

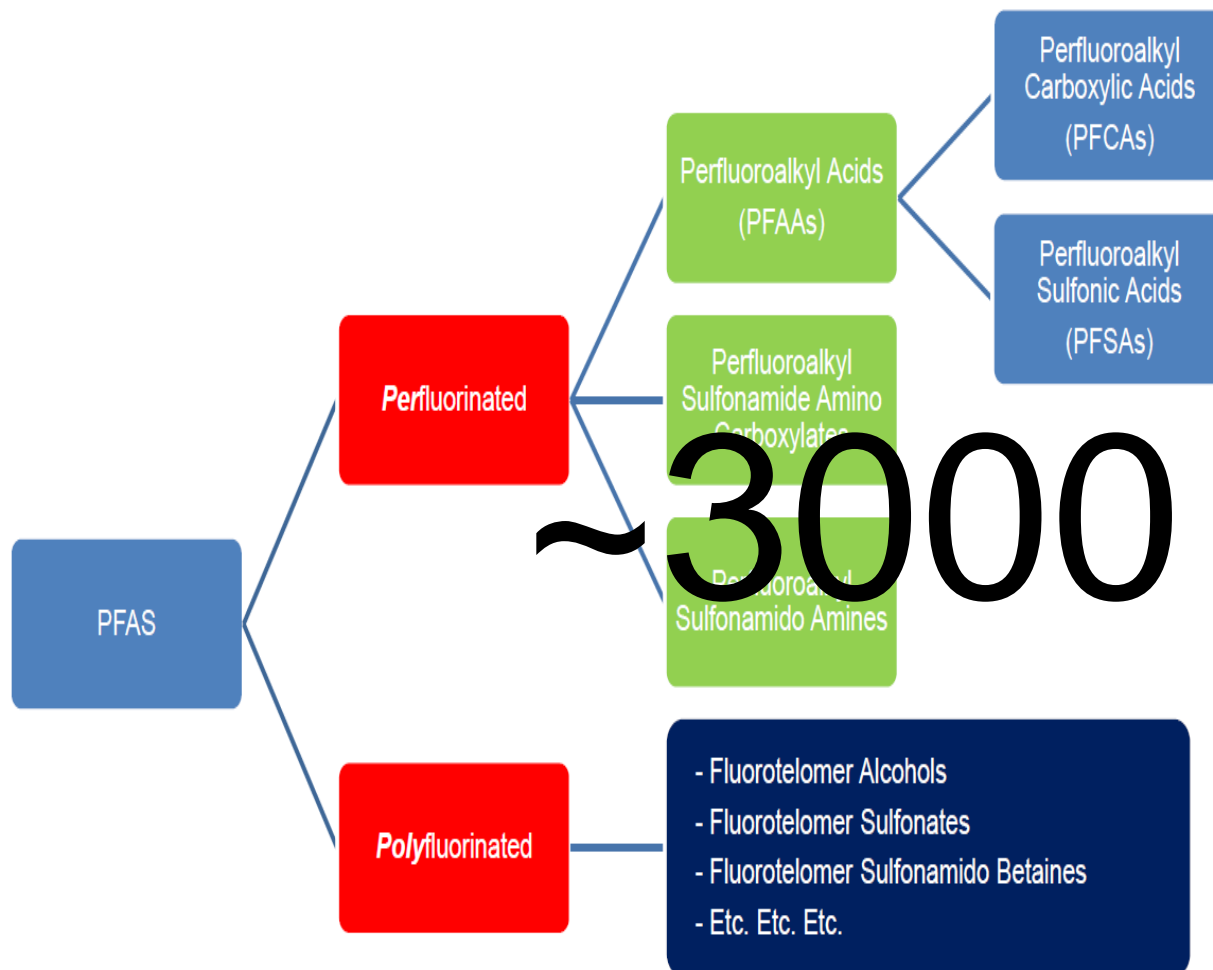


Quantitative comparison of perfluorinated active substances in drinking water between tandem triple quadrupole MS/MS and high resolution mass spectrometry using orbitrap technology – knowns and unknowns

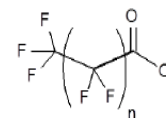
Ali Wolfgang Haghani (Eurofins Eaton Analytical)

Andy Eaton, PhD, BCES (Eurofins Eaton Analytical)

Perfluorinated compounds as emerging contaminants

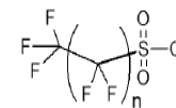


PFCAs incl. PFOA



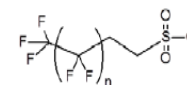
n=2, PFBA; n=3, PFPeA;
n=4, PFHxA; n=5, PFHpA;
n=6, PFOA; n=7, PFNA;
n=8, PFDA; n=9, PFUnDA;
n=10, PFDoDA;

