PFAS Analysis Using High Resolution Accurate Mass Spectrometry

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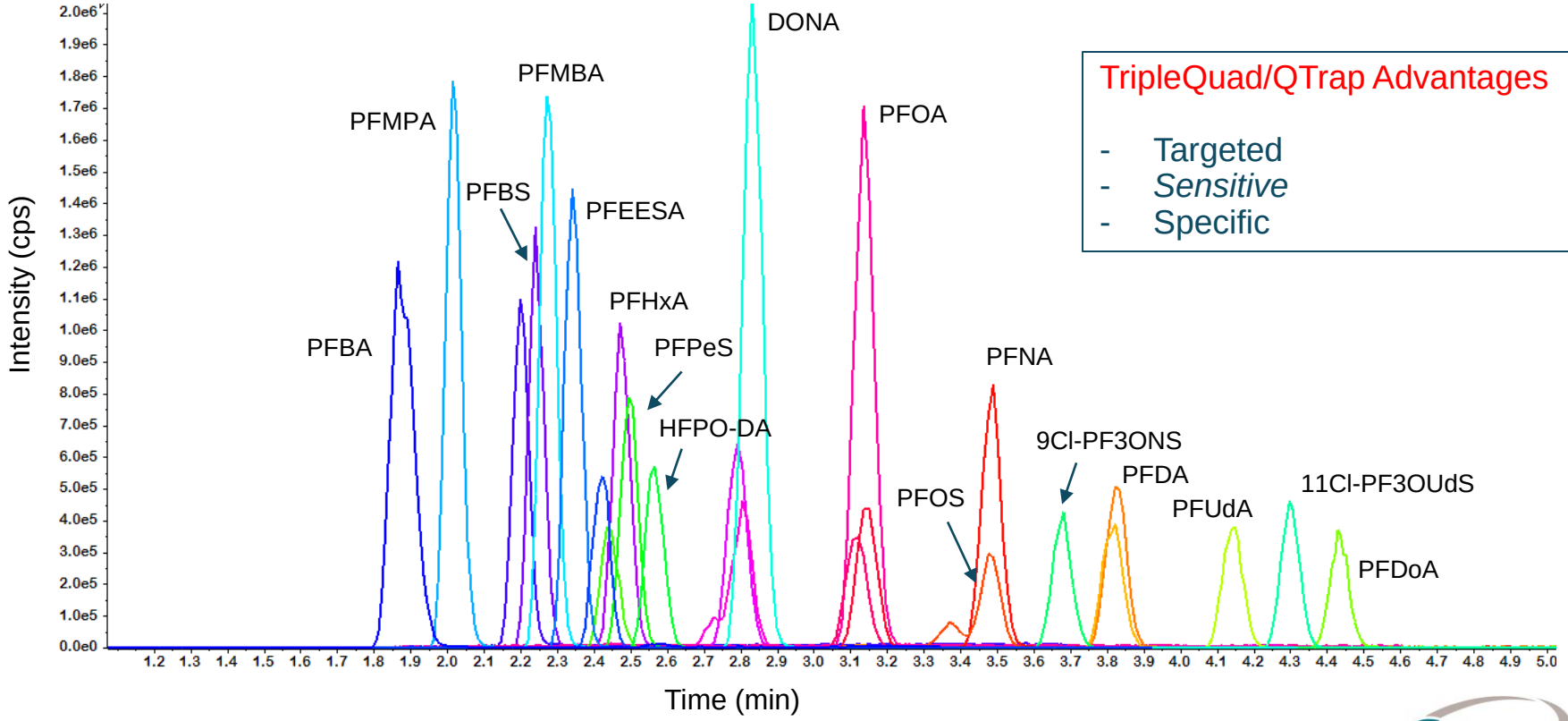
Outline

- What additional information can HRMS provide for PFAS analysis?
- Targeted MRMHR Acquisition
  - Similar to MRM acquisition but monitoring high resolution fragments
- Non-Target Analysis Using SWATH™ Acquisition
  - Unknown ID using MS/MS fragmentation spectra (GenX impacted)
  - MS/MS library matching in AFFF-impacted groundwater

EPA Method 533 Mix: 25 ppb (SCIEX 5500+ TripleQuad)



TripleQuad/QTrap Advantages

- Targeted
- *Sensitive*
- Specific

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Unique Features of a HRAM QTOF versus TripleQuad MS

- Q1 (mass filter) and Q2 (collision cell) are same as TripleQuad
- Q3 is replaced by very fast scanning time-of-flight tube (TOF)
  - Allows for *high quality, high resolution* full scan MS data
  - Precursor scans (TOF MS) and Fragment Scans (TOF MSMS)
- Applications:
  - High resolution MRM Quantitation; HRAM fragments results in greater compound specificity
  - Non-Target Acquisition with Suspect Screening; HRAM product scan for compound confirmation
  - Unknown Compound ID

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SCIEX X500R QTOF System

DESIGN IMPROVEMENTS AND DETAILS

Heated Chamber & N-Shaped Flight Path
Minimized height, flight chamber heated to 60ºC to maintain mass accuracy.

TwinSpray
An independent calibrant delivery path for reliable auto-calibration.

Legendary Turbo V source and Curtain Gas interface
Renowned ionization performance and ruggedness for high sensitivity and sample throughput

Minimized footprint
The benchtop stature (110 x 57 x 112 cm)* occupies less lab space than any other HRMS system on the market.

Integrated calibration
~1.5 min for mass calibration; negligible impact on batch time.

