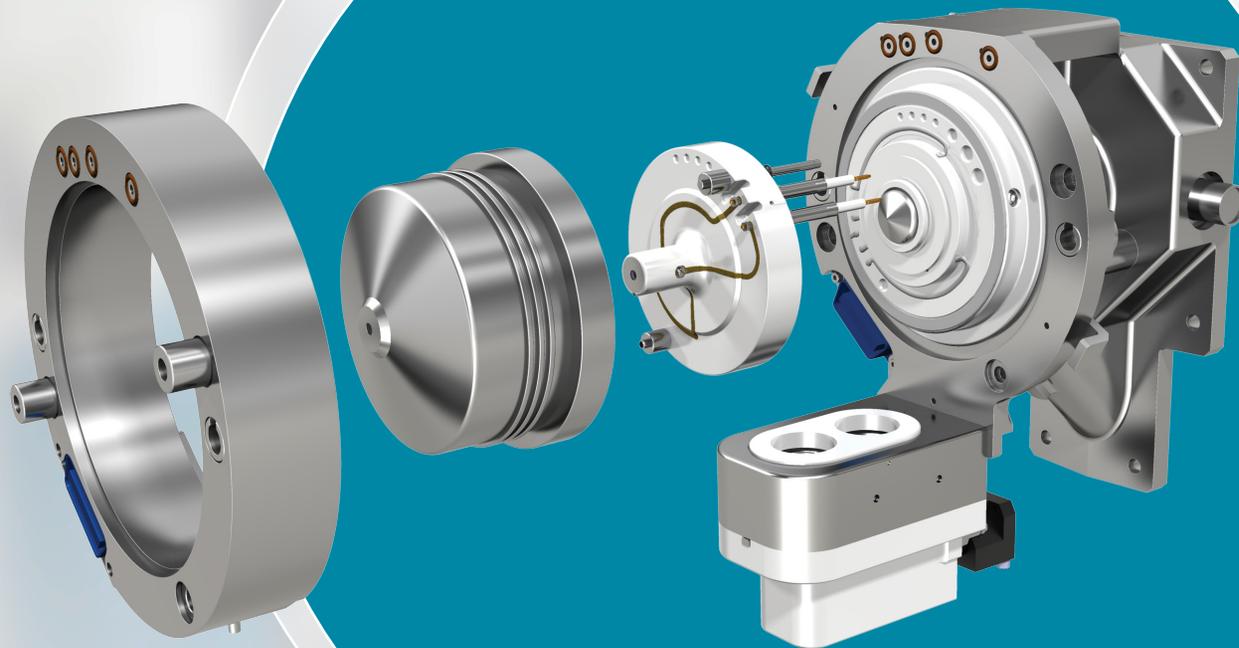


A new dimension in selectivity

SCIEX SelexION differential mobility spectrometry



Advanced separation **for challenging analytes**

Advanced performance

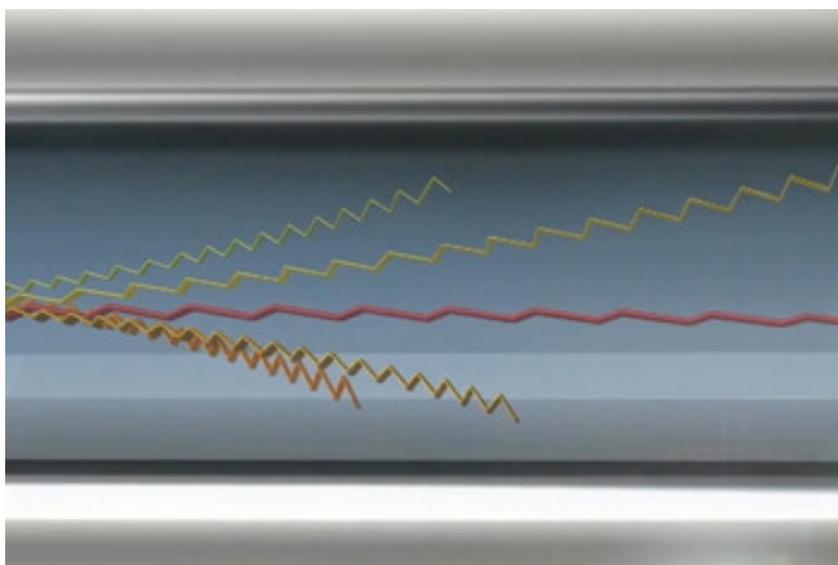
SCIEX SelexION differential mobility spectrometry (DMS) is an effective ion mobility separation tool for improving data quality in the quantification and characterization of challenging samples requiring advanced analytical selectivity.

