analysis by IEX-UPLC.
- Oxidation analysis by HIC-UPLC.

**HOST CELL PROTEIN ANALYSIS**

**Mass spectrometry based quantification and identification of Host Cell Proteins**
- 2-D LC-MS® analysis with Hi-3 quantification.

**Disulphide Bond**
- LC-MS/MS peptide mapping of reduced and non-reduced protein samples are differentially analysed to identify each disulphide linkage.

**OTHER**

Where methods are not available we aim to provide solutions supported by world class facilities including; HPLC, UPLC, mass spectrometry and capillary electrophoresis.
CLIENT TESTIMONIAL

“NIBRT Contract Research has enabled Levicept to access a wide range of analytical services delivered through the provision of top specification analytical instrumentation. In addition to providing protein and glycan analytical services their ability to develop new methods to meet our specific needs enables us to quickly resolve our analytical queries in timely and cost effective manner. Working with NIBRT Contract Research has enabled us to gain a greater understanding of our clinical candidate.”

Dr. Simon Westbrook, CEO Levicept.

To talk directly with our contract research manager please contact:

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