Advanced Analysis of Controlled Substances Using DART-TIMS-QTOF Mass Spectrometry

Leon Groeschel^{1,2}, Ilona Nordhorn¹ Birgit Schneider¹, Jürgen Kempf³, Artem Filipenko⁴, Carsten Baessmann¹

¹ Bruker Daltonics GmbH & Co. KG, Bremen, HB, Germany; ²University of Muenster, Muenster, NRW, Germany; ³Institute of Forensic Medicine, Medical Center – University of Freiburg, Freiburg, BW, Germany; Bruker Daltonics Inc., Billerica, MA, USA

Introduction

Forensic analytics are constantly facing growing demands like an increasing number of targets due to new psychoactive substances (NPS). The caseloads in these laboratories are increasing. These issues lead to the need of fastened up preparation and analysis time although not lacking the high sensitivity and selectivity needed in this field. The use of Direct Analysis in Real Time-Mass Spectrometry (DART-MS) is a technique that combines these aspects. With nearly no sample preparation and fast analysis times it is a valuable tool for the high throughput analysis and fast identification of drugs and their mixtures. The use of Trapped Ion Mobility Spectrometry (TIMS) in combination with DART adds another dimension to the analysis, allowing isomeric drugs to be separated.

timsTOF-MS - Add a new dimension!

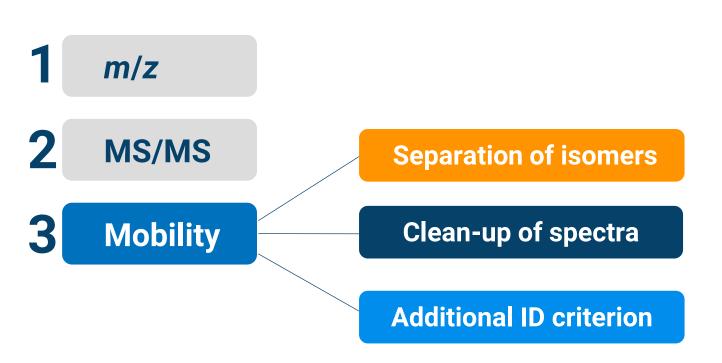


Fig. 1: The addition of the ion mobility dimension provides three benefits.

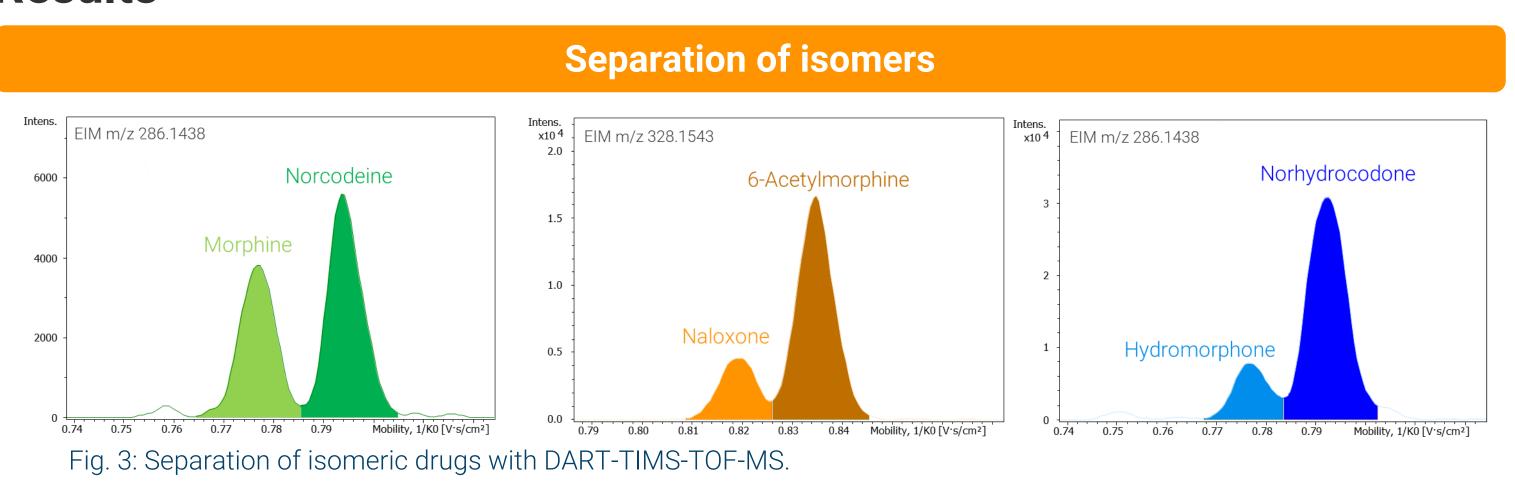
Methods

A Bruker timsTOF Pro 2 mass spectrometer equipped with a Bruker DART JumpShot ion source was used for analysis. Reference standards and mixtures were analyzed after spotting aliquots of 3 µL onto a QuickStrip.