PFSA incl. PFOS



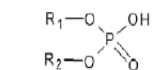
n=3, PFBS
n=5, PFHxS
n=7, PFOS

FTS



n=3, 4:2 FTS
n=5, 6:2 FTS
n=7, 8:2 FTS

PAP, DiPAP



R₁=C₂H₄C₈F₁₇ } 6:2 diPAP
R₂=C₂H₄C₈F₁₇ }

R₁=C₂H₄C₈F₁₃ } 8:2 diPAP
R₂=C₂H₄C₈F₁₃ }

R₁=C₂H₄C₈F₁₃ } 6:2 PAP
R₂=H }

R₁=C₂H₄C₈F₁₇ } 8:2 PAP
R₂=H }

PFPA/PFPiA



R₁=OH } PFHxPA R₁=C₈F₁₃ } 6:6 PFPiA
R₂=C₈F₁₃ } R₂=C₈F₁₃ }

R₁=OH } PFOPA R₁=C₈F₁₃ } 6:8 PFPiA
R₂=C₈F₁₇ } R₂=C₈F₁₇ }

R₁=OH } PFDDPA R₁=C₈F₁₇ } 8:8 PFPiA
R₂=C₁₀F₂₁ } R₂=C₈F₁₇ }

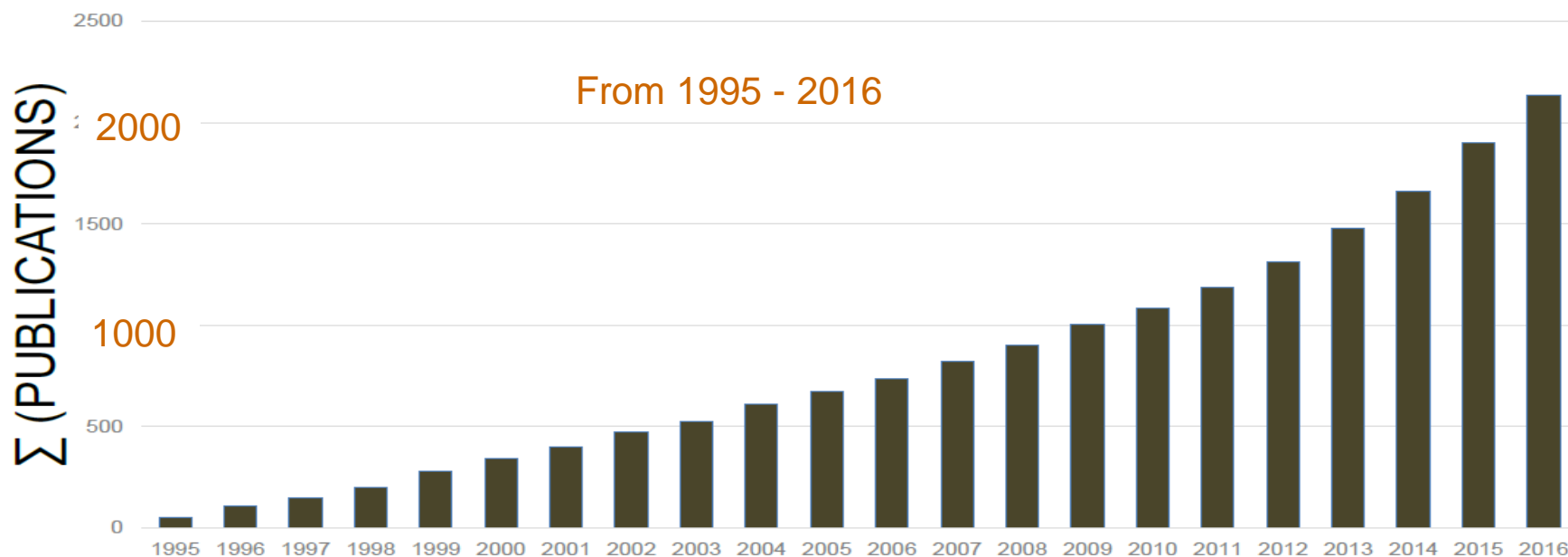
FTOH



Publications shows continued interest in PFAS.