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MRM^{HR}: Targeted Acquisition

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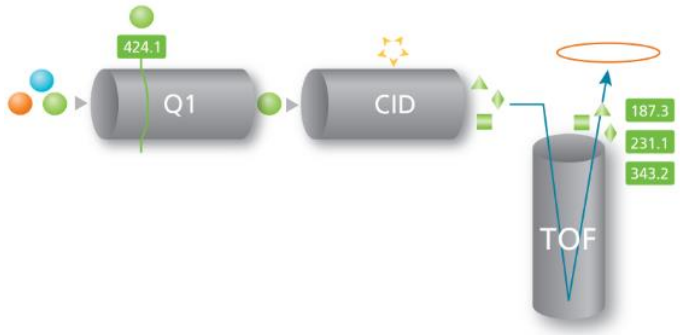
Targeted Acquisition: MRM^{HR} Acquisition Method

HIGH RESOLUTION FRAGMENT IONS



- High resolution fragment ions results in greater compound specificity
- Optimized CE for each MRM
- Scheduled MRM capability to minimize scan time; unique retention time window for each MRM
- Increased method flexibility

TOF MSMS

Mass Table | Apply fragment ion mass | Apply TOF start/stop mass | Apply Scan Schedule | Import and autofill... | Sort by precursor ion

	Compound ID	Group name	Precursor ion (Da)	Fragment ion (Da)	Accumul...	Declusteri...	Collision energy (V)	Retention time (min)	Retention ti...
1	A5760 1	A5760	205.97	122.0255	0.1500	-100	-20	3.40	30
2	A5760 2	A5760	205.97	106.0305	0.1500	-100	-20	3.40	30
3	A5760 3	A5760	205.97	78.0354	0.1500	-100	-24	3.40	30
4	F4106 1	F4106	219.94	156.0239	0.1500	-60	-18	6.24	30
5	F4106 2	F4106	219.94	77.9664	0.1500	-60	-32	6.24	30
6	F4106 3	F4106	219.94	141.0004	0.1500	-60	-24	6.24	30
7	UJV12 1	UJV12	293.00	205.9705	0.1500	-60	-24	2.49	30
8	UJV12 2	UJV12	293.00	77.9662	0.1500	-60	-72	2.49	30
9	UJV12 3	UJV12	293.00	142.0080	0.1500	-60	-36	2.49	30
10	UNS90 1	UNS90	293.99	205.9688	0.1500	-60	-26	3.61	30
11	UNS90 2	UNS90	293.99	77.9657	0.1500	-60	-62	3.61	30
12	UNS90 3	UNS90	293.99	142.0073	0.1500	-60	-32	3.61	30
13	QZY47 1	QZY47	307.02	219.9870	0.1500	-60	-20	5.10	30
14	QZY47 2	QZY47	307.02	77.9668	0.1500	-60	-48	5.10	30
15	QZY47 3	QZY47	307.02	156.0244	0.1500	-60	-32	5.10	30

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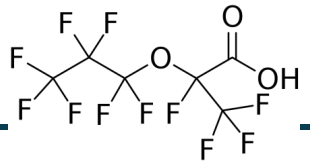
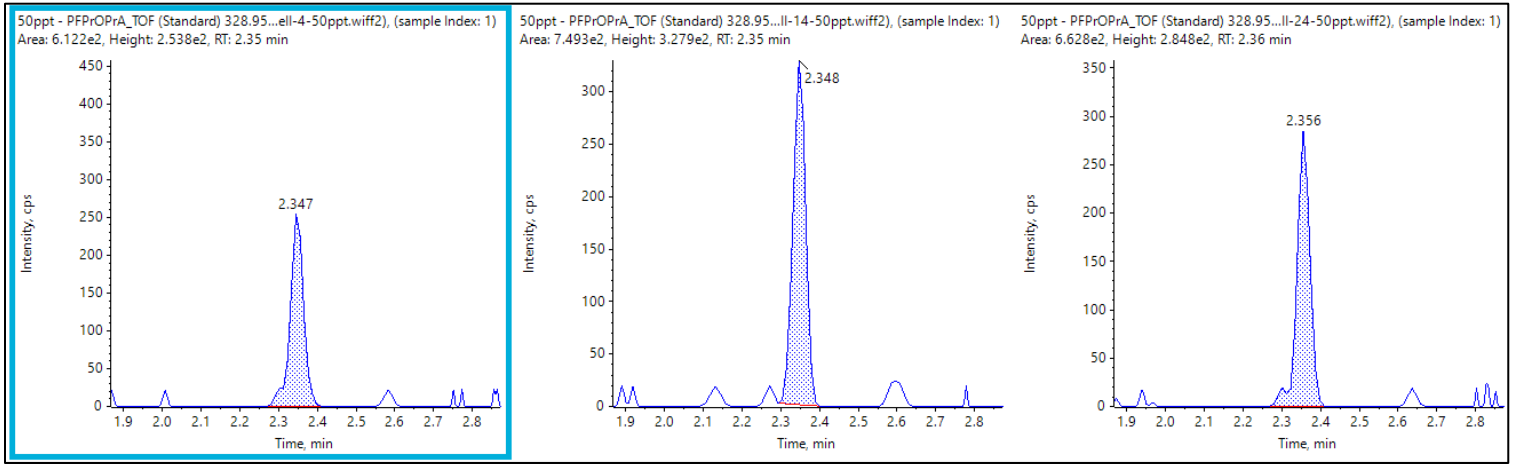
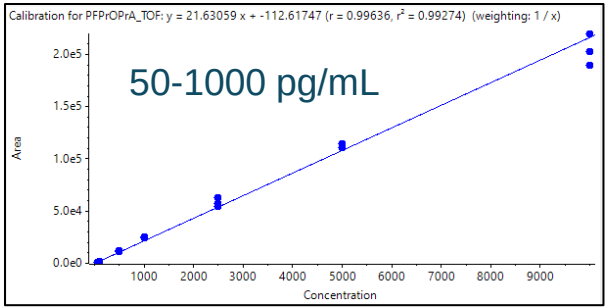
GenX (PFPrOPrA, HFPO-DA), TOF MS