Enhanced selectivity

SelexION DMS delivers a new dimension of selectivity and performance for any applications requiring the separation of isobaric species, isolation of challenging co-eluting analytes and reduction of high background noise.

Transformational analytical power

SelexION DMS brings unprecedented analytical selectivity and data quality improvements for your most challenging assays. It turns the most sensitive SCIEX Triple Quad, QTRAP and TripleTOF systems into the most sensitive and selective SCIEX systems.



Two parallel flat plates define a mobility region, allowing nitrogen carrier gas to create forward directional flow between the ion source and the mass spectrometer. Analytes are separated based on their respective size, shape, charge state and chemical interaction, prior to entering the mass spec.

Reproducible, robust **and easy to use**

SelexION DMS supports highly selective quantitative and qualitative LC-MS/MS workflows on SCIEX Triple Quad, QTRAP and TripleTOF systems.

Bring a new dimension of selectivity, simplicity and cost-effective efficiency to your LC-MS/MS analysis.

- Quickly add SelexION DMS to your mass spectrometry system with a small, easily interchangeable cell
- Increase peak separation power further through the use of chemical modifiers
- Meet analytical standards for quantitative reproducibility and robustness
- Quantitative and qualitative workflows
- Match cycle and run times with multi-component analysis and UHPLC time scales
- On demand operation can be turned off and on as needed without removing hardware



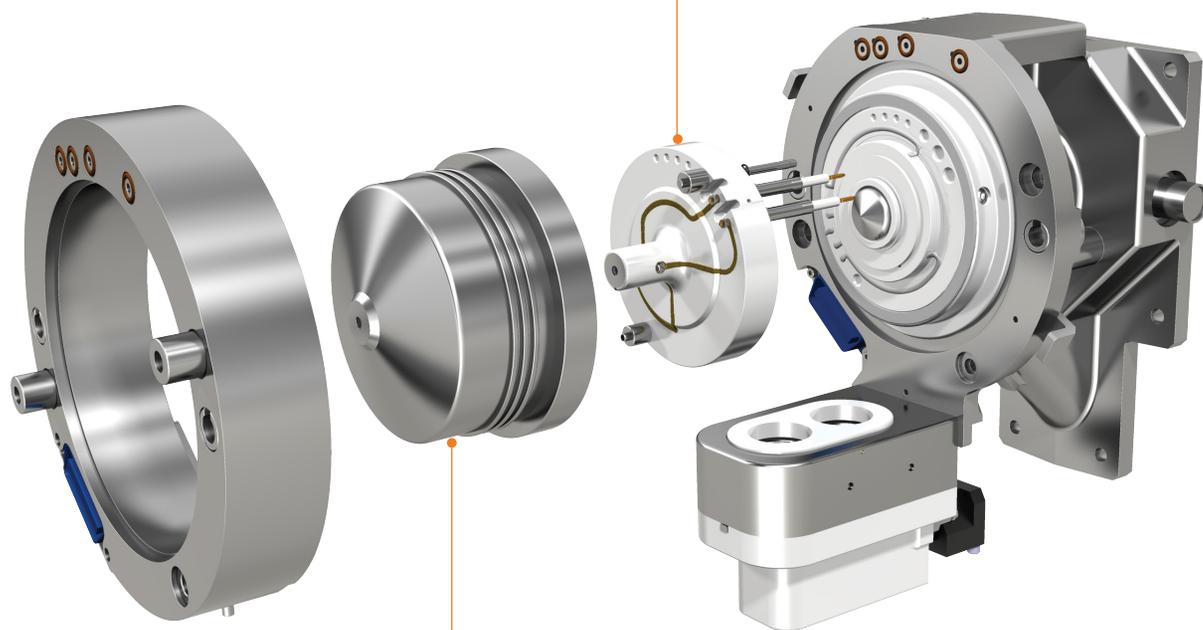
The tool to take on your **most challenging assays**