■ Rapidly Evolving Science



Google Scholar search of "Perfluoroalkyl" in title

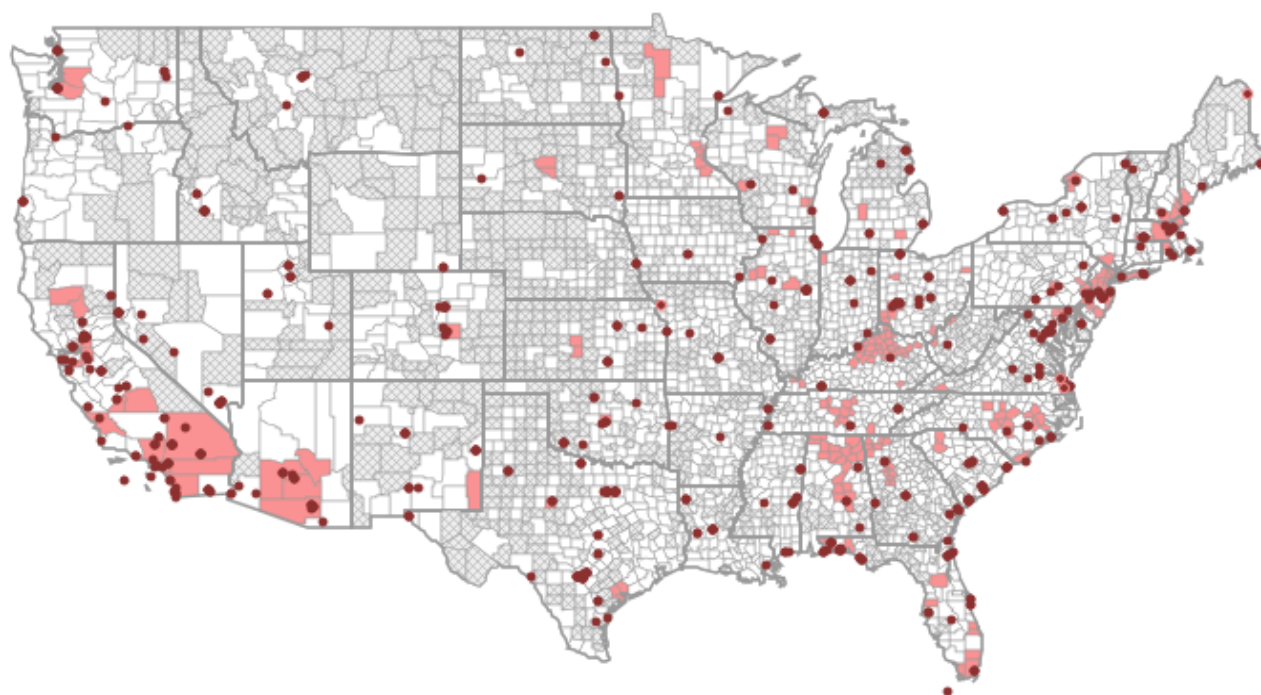
Dr. Richard (Hunter) Anderson
AFCEC/CZTE
February 2017

PFAS Occurrence – UCMR 3



2012: Six PFASs added to Unregulated Contaminant Monitoring Rule 3 (UCMR 3) list, including PFOS and PFOA using **EPA 537 method**.

October 2015 UCMR 3 data summary



Contaminant	Minimum Reporting Level
PFOS	0.04 µg/L
PFOA	0.02 µg/L
PFNA	0.02 µg/L
PFHxS	0.03 µg/L
PFHpA	0.01 µg/L
PFBS	0.09 µg/L

PFAS Contamination in US Drinking Water

- PFCS detected
- No PFCS detected
- Not tested
- U.S. Military Fire/Crash Training Area Sites

Data visualization: Moiz Syed. Sources: EPA and Department of Defense.
<https://theintercept.com/2015/12/16/toxic-firefighting-foam-has-contaminated-u-s-drinking-water-with-pfcs/>

EPA 537 Method Used – Summary: Extraction



- A 250-mL preserved water sample with Trizma is fortified with surrogates and passed through a solid phase extraction (SPE) cartridge containing **Solex HRPHS** in lieu of polystyrenedivinylbenzene (SDVB) to extract the method analytes and surrogates. The compounds are eluted from the solid phase with a small amount of methanol. The extract is concentrated to dryness with nitrogen in a heated water bath, and then adjusted to a 1-mL volume with 96:4% (vol/vol) methanol:water after adding the IS(s). A **5- μ L** in lieu of 10- μ L injection is made into an LC equipped with a C18 column.