Row	Component...	Actual...	Num...	Mean	Standa...	Percent CV	Accuracy	Value #1	Value #2	Value #3
1	PFPrOPrA_TOF	10.00	0 of 3	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	PFPrOPrA_TOF	25.00	0 of 3	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	PFPrOPrA_TOF	50.00	3 of 3	36.4	3.2	8.80	72.81	33.5	39.8	35.9
4	PFPrOPrA_TOF	100.00	3 of 3	97.8	6.1	6.25	97.84	94.6	104.9	94.0
5	PFPrOPrA_TOF	500.00	3 of 3	539.2	9.1	1.69	107.85	529.6	547.8	540.3
6	PFPrOPrA_TOF	1000.00	3 of 3	1151.4	22.2	1.93	115.14	1142.4	1176.7	1135.1
7	PFPrOPrA_TOF	2500.00	3 of 3	2713.9	198.8	7.33	108.55	2540.1	2930.7	2670.8
8	PFPrOPrA_TOF	5000.00	3 of 3	5170.1	110.3	2.13	103.40	5103.9	5109.0	5297.5
9	PFPrOPrA_TOF	10000.00	3 of 3	9441.1	686.4	7.27	94.41	8790.2	9375.1	10158.2



- TOF MS, C6HF11O3 [m/z = 328.9677], LOQ = 50 ppt

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GenX (PFPrOPrA, HFPO-DA): MRMHR 1

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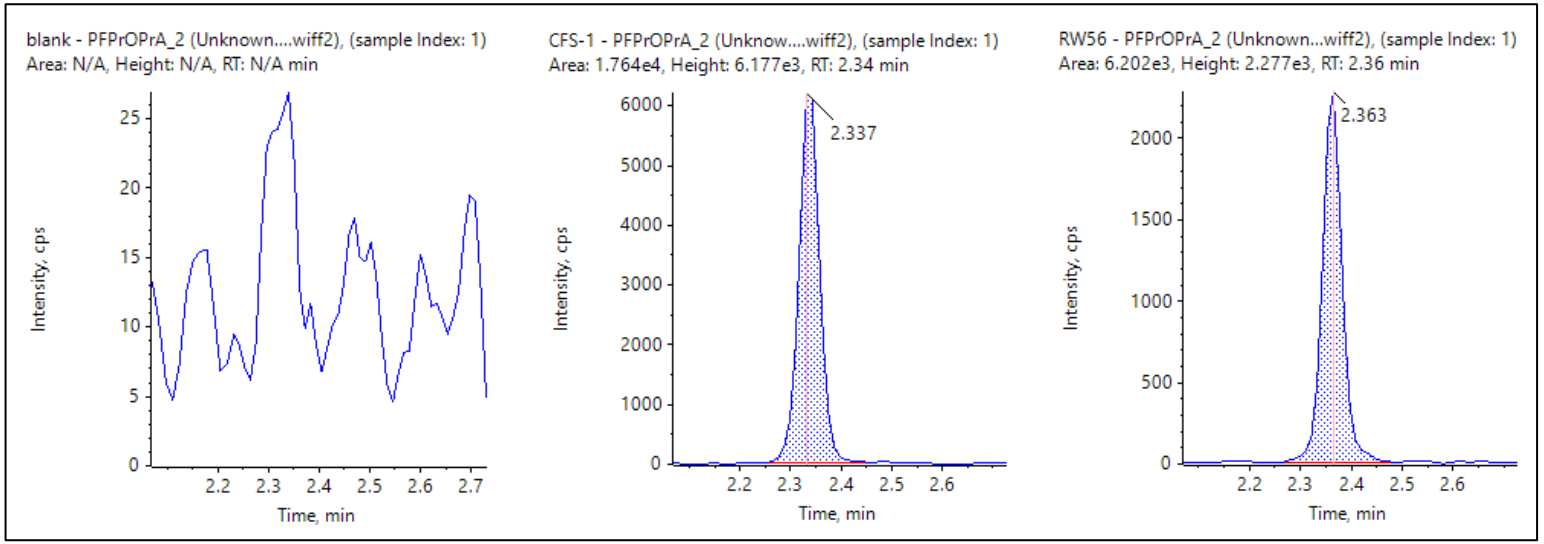
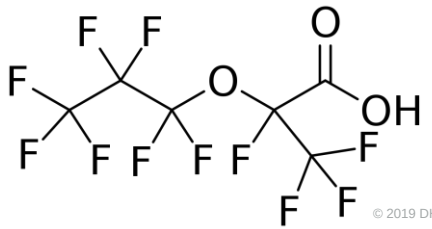
Sediment

River Water



- MRMHR 1, [m/z = 329.0 -> 284.9795]



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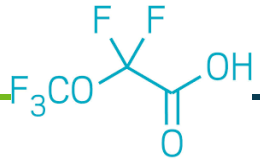
PFMOAA: MRMHR 1



