Example of True Signal Deconvolution® in an Automated SPME-GCxGC-TOFMS Analysis of Non-Derivatized Drugs in Urine

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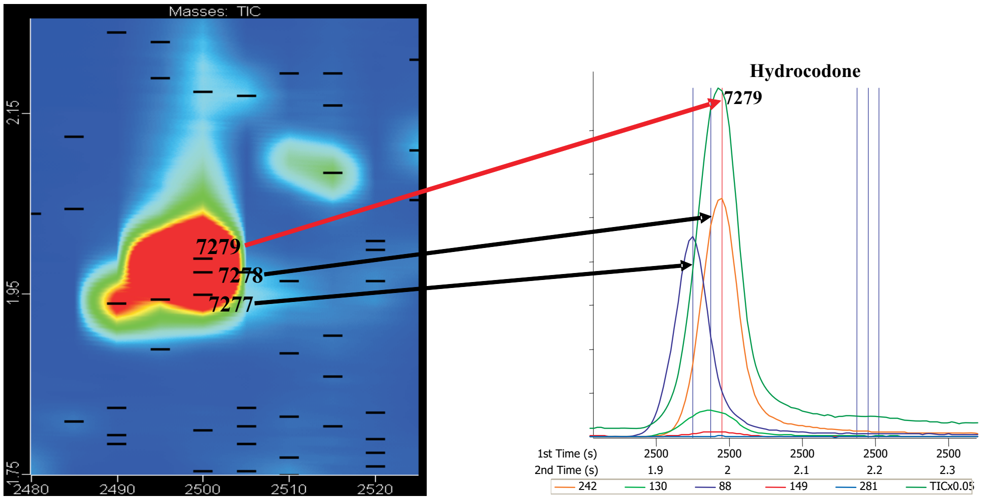

Peak #	Name	R.T. (s)	UniqueMass	Similarity
7277	Cyclohexaneacetic acid, à-ethyl-	2500 , 1.950	88	511
7278	Undeca-2,4,6,8,10-pentaenal, 11-(2-furyl)-, oxime	2500 , 1.975	130	622
7279	Hydrocodone	2500 , 1.990	242	893

The illustration above shows the benefits of time-of-flight mass spectrometry to allow fast acquisition rates which provide the data density and non-skewed mass spectra required to facilitate deconvolution algorithms that successfully identify trace components even in heavy sample matrices. Hydrocodone (Peak 7279) is identified with a similarity of 893 as well as 2 other components in approximately 40 milliseconds.

Columns:
30 m x 0.25 mm x 0.25 µm Rxi-5MS
1.5 m x 0.18 mm x 0.20 µm Rtx-200

TOFMS:
45 to 550 m/z @ 200 spectra/s

For questions on this analysis
e-mail us at: life_science@leco.com

For a complete listing of snapshots
and application notes visit us on the
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