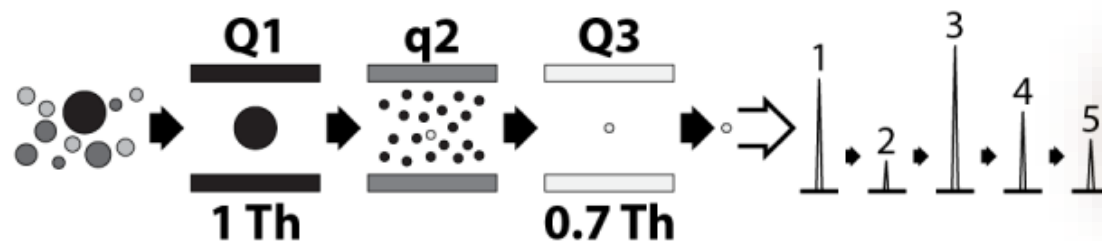
- **Q-Exactive hybrid HRAM capable of producing MS/MS data** in lieu of “low resolution triple” -MS/MS. The analytes are separated and identified by comparing the acquired mass spectra and retention times to reference spectra and retention times for calibration standards acquired under identical LC/MS/MS conditions. The concentration of each analyte is determined by using the internal standard technique. Surrogate analytes are added to all Field and QC Samples to monitor the extraction efficiency of the method analytes.

Hybrid HRAM can be used for EPA LC-MS/MS Analysis



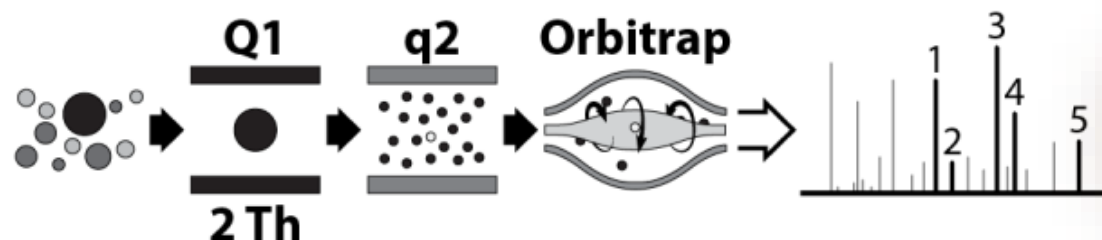
Using Parallel Reaction Monitoring (PRM) - Targeted MS2

A SRM



Serial monitoring

B PRM



Parallel monitoring

Parallel reaction monitoring for high resolution and high mass accuracy quantitative, targeted proteomics. Peterson et al., MCP 2012, O112.020131

Q-Exactive tune page: the setup.



```

040216-IDOC-PRM-FS-006
10
040216-IDOC-PRM-FS-006
Q Exactive - Orbitrap-MS

FULL MS - SIM
General
Runtime
Polarity
In-source CID
Full MS - SIM
Microscans
Resolution
AGC target
Maximum IT
Number of scan ranges
Scan range
Spectrum data type

PRM
General
Runtime
Polarity
In-source CID
Default charge state
Inclusion
MS2
Microscans
Resolution
AGC target
Maximum IT
MSX count
MSX isochronous ITs
Isolation window
Isolation offset
Fixed first mass
NCE / stepped NCE
Spectrum data type

0 to 19.2 min
Negative
0.0 eV
1
70,000
1e6
100 ms
1
100 to 1100 m/z
Profile

0 to 19.2 min
Negative
0.0 eV
1
on
1
35,000
2e5
100 ms
1
on
1.0 m/z
0.0 m/z
-
10, 55
Profile

Setup

TUNEFILES
General
Switch Count 0
Base TuneFile C:\Xcalibur\methods\5000UL-EPA-537-TUNE.mstune

CONTACT CLOSURE
    
```

Full Scan Set up

70000 Resolution

100-1000 m/z

PRM Set up

35,000 Resolution

Isolation window

No need for optimization

**Targeted +
Non Targeted**

Targeted

Needs RT and specific collision E.

EPA 537 – FULL-MS at 70K resolution showing good peak shapes, and S/N for a 2.5ppt standard.

