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Taylor-Aris Dispersion Assisted Mass Spectrometry for the Direct Injection Analysis of Proteins with High Matrix Content

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Summary

Electrospray ionization mass spectrometry (ESI-MS) is a predominant tool in the analysis of proteins; however, protein samples often contain ESI-MS incompatible components. This is the case for protein pharmaceuticals such as monoclonal antibodies (mAbs), which are stabilized with non-volatile salts, buffer components and often detergents as well. In case of native protein analysis, the use of phosphate-buffered saline (PBS) solution is a prevalent option for mimicking the native conditions. Although direct infusion is the fastest and most straightforward method for introducing samples to the MS, due to the interferences of the aforementioned MS incompatible components the results often provide low-quality spectra or no information at all.

Taylor-Aris dispersion occurs in case of sample plugs moving slowly through a small inner diameter capillary, causing symmetrical band broadening due to the radial diffusion of analytes across the pressure-driven parabolic velocity profile [1]. This dispersion is more substantial in case of high molecular weight components with low diffusion coefficients, resulting in relatively wide peaks for proteins and narrow peaks in case of low molecular weight matrix components. Consequently, a matrix-free zone forms in the front and rear portions of the sample plug, where ESI-MS measurements can provide clean spectra of the protein, without the need for any conventional separation technique.

We have recently demonstrated the use of Taylor-Aris Dispersion Assisted Mass Spectrometry (TADA-MS) for the simple, fast and low-cost analysis of large molecules in MS incompatible matrices, such as mAbs in their original formulation or native protein complexes in PBS solution [2].

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References

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