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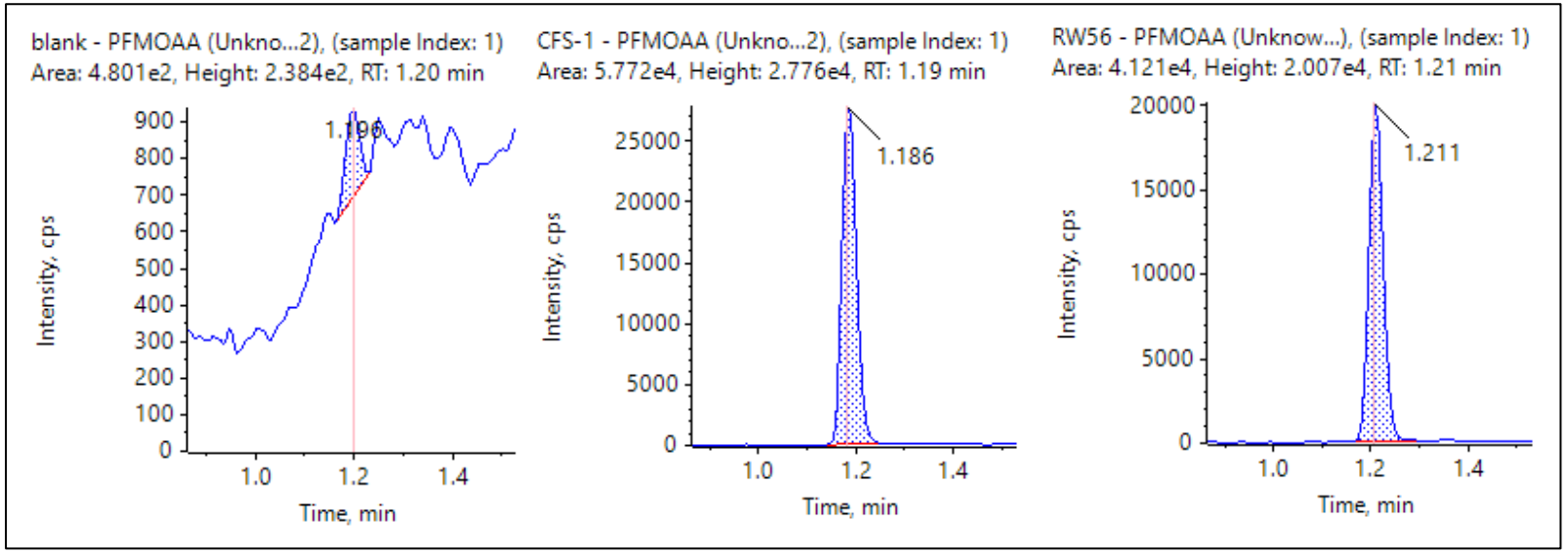
Sediment

River Water



- MRMHR 1, [m/z = 179.0 -> 84.9899]

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Non-Target Analysis with SWATH™ Acquisition

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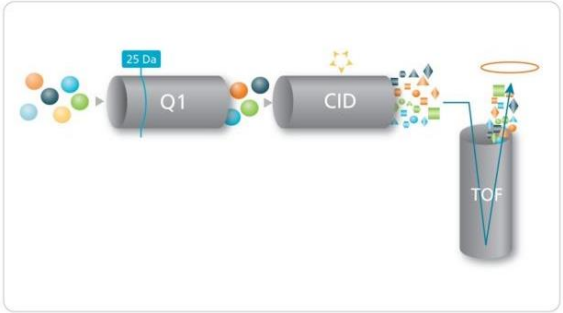
Non-Target Acquisition: MS/MS^{ALL} using SWATH™ Acquisition

A MODE OF DATA INDEPENDENT ACQUISITION PROVIDING MS/MS^{ALL}



- Wide Q1 isolation window is stepped across the mass range
- Can use variable mass windows to reduce complexity of MS/MS spectra, increased specificity
- *Unlike IDA (Information Dependent Acquisition), MS/MS acquisition is NOT dependent on precursor intensity*
- **Advantage: Sequentially acquired MS/MS spectra of all precursor ions across the mass range**
- **Retrospective data analysis**

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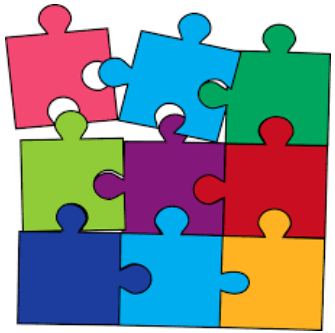
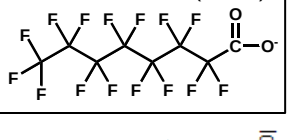
Molecule Fragmentation

- Compounds will break apart into characteristic fragments which generally represent pieces of the original (precursor) molecule
- **Fragmentation pattern can reveal the chemical structure**
- TOF instruments obtain high resolution fragment masses resulting in greater specificity



Perfluorooctanoate (PFOA)



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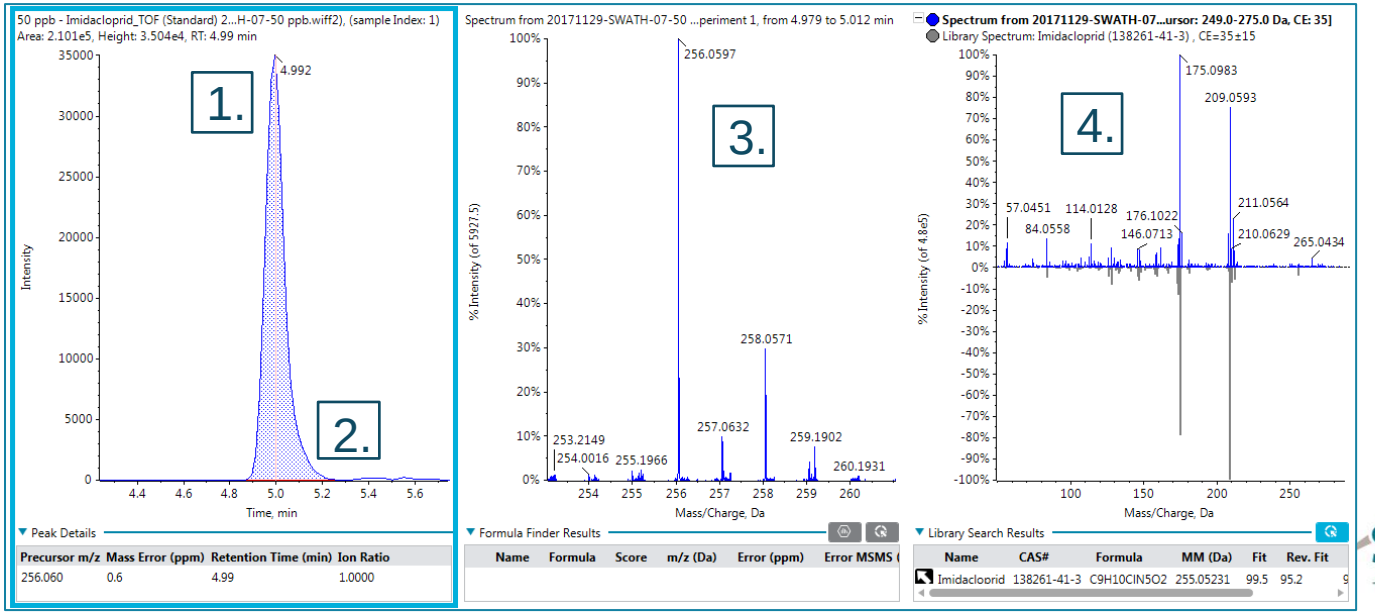
HRMS – Multiple Lines of Evidence for Compound ID