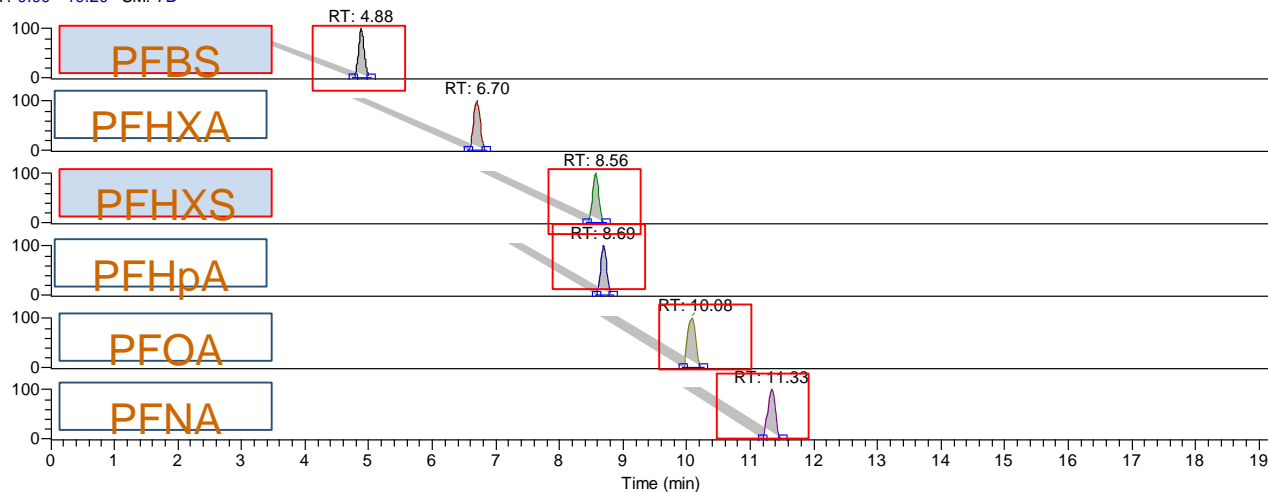


040216-IDOC-PRM-FS-003
1.0

04/02/16 01:11:20

ICAL-2

RT: 0.00 - 19.20 SM: 7B



NL: 2.83E4

Base Peak m/z= 79.95564-79.95644 F: FTMS - p ESI Full ms2 298.94@hcd55.00 [50.00-325.00] MS Genesis 040216-IDOC-PRM-FS-003

NL: 1.43E4

Base Peak m/z= 268.98166-268.98434 F: FTMS - p ESI Full ms2 312.97@hcd10.00 [50.00-335.00] MS Genesis 040216-IDOC-PRM-FS-003

NL: 2.39E4

Base Peak m/z= 318.97821-318.98139 F: FTMS - p ESI Full ms2 362.97@hcd10.00 [50.00-390.00] MS Genesis 040216-IDOC-PRM-FS-003

NL: 2.29E4

Base Peak m/z= 79.95564-79.95644 F: FTMS - p ESI Full ms2 398.94@hcd50.00 [50.00-425.00] MS Genesis 040216-IDOC-PRM-FS-003

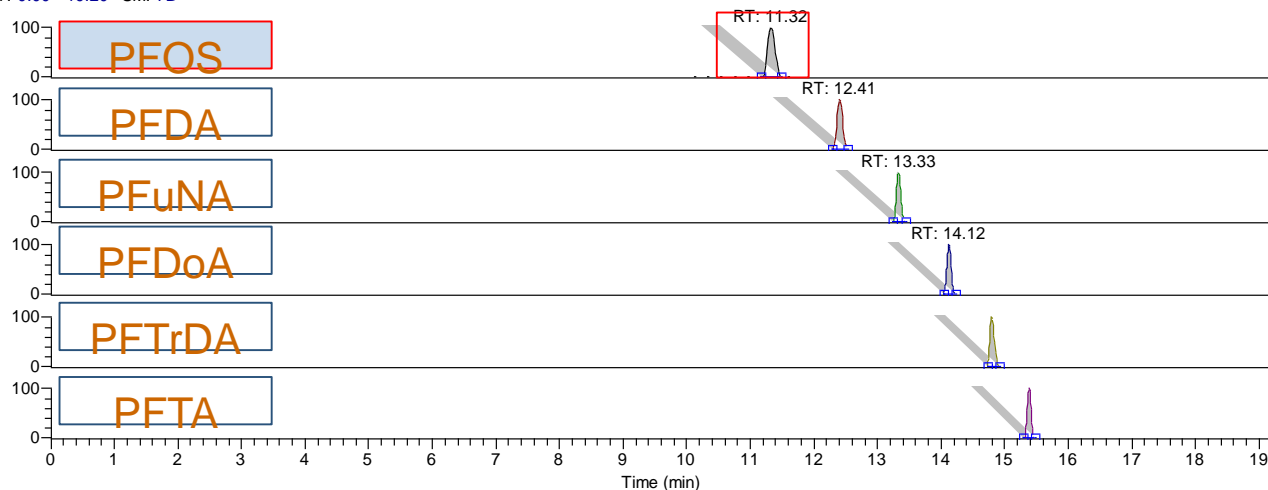
NL: 2.29E4

Base Peak m/z= 368.97481-368.97849 F: FTMS - p ESI Full ms2 412.97@hcd10.00 [50.00-440.00] MS Genesis 040216-IDOC-PRM-FS-003