No other ion mobility separation tool has the reproducibility, robustness and ease of use to deliver highly selective and sensitive quantitative and qualitative analyses, within a UHPLC time scale – all on the most sensitive SCIEX Triple Quad, QTRAP and TripleTOF systems.

Perform a gas phase differential ion mobility separation within the planar mobility cell, based on the ion's size and shape, prior to entering the mass analyzer where the compounds are further separated by m/z ratios. Separate ions based on the difference between their unique differential mobilities across high and low energy fields. Enhance separation power with the use of chemical modifiers such as isopropanol.

SelexION differential ion mobility cell

Compact and simple design allows the cell to be installed without the use of any tools and in less than 2 minutes



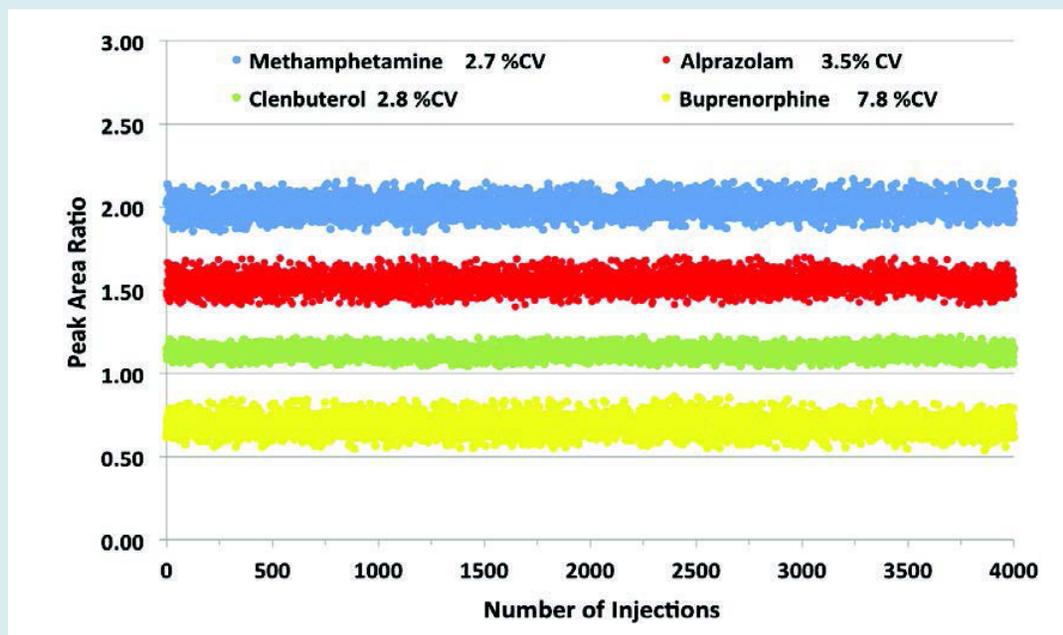
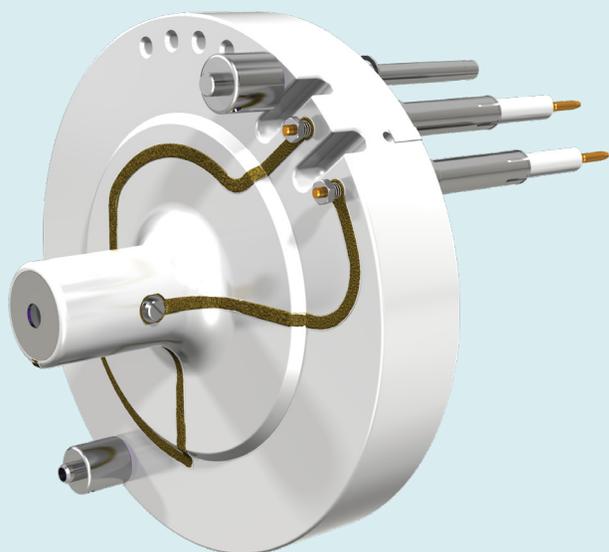
SelexION curtain plate

Updated version of the traditional curtain plate to accommodate the differential ion mobility cell. Maintains the same level of robustness and stability associated with the original design.

