Membrane Proteins

OMASS

A native mass spectrometry platform, technology innovation and consultancy provider, meeting the needs of pharmaceutical and biotechnology companies

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

Intact membrane proteins

Our technology is primed for studying challenging membrane protein targets such as GPCRs, channels, pores, transporters and receptor kinases.

We introduce intact membrane protein assemblies into the mass spectrometer under the protection of detergent micelles. The ability to remove the detergents from membrane proteins once inside the mass spectrometer allows membrane proteins to be studied in native-like environments.

Oligomeric state and ligand binding

The instability and dynamic nature of these proteins render them intractable to many biophysical techniques. Native mass spectrometry is providing a new way of understanding the structure and interactions of these targets.

The oligomeric states of membrane proteins is directly observed. The presence of mass discrepencies, such as post-translational modifications is inferred from the measured mass. Co-purifying species, such as cofactors or lipids, are typically observed as adducts in the mass spectrum.

OMASS

Native Mass Spectrometry

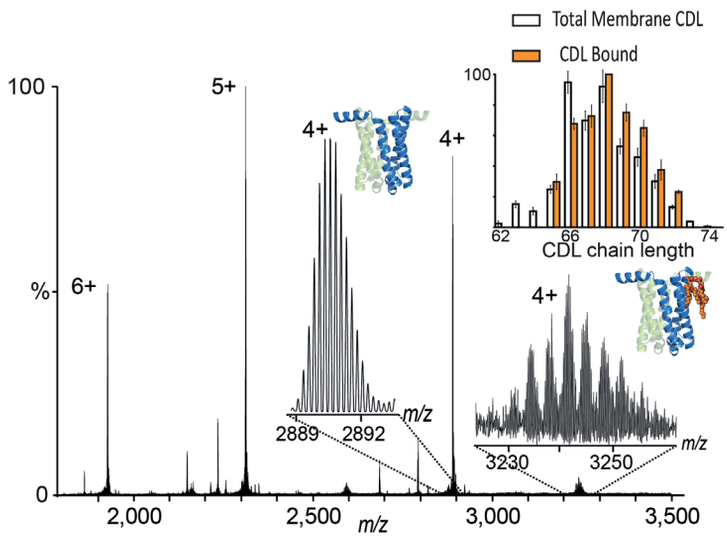
Based on preserving the non-covalent interaction networks of proteins, thereby capturing folded, native-like states along with their interactions with biomolecules or drugs. This allows access to a variety of structural and functional information, such as stoichiometry, binding strengths, dynamics and stability.

Understanding lipid interactions

We have developed a new platform that not only allows a global lipid assessment of samples, but identifies those lipids which interact directly with proteins of interest.

High-resolution measurements on intact protein-lipid complexes are capable of distinguishing different lipid classes as well as the populations of chain lengths bound.

OMass instruments with modified sources allow the dissociation and interrogation of these species, allowing further confirmation. Protein unfolding experiments allow lipids which provide structural stability to receptors to be identified.

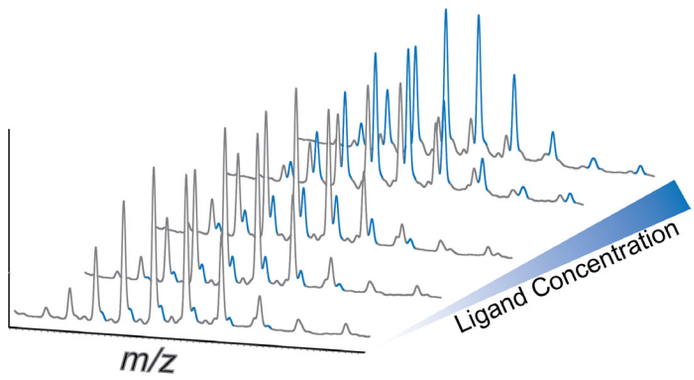


Affinity measurements

The resolution of mass spectrometry allows multiple binding equilibria to be captured simultaneously.

As well as revealing the stoichiomery of bound ligands to receptors, the interactions can be quantified when monitored over several concentrations or time points.

The ability to monitor and resolve several equilibria provides the opportunity to measure ligand binding affinity and allostery.



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