NL: 2.03E4

Base Peak m/z= 418.97142-418.97560 F: FTMS - p ESI Full ms2 462.96@hcd10.00 [50.00-490.00] MS Genesis 040216-IDOC-PRM-FS-003

RT: 0.00 - 19.20 SM: 7B



NL: 2.04E4

Base Peak m/z= 79.95565-79.95645 F: FTMS - p ESI Full ms2 498.93@hcd55.00 [50.00-525.00] MS Genesis 040216-IDOC-PRM-FS-003

NL: 2.74E4

Base Peak m/z= 468.96778-468.97246 F: FTMS - p ESI Full ms2 512.96@hcd10.00 [50.00-540.00] MS Genesis 040216-IDOC-PRM-FS-003

NL: 3.13E4

Base Peak m/z= 518.96439-518.96957 F: FTMS - p ESI Full ms2 562.96@hcd10.00 [50.00-590.00] MS Genesis 040216-IDOC-PRM-FS-003

NL: 2.58E4

Base Peak m/z= 568.96097-568.96665 F: FTMS - p ESI Full ms2 612.95@hcd10.00 [50.00-645.00] MS Genesis 040216-IDOC-PRM-FS-003

NL: 2.42E4

Base Peak m/z= 618.95754-618.96372 F: FTMS - p ESI Full ms2 662.95@hcd10.00 [50.00-695.00] MS Genesis 040216-IDOC-PRM-FS-003

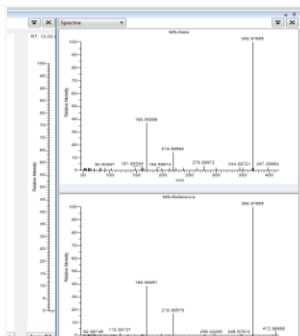
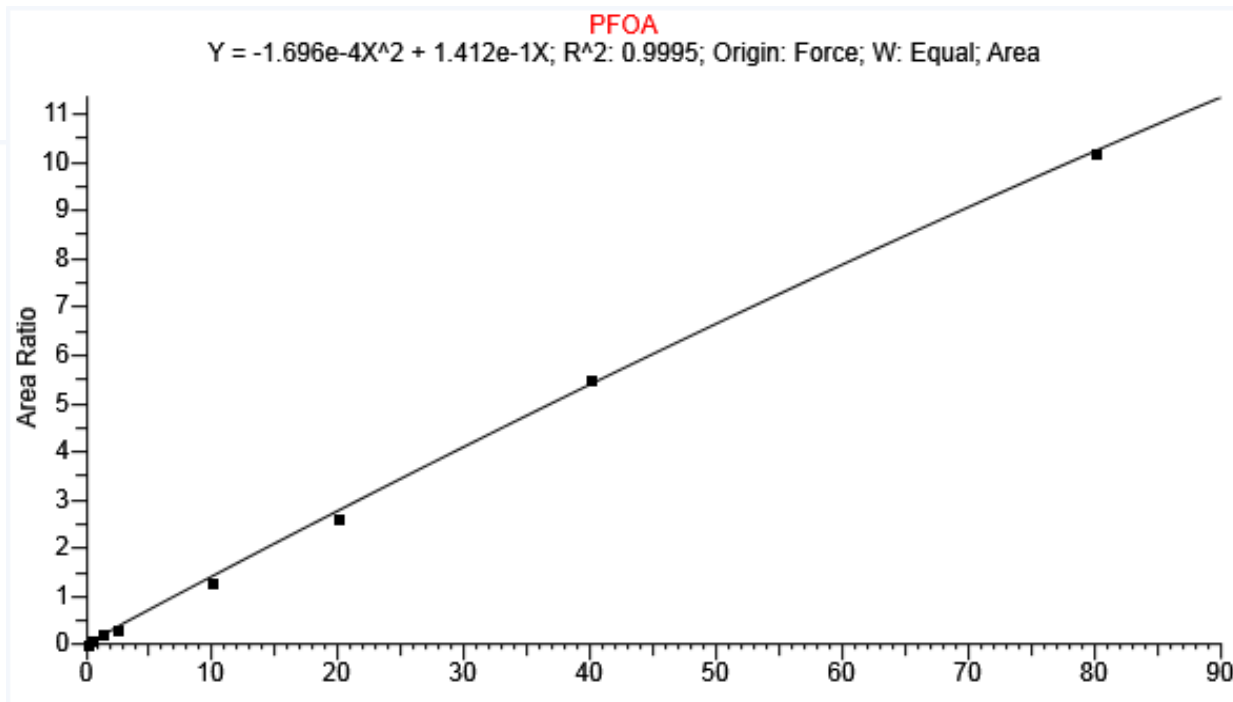
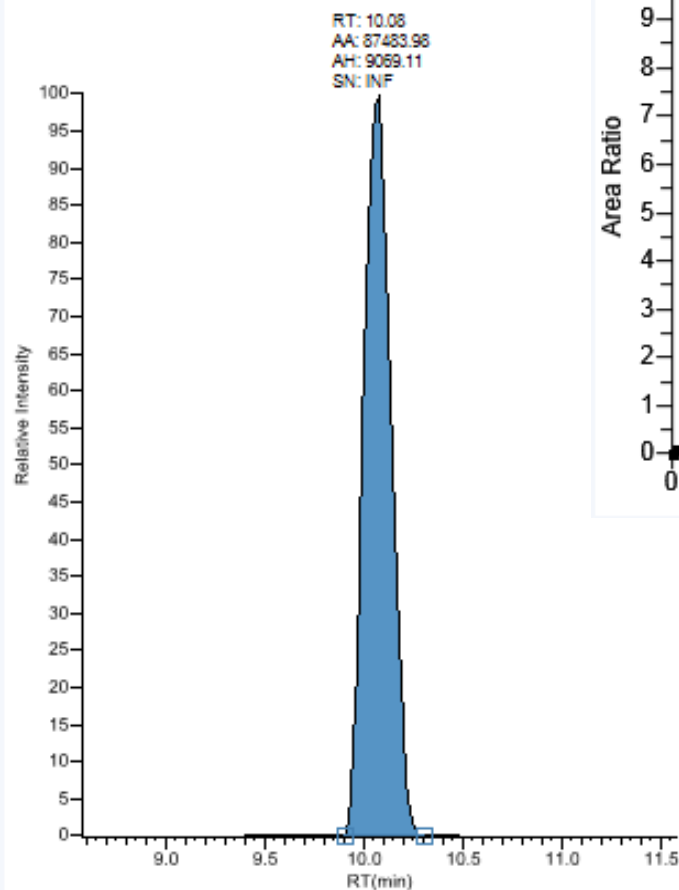
NL: 2.06E4

