

OMASS



Mass spectrometry for challenging targets

At Oxford Mass Technologies (OMass) we specialise in applying our [state-of-the-art mass spectrometry](#) platform to characterising intact protein assemblies.

We provide our technology and expertise to assist biotechnology and pharmaceutical companies in tackling the [characterisation of challenging drug targets and biotherapeutics](#).

We help our partners to understand their target proteins in detail, more quickly, with reduced ambiguity, and in new ways that are either not possible or much harder with other analytical techniques.

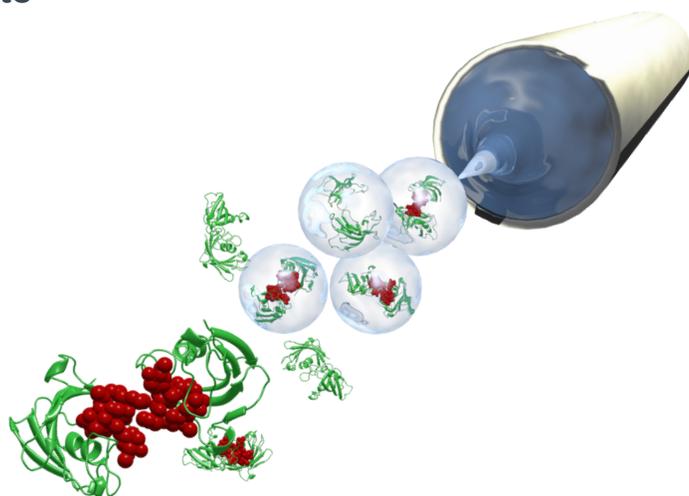
The characterisation information we provide empower scientists to make more informed decisions with greater confidence.

Partnering opportunities

We work together with our partners, providing access to and know-how in advanced native mass spectrometry technology via [collaborative research partnerships](#). Rather than just results, we use our expertise to advise you on the best strategies for success.

Access to frontier technology

We have close relationships with instrument manufacturers, and unrivalled access to the frontiers of native mass spectrometry research at the University of Oxford. This enables us to provide you the [latest instrumentation and applications](#) of the technology.



The OMass Story

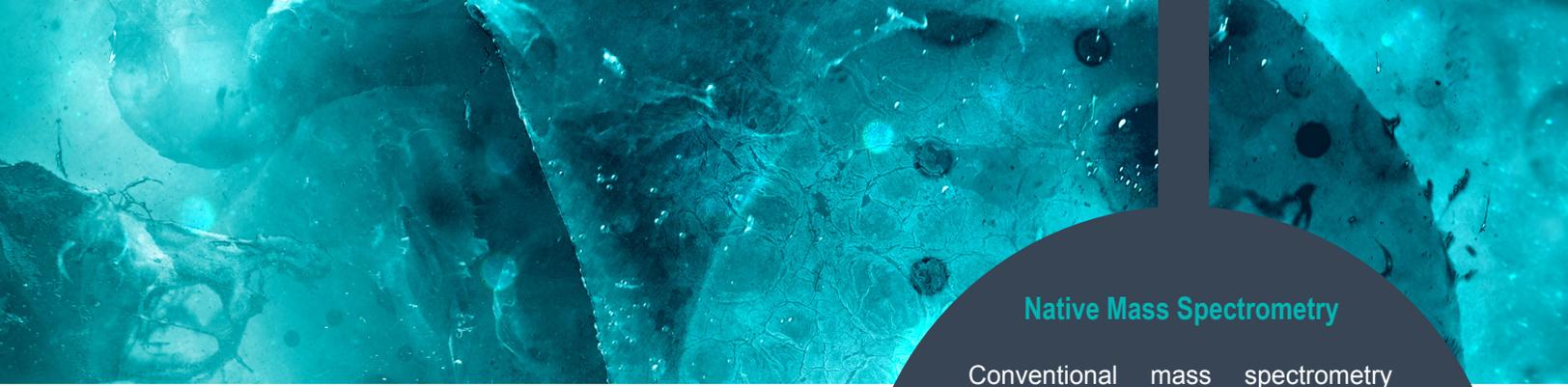
OMass is built on discoveries made over 25 years of research at the University of Oxford and University of Cambridge by our founder Professor Dame Carol Robinson.

These discoveries have taken mass spectrometry from the realm of small molecules to the analysis of large intact protein assemblies. This now mature platform has a track record of providing breakthroughs in the structural biology of proteins. These successes prompted considerable interest from biotechnology and pharmaceutical companies for access to the technology, leading to the creation of OMass in 2016.

OMass and our expert team of scientists are committed to delivering native mass spectrometry technology to drive new advances and understanding in pharmaceutical and biotechnology research.

Providing a native mass spectrometry platform for a new perspective in drug discovery





Native Mass Spectrometry

Conventional mass spectrometry has revolutionized the analysis of small compounds and the primary protein sequence. However, in conventional proteomics and for intact mass measurements denaturing solutions are used and the folded native-like states of the proteins are not preserved. In native mass spectrometry this is not the case: non-covalent interactions are preserved. Protein-protein and protein-ligand interactions are maintained and can be interrogated to reveal stoichiometry, binding strengths, dynamics, and stabilities.

Our technology

With **native mass spectrometry** we extend mass spectrometry to be able to **maintain the non-covalent structure and interactions** of proteins enabling novel types of analyses.

The technology requires only small sample amounts and rapid determination of results provides fast answers to discovery dilemmas.

Application areas

Including:

Biologics

- Full glycan characterisation
- Antibody-drug ratio
- Biologic-receptor binding
- Allostery

Membrane Proteins

- Oligomeric state
- Cofactor/ligand binding
- Bound lipids
- Gas-phase stabilisation

Purity Insights

- Detergent screening
- Delipidation
- Protein integrity
- Post-translational modifications

Binding Interactions

- Binding stoichiometry
- Affinity constants
- Allosteric binding effects

GPCRs

- Drug binding
- Effect of lipids
- Nanobodies
- G-protein coupling

Our technology is used to:

- Analyse intact protein complexes, including membrane proteins
- Resolve structural and binding complexity
- Record ligand and drug binding, affinity, cooperativity, and stabilising effects



We provide a complete suite of mass spectrometry-based services by complementing our native mass spectrometry with **lipidomics**, **proteomics** and **hydrogen-deuterium exchange**.

Genentech say:

OMass currently supports several challenging analytical areas for Genentech including a structural characterization effort for various challenging drug targets. The technology allows us to rapidly assess the oligomeric and often heterogeneous structure of cell surface receptors and has been extremely valuable in highlighting conditions which preserve the structure and non-covalent interactions of important co-factors and lipids. The information provided by this technology is extremely valuable and we have enjoyed the strong collaborative relationship which OMass provides and their expertise in this area has been exceptional. We look further to expanding this collaboration as the technologies expand.



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