Purity Insights

OMASS

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

- Detergent screening
- Delipidation
- Protein integrity
- PTM identification

Feeding purity into expression and purification optimisation

Native mass spectrometry can be used to monitor protein purity, including to measure sample quality, reproducibility and homogeneity. This can aid the development and improvement of protocols for protein expression and purification.

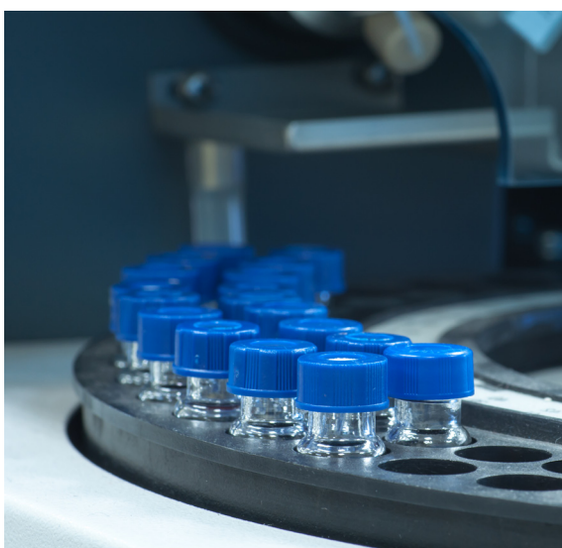
It can be difficult to purify proteins to a level acceptable for many biophysical investigations or applications in biotechnology or pharmaceutical areas. Identifying the contaminants that co-purify with a protein can enable strategies to be developed to enhance sample purity.

With a single mass measurement we directly identify co-purified contaminants and use this information to adjust protocols to increase sample purity.

Detergent screening

The choice of detergent is critically important when studying a membrane protein, as detergents can affect the structure and oligomeric state, the stability in solution, and function.

Native mass spectrometry can measure quaternary structure, and can detect all states present in solution. Coupled with detergent screening this can be used to find conditions that preserve the native state of membrane proteins *in vitro*.



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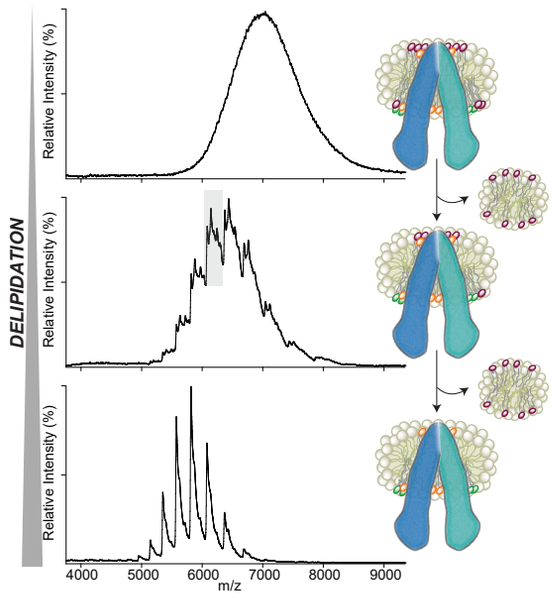
Native Mass Spectrometry

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.

Delipidation

Detergent-solubilised membrane proteins frequently co-purify with lipids. This large source of heterogeneity can influence the reproducibility of preparations, through the effects of lipids on the structure, stability, and function of membrane proteins.

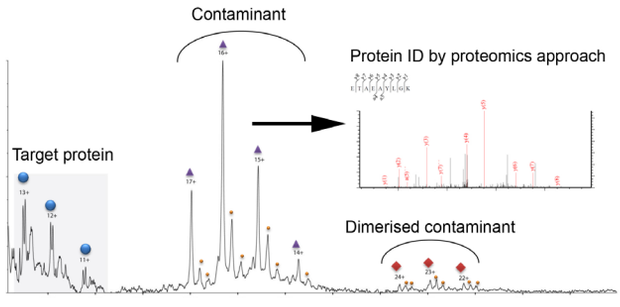
Native mass spectrometry can be used to optimise purification protocols, and can also be used to guide purification in finding conditions where only structurally important lipids are preserved while other bulk lipids are removed.



Protein integrity

We can use native mass spectrometry to assess sample quality, reproducibility and homogeneity by monitoring oligomeric state, sequence integrity, and for the presence of post-translational modifications.

Expression variations can be observed as truncations in sequence, or by the addition of post-translational modifications, such as acetylation, phosphorylation, and glycosylation. These changes can be readily detected by mass spectrometry allowing both the integrity and homogeneity of expressed proteins to be rapidly assessed.



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