DC BIOSCIENCES

Pioneers in Proteomics

DC BIOSCIENCES

Pioneers in Proteomics

CONTENTS PAGE



Our mission

***"To deliver on the promise of novel proteomic science in drug discovery and advancement."***

DC BIOSCIENCES

Pioneers in Proteomics

INTRODUCTION

## Global Proteomic Services

DC Biosciences has been involved with innovative proteomics for over 15 years, working on projects with researchers in large pharmaceutical companies, biotech firms, and academic institutions in Europe, the US, and Middle East.

Our work has also been key in a recent EU project aimed at identifying new medicines to treat Alzheimer's Disease through investigating a previously little understood gene.

We are well-positioned to apply our extensive knowledge and experience across a broad range of proteomic disciplines including protein profiling, quantitative proteomics, protein post-translational modifications, and affinity proteomics; and also to deliver solutions in key areas of drug discovery and development.

DC BIOSCIENCES

Pioneers in Proteomics

## Protein Identification

At DC Biosciences, we offer a broad range of mass spectrometry-based protein identification methods.

To identify your proteins, it is often much easier to digest protein mixtures into smaller components called peptides. These peptides can then be fragmented in a mass spectrometer to generate $MS^2$ spectra. This commonly used approach is known as "bottom-up" proteomics.

It is quite challenging and time-consuming to routinely evaluate and annotate $MS^2$ spectra and determine the identity of every individual peptide. Thus, the $MS^2$ spectra are searched against a protein database. High-quality matches between $MS^2$ spectra and peptides in the database confirms identity. *De novo* sequencing can be necessary when the protein sequence is unknown, or amino acid substitutions are suspected.

For samples of low complexity, *e.g.*, assessing the purity of an isolated or recombinant protein, intact protein mass determination can provide valuable information.

**Read more.....**

DC BIOSCIENCES

Pioneers in Proteomics

## Quantitative Proteomics

DC Biosciences quantitative proteomic service enables you to answer all your protein quantitation questions.

Why be content with qualitative data when you can also have quantitative data? DC Biosciences offer the most commonly used relative quantitation methods: isobaric labelling with tandem mass tags (TMT), label-free, SILAC, and data-independent acquisition (DIA).

- TMT (Tandem Mass Tag) is a chemical labelling method that utilises isobaric tags to modify peptides.
- Label-free enables relative quantitation between multiple LC-MSMS analyses and is highly-applicable to large patient cohorts in clinical proteomic studies.
- SILAC (Stable Isotope Labelling by Amino acids in Cell culture) is based on the *in vivo* metabolic labelling of the proteins in cells with heavily-labelled versions of specific amino acids.
- DIA (Data Independent Acquisition) is the latest development in LC-MSMS data acquisition.

DC BIOSCIENCES

Pioneers in Proteomics

## Affinity Proteomics

Affinity pull-downs are one of the most common types of proteomic experiments performed in any research laboratory. Combining such experiments with mass spectrometry can be challenging; but it is a very powerful approach when studying protein-protein interactions.

Understanding protein-protein interactions in cellular pathways is essential for comprehending biological processes. Mass spectrometry (MS)-based proteomics is a powerful tool to analyse interactomes. Unlike traditional western blot (WB) analysis, MS can identify all the enriched proteins in a completely unbiased manner.

DC Biosciences offer a range of pull-down proteomic experiments, our experts will guide you from experimental design through to completion and assist you in avoiding the many pitfalls associated with mass spectrometry analysis of affinity-based experiments.

**Contact us....**

DC BIOSCIENCES

Pioneers in Proteomics

## Post Translational Modification

DC Biosciences PTM service enables you to answer questions about the post-translational modifications on your proteins.

Post-translational modifications (PTMs) on proteins are an often understudied and neglected area of proteomics. Yet, PTMs have a huge impact on the cellular function of proteins.

The diversity and relatively low-abundance of modified peptides compared to the unmodified counterparts complicates the study of PTMs. The detection and identification of PTMs by LC-MSMS can be improved by selectively enriching for modified peptides/proteins using a variety of methods (affinity resins, antibodies, *etc.*). The PTM-enriched fraction is then analysed separately from the non-enriched sample.

This can be a complex process but highly rewarding for the researcher. DC Biosciences has the knowledge and experience to use the most innovative methods to secure high quality results.

**Read more....**

DC BIOSCIENCES

Pioneers in Proteomics

## Bioinformatic Data Analysis Service

The overwhelming quantity of data produced by a mass spectrometer from a single experiment can confound the savviest & most experienced of researchers.

At DC Biosciences we have partnered with highly experienced bioinformaticians with a broad range of knowledge to analyse your data. We can combine our own understanding of the field of proteomics with bioinformatic expertise to produce clear and robust results.

Our bioinformatic data analysis service aims to give you quick yet accurate results, a flexible and efficient service, with access to the most innovative and accomplished experts.

We perform and deliver the data analysis, while you concentrate on the science.

**Find out more...**

DC BIOSCIENCES

Pioneers in Proteomics

## Start your project today

At DC Biosciences we offer a friendly and flexible approach with open communication and support at every stage. Contact us today to discuss your project.

DC Biosciences Ltd

Millars House

41a Gray Street

Dundee

DD5 2BJ

customerservices@dcbiosci.com

dcbiosci.com

+44 (0)1382 843413