1. Retention time (<2.5%) ✓
2. High resolution accurate mass (<5 ppm) ✓
3. Isotope Pattern (>80%) ✓
4. MS/MS Fragmentation Pattern Match with HRMS Library ✓



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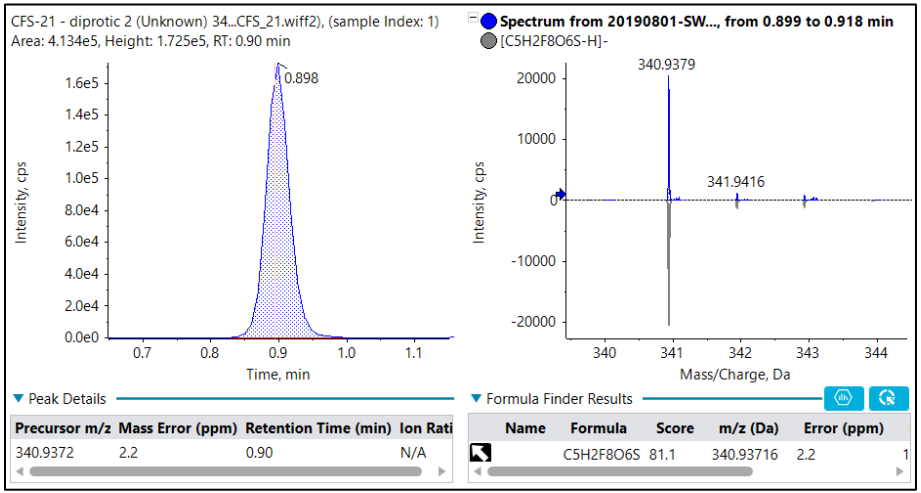
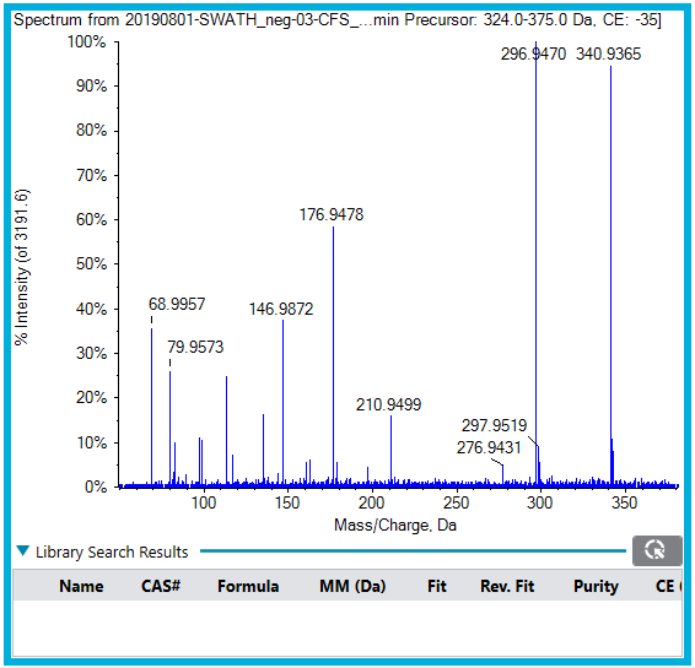
Results – Diprotic Compound, C5H2F8O6S (m/z 340.9372)



MS/MS Fragmentation Spectrum



Sediment Sample, CFS-21

Precursor mass error = 2.2 ppm

MS/MS Fragment Spectrum:

- CO2 neutral loss (m/z 296.9470)
- SO3 (m/z 79.9573)
- CF3 (m/z 68.9957)

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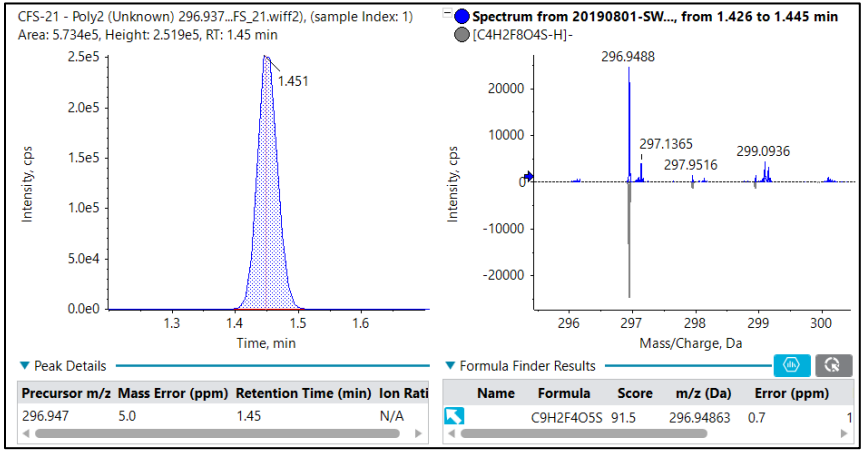
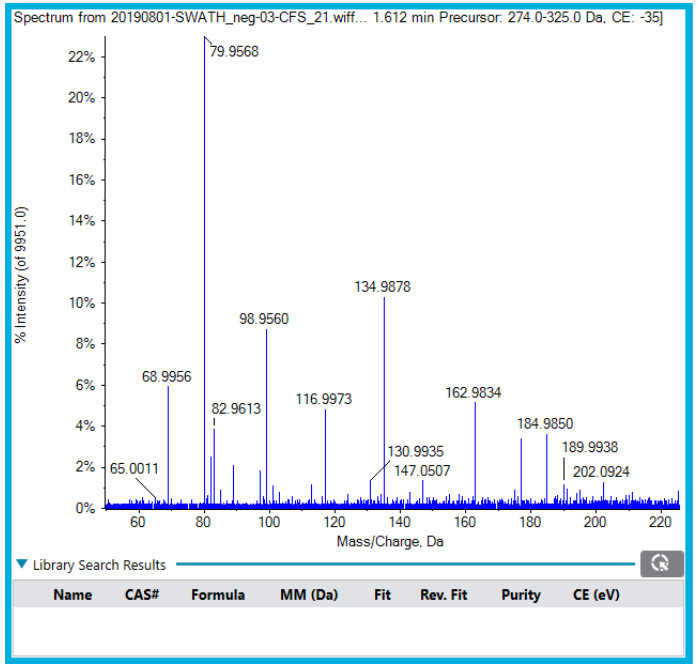
Results – NVHOS, C4H2F8O4S (m/z 296.9473)