Fig. 2: Bruker timsTOF Pro 2 equipped with a Bruker DART JumpShot ion source.

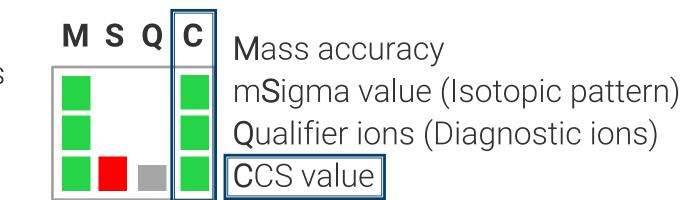
Results



All mobilograms revealed a separation of the substances in the mobility dimension

Additional ID criterion

TIMS adds an ID criterion in form of the Collisional Cross Section (CCS) which enhances the confidence in the compound identification



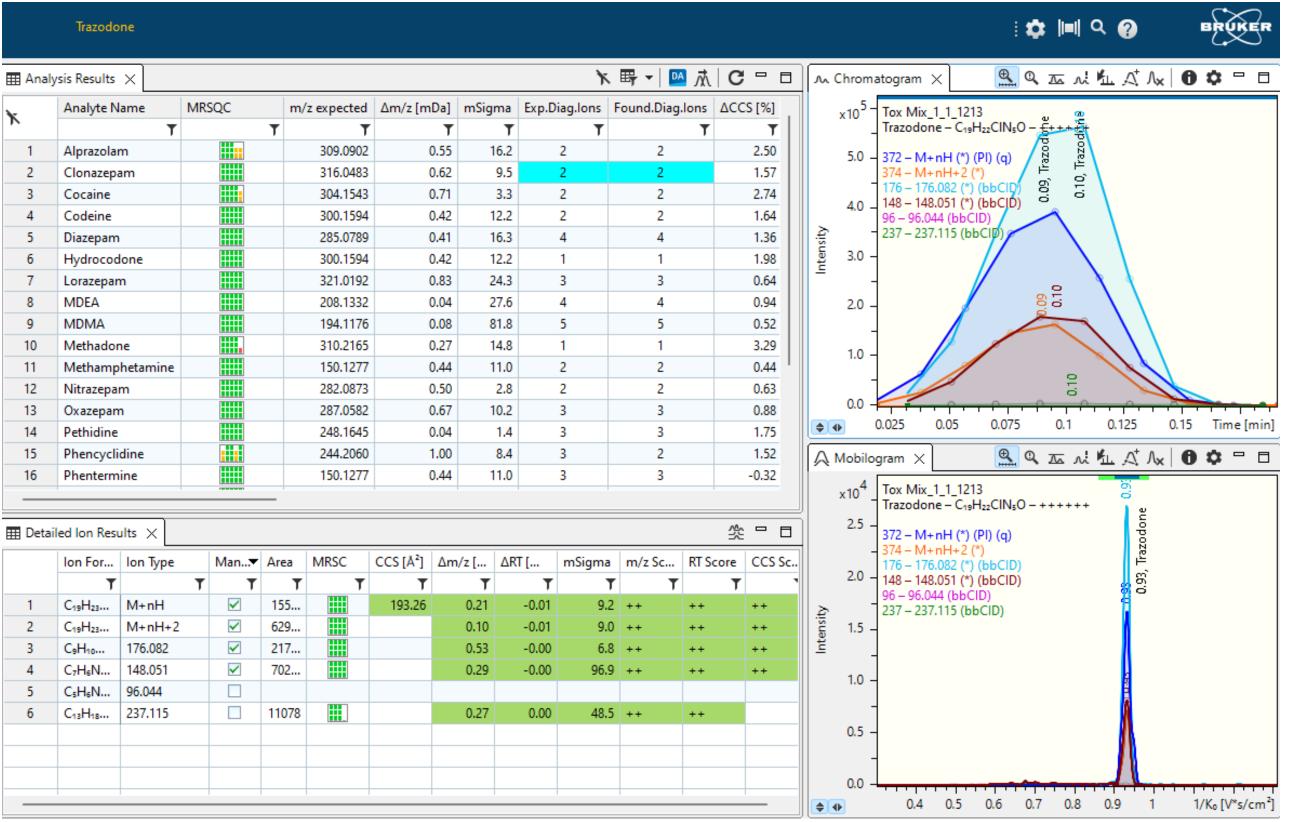
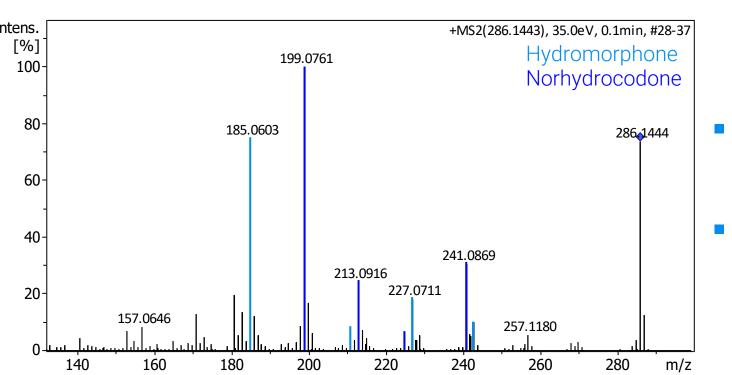