SelexION+ DMS - enhanced selectivity in a robust and elegantly simple package

The SelexION+ DMS is enhanced with a jet injector lens to help accelerate ions and deliver up to a 2x improvement in ion transmission.

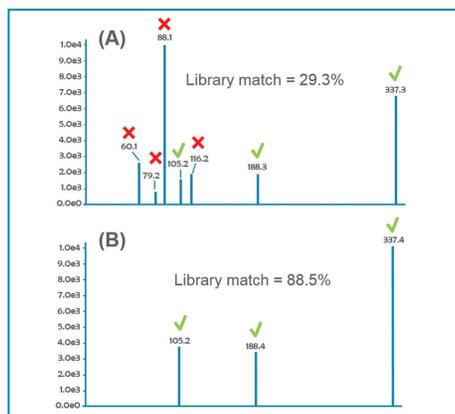
Currently available for use only on the new SCIEX 6500+ series mass spectrometers, the SelexION+ ion mobility cell is enhanced by a jet injector that reduces the ion residence time within fringing fields at the DMS inlet. This increases the size of the acceptance region, providing a 2-fold increase in transmission over the standard SelexION DMS.



4000 replicate injections of methamphetamine, clenbuterol, alprazolam, and buprenorphine spiked in protein precipitated human plasma demonstrates the unique reproducibility, robustness and stability of SelexION+ DMS in combination with the QTRAP 6500+ system. A total of 7 days of consecutive analysis produced a % CV of less than 8% in the peak area (internal standard corrected) for methamphetamine, clenbuterol, alprazolam, and buprenorphine.

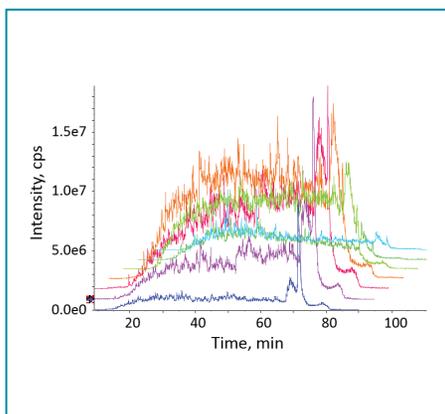
Illuminate your data **by removing isobaric interferences** and **co-eluting analytes**.

SelexION DMS brings clarity to your data, allowing you to dig deeper. Take advantage of the resolving power of ion mobility separations to remove spectral interferences, make use of gas-phase fractionation to reduce the complexity of your data, or de-convolute difficult to separate chromatographic interferences.



A clear difference

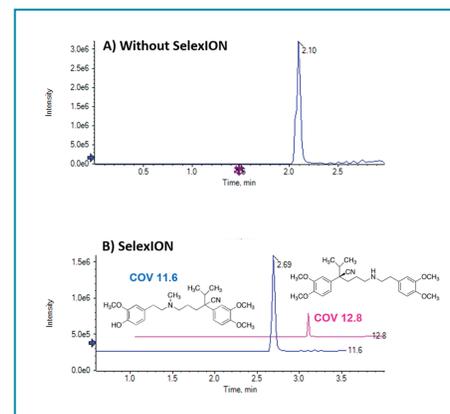
- In some cases, compound identification via automated MS/MS library searching might be challenging due to the presence of isobaric interferences.
- When SelexION DMS is employed, isobaric interferences are removed prior to analysis by MS/MS. In the example presented here, the library match score for fentanyl increases from 29% to 88% when SelexION DMS is employed.



