

Di-Nitro Compound Internal Exchange Reporter for Mass Spectrometry

The innovation offers a collection of compounds that serve as internal exchange reporters (IERs) of exchange conditions with a superior ability to overcome challenges in reproducibility of Hydrogen/Deuterium exchange studies for the determination of protein structure.

What is the Problem?

Hydrogen/Deuterium exchange with mass spectrometry is a widespread tool for the characterization of protein stability and mapping protein interactions and is becoming more widely used for biotherapeutic development. One of the major drawbacks to this method is the high day-to-day variation of results leading to low reproducibility. Currently available internal exchange reporters designed to reduce variation between runs are limited in that they only function within a narrow temporal window and can exhibit complex solution dependent exchange behavior.

What is the Solution?

The solution is a collection of highly stable internal exchange reporter (IER) compounds that exhibit predictable exchange behavior under a wide range of reaction conditions. These compounds can be easily modified to exchange over a broad temporal window, allowing for more robust empirical exchange correction and improved reproducibility in Hydrogen/Deuterium exchange studies.

What is the Competitive Advantage?

The competitive advantage of this innovation lies in its potential to significantly improve the reproducibility of Hydrogen/Deuterium exchange studies. Unlike currently available internal exchange reporters, these compounds exhibit predictable exchange behavior across various conditions and can be modified to exchange over a broader temporal window, leading to greater reproducibility and more accurate results. This can lead to increased resolution in studying protein conformational dynamics and function, enhanced protein-protein interaction studies, and establishing "equivalence" for FDA standards between existing biologics and emerging biosimilars. As the mass spectrometry market is expected to grow to USD 5.6 billion

Technology ID

BDP 8135

Category

Selection of Available Technologies

Authors

Miklos Guttman

Learn more



by 2025, this innovation can play a crucial role in advancing the field and addressing the ongoing need for reliable and reproducible protein structure determination methods.

References

1. Murphree, T. A., Vorauer, C., Brzoska, M., & Guttman, M. (2021), <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8106947/>, <https://pubs.acs.org/journal/ancham>, 92, 9830–9837