Fig. 7: Results of the analysis of a mixture of drugs with DART-TIMS-TOF-MS in bbCID mode.

Clean-up of spectra

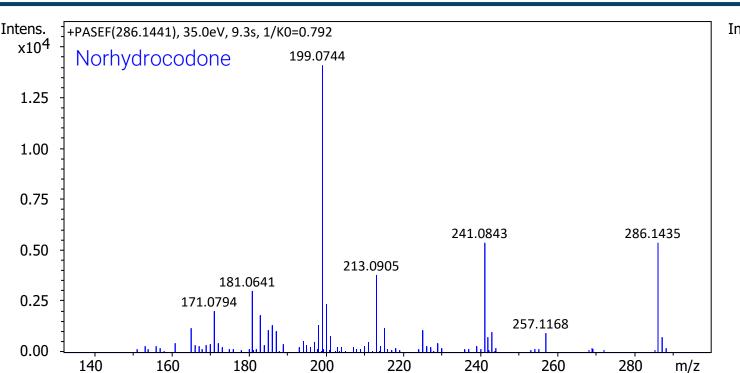
TIMS OFF: AutoMS/MS



- m/z based precursor selection leads to mixed fragmentation spectra for isomers
- Lower library match scores and false negative results

Fig. 4: AutoMS/MS spectrum for m/z 286.144 obtained with AutoMS/MS for a mixture of Hydromorphone and Norhydrocodone.

TIMS ON: Parallel Accumulation Serial Fragmentation (PASEF)



obtained with for a mixture of Hydromorphone and Norhydrocodone.

- Mobility based separation prior to precursor isolation for fragmentation
- Cleaner MS/MS spectra and therefore higher library match scores

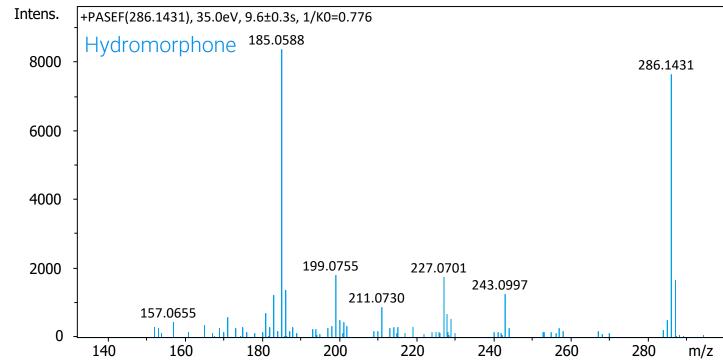


Fig. 5: PASEF spectrum for m/z 286.144, $1/K_0 = 0.792 \text{ Vs/cm}^2$ Fig. 6: PASEF spectrum for m/z 286.144, $1/K_0 = 0.776 \text{ Vs/cm}^2$ obtained with for a mixture of Hydromorphone and Norhydrocodone.

Tab. 1: Library match scores obtained for the analysis of a mixture of Hydromorphone and Norhydrocodone.

Compound	Purity'	
	AutoMS/MS	PASEF
Hydromorphone	603	970
Vorhydrocodone	690	951

Conclusion

- DART-TIMS-TOF-MS provides a chromatography-free approach for the analysis of isomeric drugs
- Fast generation of reliable results

DART-timsTOF