



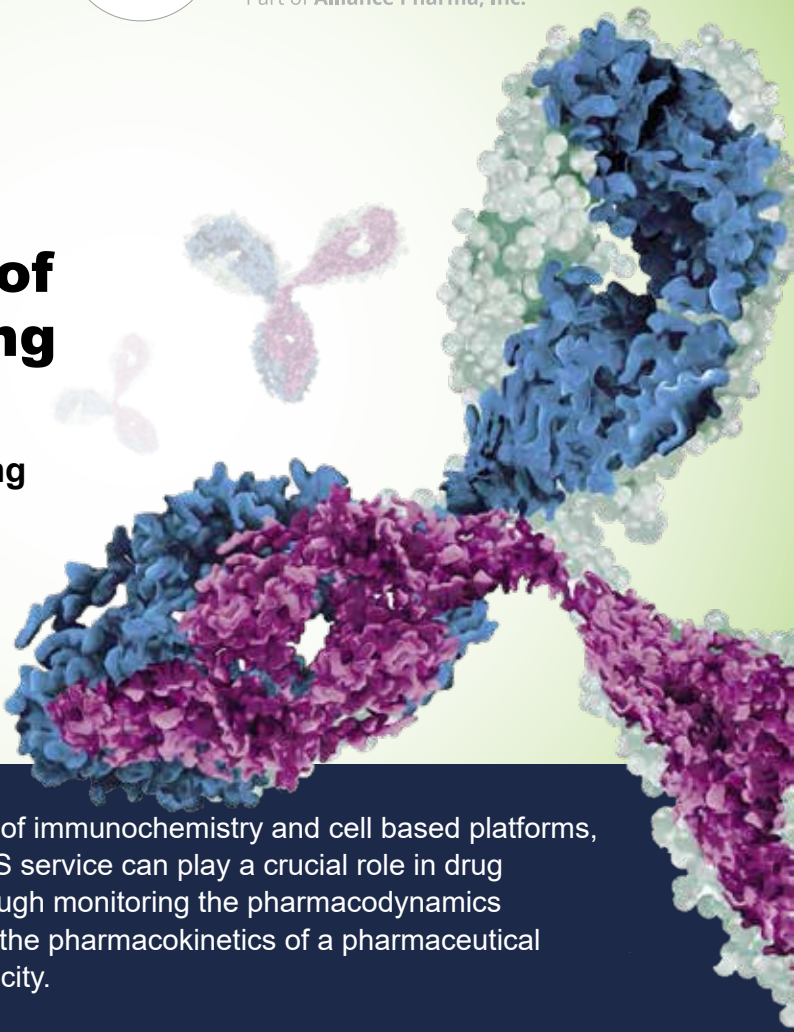
**DRUG DEVELOPMENT  
SOLUTIONS**

Part of Alliance Pharma, Inc.

# Protein LC-MS

## Our specialist service providing quantitation of large molecules utilising LC-MS technology

For over a decade we have been harnessing our small molecule LC-MS expertise to offer a complimentary technique for the quantitation of proteins and peptides in biological matrices.



CENTRE OF  
EXCELLENCE

PROTEIN LC-MS

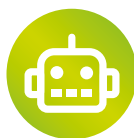
Alongside a suite of immunochemistry and cell based platforms, our Protein LC-MS service can play a crucial role in drug development through monitoring the pharmacodynamics with a biomarker, the pharmacokinetics of a pharmaceutical or its immunogenicity.

Within our Cambridge (Fordham) facility we have over 10 years' experience in the implementation of LC-MS for the bioanalysis of large molecules, first publishing back in 2007 on the utilisation of UPLC-MS/MS for the quantification of proteins in biological fluids. We have continued to contribute to the field through production of peer reviewed publications and white papers demonstrating the depth of our knowledge and scientific competence.

## Supporting your Protein LC-MS project



High sensitivity triple quadrupole platforms



Robust automated platform for bead based affinity capture



HR-MS capability for intact analysis and rapid optimisation of bottom-up workflows



Dedicated team of multidisciplinary staff



All MS systems coupled to UHPLC for fast chromatographic separations

Research partnership with University of Cambridge (Institute of Metabolic Science)



## Protein LC-MS expertise

A major challenge with LC-MS analysis of large molecules is their isolation from similar endogenous components within biological samples. We possess a wealth of experience in various extraction and purification techniques to achieve the required levels of sample cleanliness and sensitivity.

We can recommend and develop robust analytical workflows tailored to your individual project, either through bottom-up proteolytic digestion or top-down intact analysis.



## Why use LC-MS for the quantitation of large molecules?

### Rapid development of assays

- » Not reliant on development of high quality, assay specific antibody reagents
- » Assay format translatable through discovery, preclinical and clinical development

### Mass based detection adds selectivity

- » Can resolve immunoassay interference issues

### Ability to distinguish closely related species

- » Provides structural information on the fate of the molecule
- » Bottom-up monitoring of specific surrogate peptides to inform in vivo stability of the molecule
- » Top-down analysis of intact protein using a HRMS platform

### Complementary to immunoassay

- » Measurement of total concentration of large molecule without the need for assay specific antibody reagents
- » Capable of achieving low pM sensitivity
- » Utility of hybrid LBA/LC-MS assays to achieve high levels of sensitivity

### Multiplexing

- » Multiple reaction monitoring (MRM) enables numerous large molecules to be quantified within a single analysis

Let's discuss your project:  
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