MS/MS Fragmentation Spectrum



Sediment Sample, CFS-21

Precursor mass error = 5 ppm

MS/MS Fragment Spectrum:

- SO3 (m/z 79.9568)
- FSO3 (m/z 98.9560)
- CF3CF2O (m/z 134.9878)

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Non-Target Analysis of AFFF-Impacted Groundwater

- 9 AFFF-impacted groundwater samples collected from near US Air Force Bases
- Water samples analyzed by large-volume injection techniques, as detailed in SCIEX Application Note (1)

  - 1 mL water combined with 0.65 mL MeOH & mass-labelled standards (Wellington Laboratories)

  - 100 µL injection using SCIEX ExionLC™ system; gradient conditions

- Instrumental analysis using SCIEX X500R QTOF system with SWATH® acquisition and MRM^{HR} in positive and negative mode
- Components list from updated SCIEX Fluorochemical HR-MS/MS Library 2.0, containing 253 compounds (positive, negative, zwitterion)

1. Roberts S, Hyland KC, Butt C, Krepich S, Redman E and Borton C. (2016) *AB Sciex Publication Number: RUO-MKT-02-4707-A*

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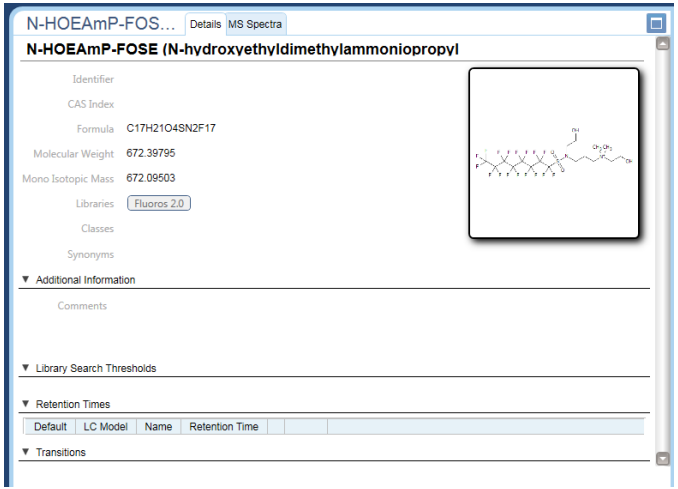
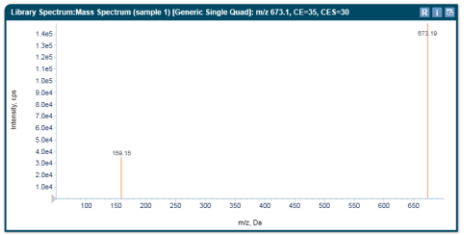
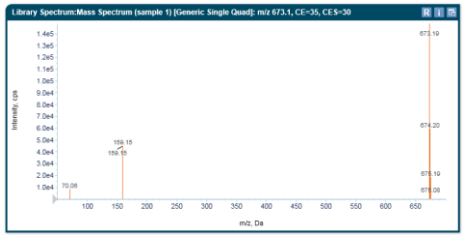
SCIEX Fluorochemical HR-MS/MS Library 2.0

HIGH RESOLUTION MS/MS SPECTRAL LIBRARY RECENTLY UPDATED TO INCLUDE ADDITIONAL COMPOUNDS DETECTED IN AFFF AND AFFF-IMPACTED WATER

- 252 PFAS compounds covering negative, positive and zwitterionic compound classes
- Built specifically for the X500R QTOF system but also compatible with SCIEX TripleTOF® and QTRAP® systems







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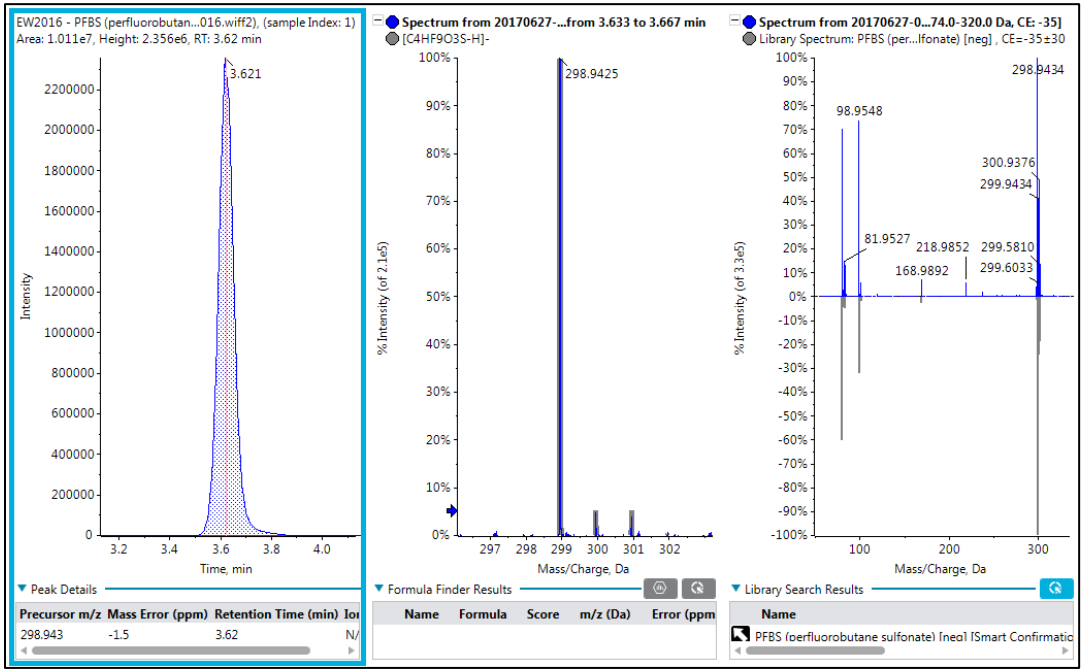
Ground Water Sample “A” – Legacy PFAS



