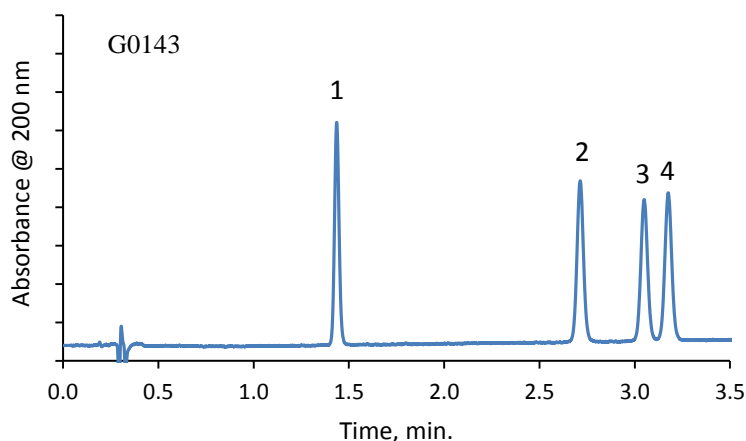


HALO | Fused-Core® Particle Technology

Application Note: 153-SC

Isocratic Separation of Synthetic Cannabinoids on HALO C18



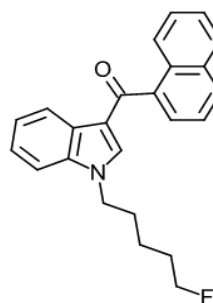
PEAK IDENTITIES:

1. AM2201 (359.44 g/mol)
2. JWH-081 (371.47 g/mol)
3. JWH-122 (355.47 g/mol)
4. JWH-019 (355.47 g/mol)

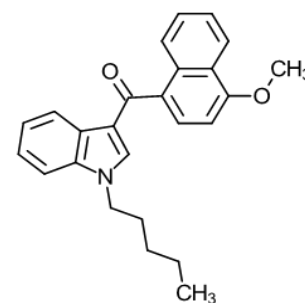
TEST CONDITIONS:

Column: HALO C18, 2.7 μ m, 2.1 x 100 mm
 Part Number: 92812-602
 Mobile Phase: Isocratic: 25/75 A/B
 A= 5 mM ammonium formate
 B= 95/5 acetonitrile/ water with 5 mM ammonium formate
 Flow Rate: 0.6 mL/min.
 Pressure: 279 bar
 Temperature: 30 °C
 Injection Volume: 0.5 μ L
 Sample Solvent: 50/50 water/acetonitrile
 Detection: UV 200 nm, VWD
 Data Rate: 100 Hz
 Flow Cell: 1 μ L
 LC System: Shimadzu Nexera X2

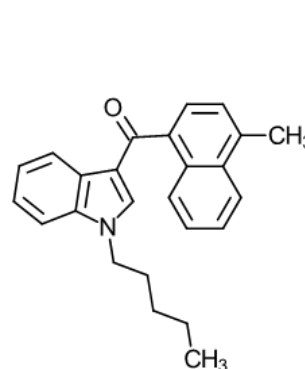
STRUCTURES:



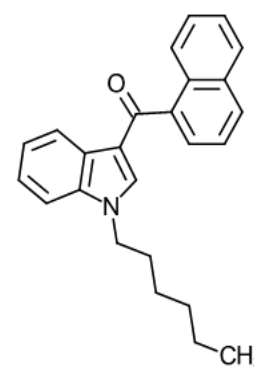
AM2201



JWH-081



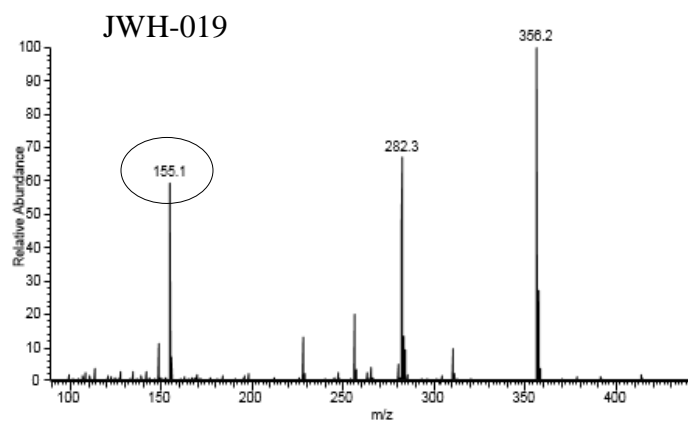
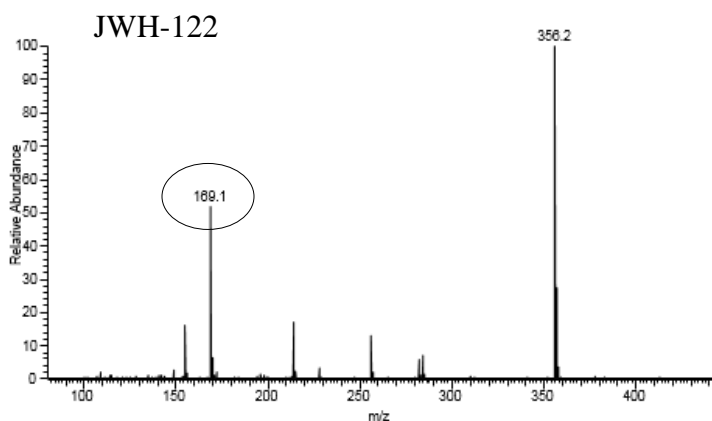
JWH-122



JWH-019

Synthetic cannabinoids are man-made compounds that act like the chemicals found in the marijuana plant. The four compounds in this mixture represent only a small number of the variations that exist. Just as one compound is made illegal, another variation will be synthesized to take its place. This represents a growing challenge for law enforcement agencies. Using a HALO C18 column gives a fast, efficient separation of these cannabinoids with ample resolution for the next generation of illegal species.

Determination of Synthetic Cannabinoid Homologues on HALO C18



MS TESTING CONDITIONS:

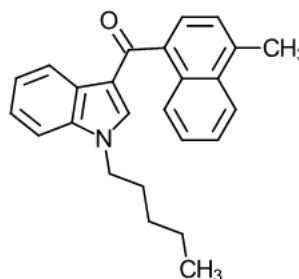
MS System: Thermo Fisher Orbitrap VelosPro ETD

Scan Time: 6 μ scans/250 ms max inject time

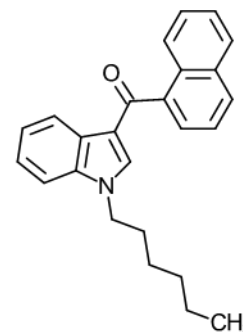
Scan range: 50-2000 m/z

MS parameters: Positive ion mode, ESI at +4.0 kV,
225°C capillary

STRUCTURES:



JWH-122 (m/z= 356.47)



JWH-019 (m/z= 356.47)

Synthetic cannabinoids can be very similar in their chemical structure. In fact, many of these cannabinoids are analogs or isomers of each other and can be difficult to distinguish. Two homologues in this particular sample were fraction collected and then identified using an orbital ion trap MS system. The Orbitrap allows us to see signature fragmentations of a particular compound, allowing positive identification of each isomer.