Dig deeper with fractionation

Use discrete compensation voltage steps to subfractionate your proteomic sample at the sample introduction stage. Easily fine tune your fractionation experiment on the fly by adjusting SelexION parameters.

Using a yeast tryptic digest, 7 injections of 1 μ g total protein were performed, each with a different compensation voltage that covered the full peptide range, providing fractionation for a significant increase in confidently detected peptides.

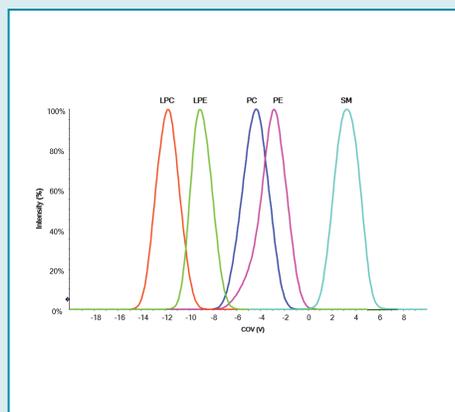


Isobaric metabolites

- Co-elution of verapamil isobaric metabolites, p-O-desmethyl verapamil and norverapamil (m/z-441.2747) prevent confident identification and quantification.
- Differential mobility separation easily separates these co-eluting isobars [p-O-desmethyl verapamil - compensation voltage (CoV) of 12.8 and norverapamil - CoV of 11.6] on TripleTOF systems with SelexION DMS.

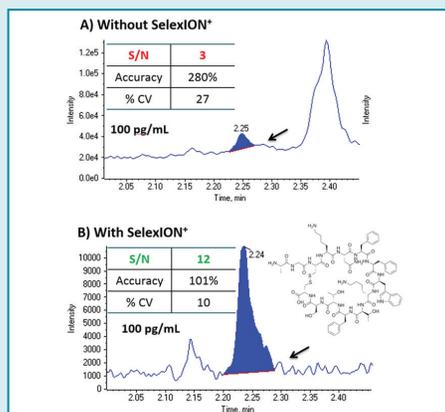
Achieve unprecedented quantitative sensitivity with powerful ion mobility separations

Isobaric interferences and co-eluting contaminants are no match for the resolving power of SelexION DMS!
Harness the power of ion mobility separations to shorten your run times and simplify your sample preparation, while achieving unprecedented levels of sensitivity.



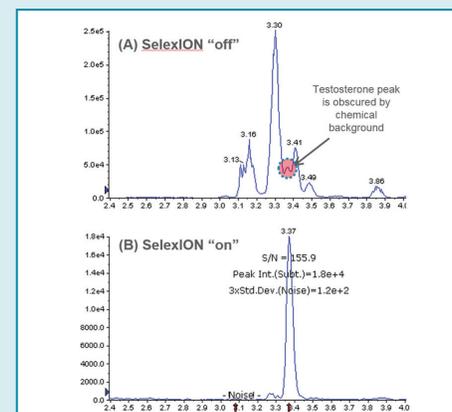
Isobaric lipid molecular species separation

Lipid classes can be separated with DMS, an orthogonal dimension to mass, to remove isobaric interferences. This provides specificity — higher confidence in lipid species assignment to generate more accurate biological insights, and simplicity. DMS also allows easy development of optimized lipid-specific assays without the use of complex, lengthy chiral chromatography.



Reduced background noise

- Somatostatin, a cyclic peptide with poor MS/MS fragmentation is acquired using a MIM (Q1 819.7 → Q3 819.7) assay in rat plasma. High background is observed limiting the signal-to-noise (S/N) ratio and limit of quantification (LOQ).
- Using the new SelexION+ jet injector on the QTRAP 6500+ system, the background noise is significantly reduced, providing a lower LOQ of 100 pg/mL (S/N ratio=12).



Enhanced workflow selectivity

- When a simple “protein precipitation” sample preparation is employed, the measurement of testosterone by LC-MS/MS can be complicated by the presence of co-eluting isobaric interferences.
- When using the SelexION DMS, interferences are removed prior to MS/MS analysis, dramatically improving the LOQ and the overall method robustness.

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