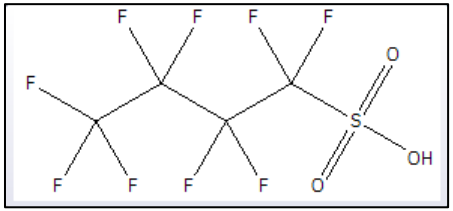
Compound Identified:

PFBS

Mass error = -1.5 ppm ✓

Isotope ratio ✓

MS/MS Library Match ✓



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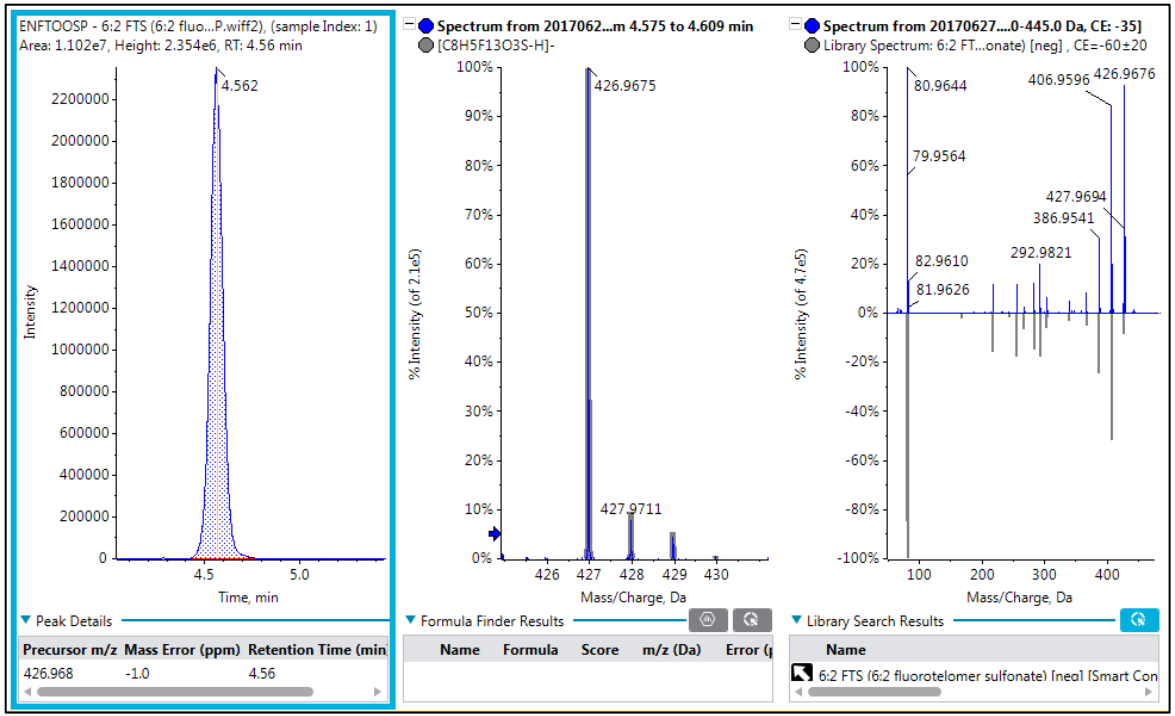
Ground Water Sample “B” – Legacy PFAS



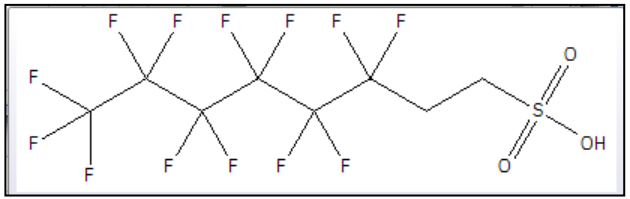
Compound Identified:

6:2 fluorotelomer sulfonate (6:2 FTS)

Mass error = -1.0 ppm ✓

Isotope ratio ✓

MS/MS Library Match ✓



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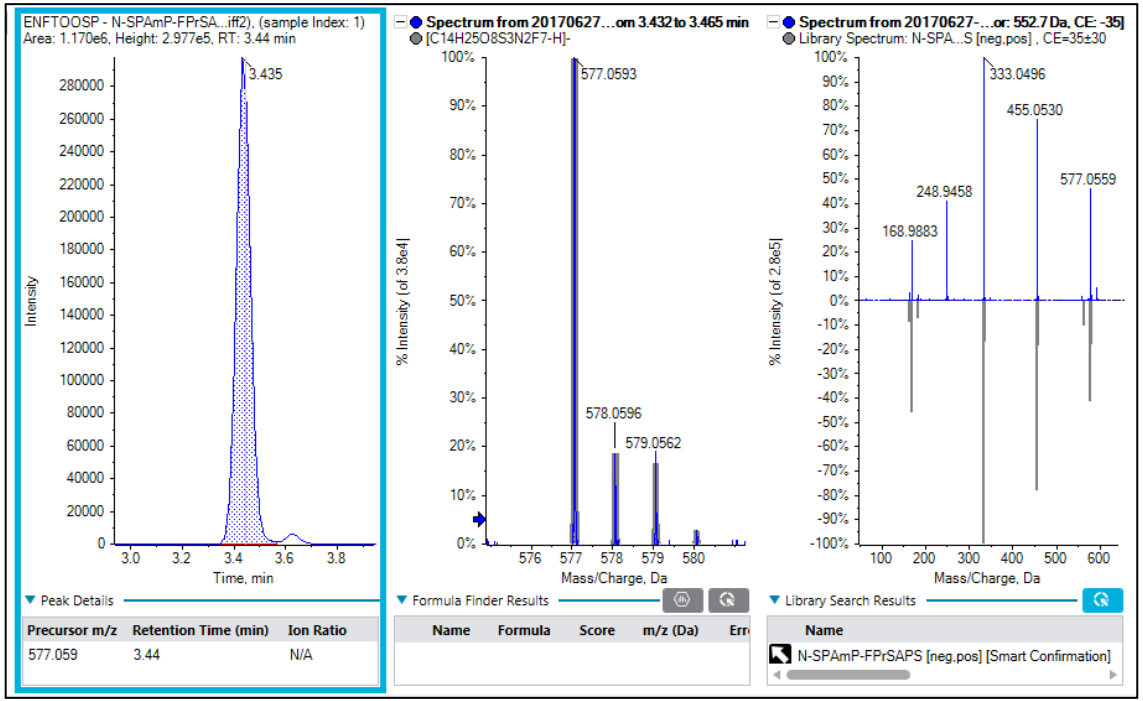
Ground Water Sample “B” – Novel PFAS



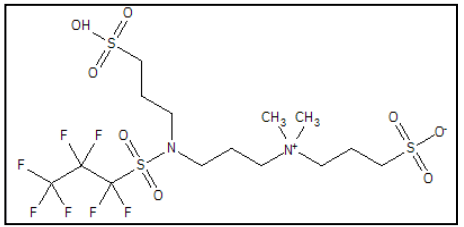
Compound Identified:

N-SPAmP-FPrSAPS

Mass error = 0.8 ppm ✓

Isotope ratio ✓

MS/MS Library Match ✓



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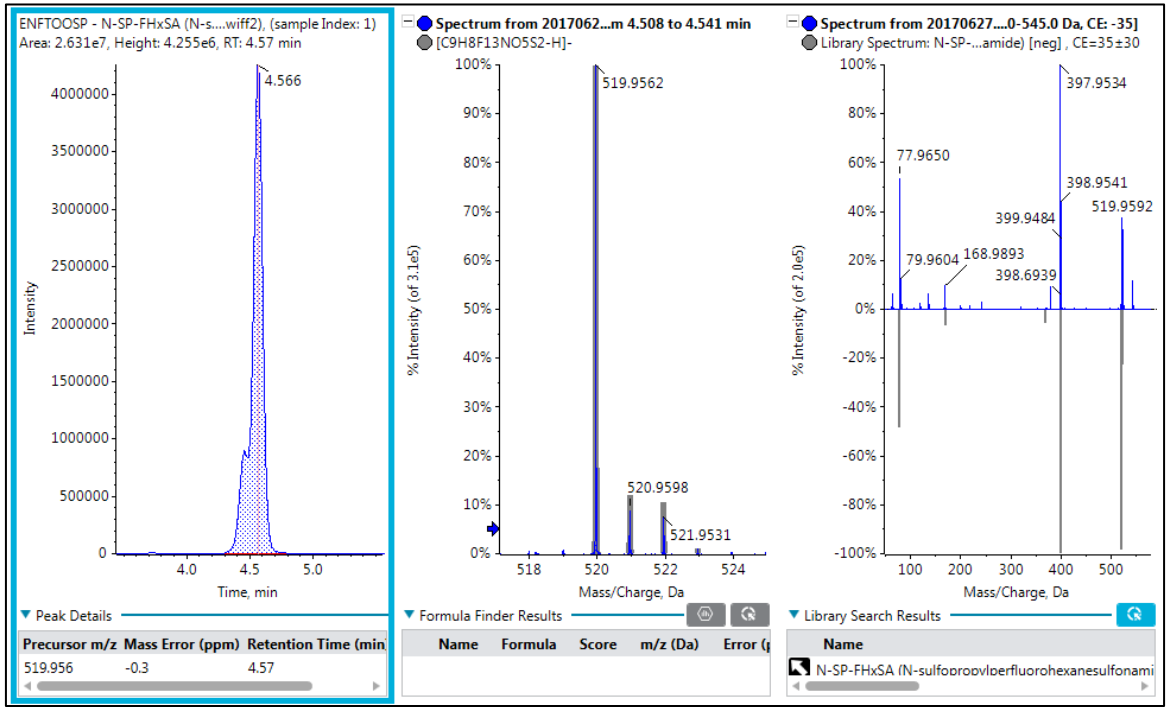
Ground Water Sample “B” – Novel PFAS



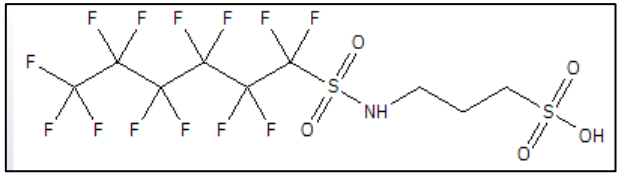
Compound Identified:

N-SP-FHxSA

Mass error = -0.3 ppm ✓

Isotope ratio ✓

MS/MS Library Match ✓



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Conclusions

- HRMS provides additional power for PFAS analysis

- Increased specificity of MRM^{HR} acquisition
  - Mass resolve matrix interferences

- Non-target Acquisition; use of MS/MS fragmentation spectra
  - Unknown identification from fragment assignment
  - Compound confirmation using MS/MS library matching

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