Base Peak m/z= 668.95430-668.96098 F: FTMS - p ESI Full ms2 712.95@hcd10.00 [50.00-745.00] MS Genesis 040216-IDOC-PRM-FS-003

EPA 537M (PRM) – targeted-MS2 for PFOA at the lowest cal std 0.5ppt shown with spectra confirmation using Trace Finder 4.1



PFOA RT: 10.08 | 040216-IDOC-PRM-FS-002



Sample MS2 Spectra

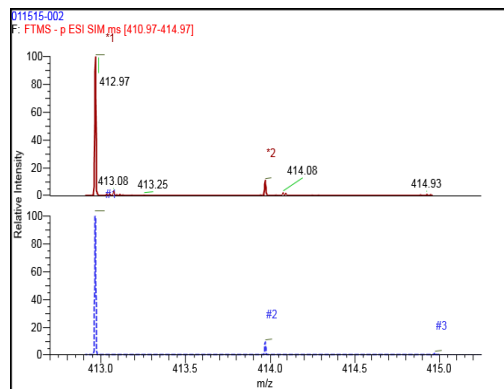
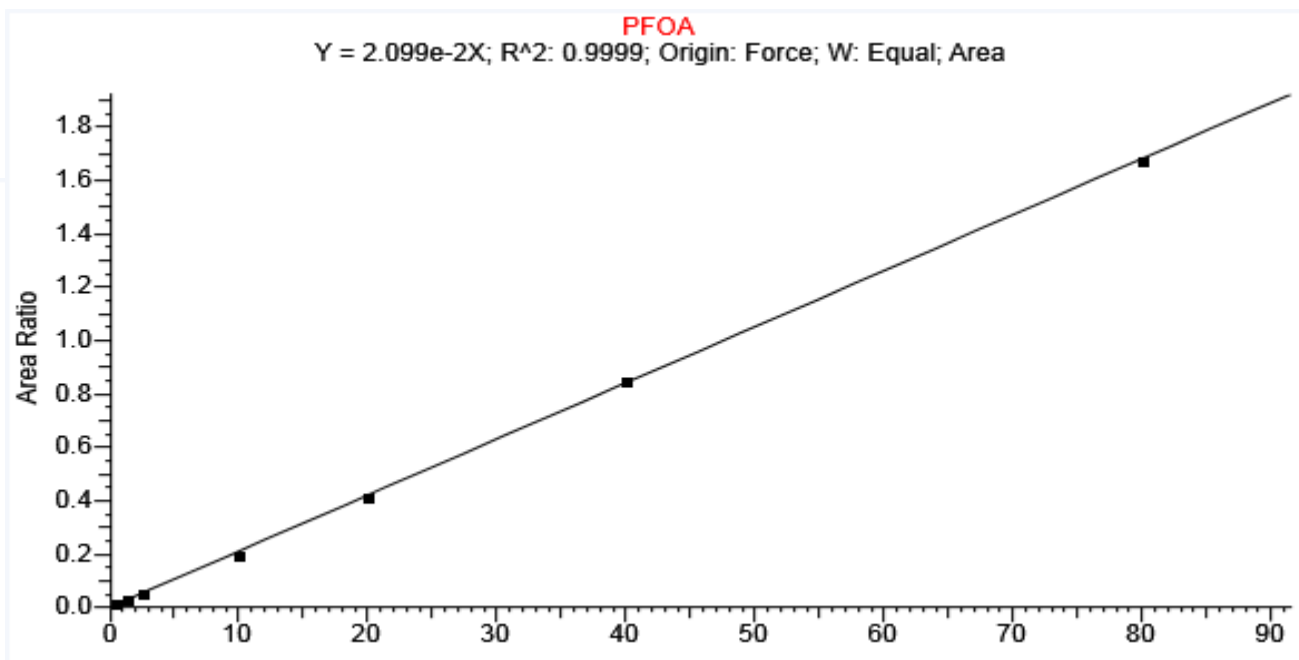
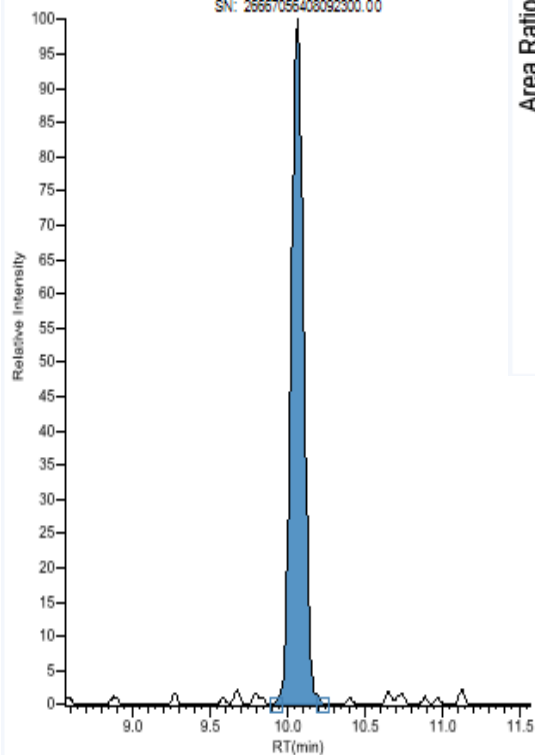
Library MS2 Spectra

By adding Full-Scan to PRM workflow – 0.5ppt PFOA shown



PFOA RT: 10.07 | 040216-IDOC-PRM-FS-002

RT: 10.07
AA: 252022.43
AH: 44360.15
SN: 26667056408092300.00



Isotopic pattern match

Determination of Minimum Reporting Limit Using LCMRL Using Regressional LOQ Calculation



Enter Test Data

Contaminant - 17 alpha-Ethynylestradiol

Method - EPA 539

Units for all measurements - Nanograms/Liter (ng/L)

NB – Calculator only works with 32 bit computers.

****Important** Please do not truncate or round any of the results. If possible, results should have a minimum of 3 significant digits.**

Use the buttons below to add a concentration (column) or measured value (row). To remove a row or column check the box next to it and click the Remove button.

↓

	<input type="checkbox"/> Conc. 1	<input type="checkbox"/> Conc. 2	<input type="checkbox"/> Conc. 3	<input type="checkbox"/> Conc. 4	<input type="checkbox"/> Conc. 5	<input type="checkbox"/> Conc. 6	<input type="checkbox"/> Conc. 7	<input type="checkbox"/> Conc. 8
Concentrations	0.225	0.45	0.9	1.8	3.6	5.4	7.2	0
Measured Concentrations								
<input type="checkbox"/> Value 1	0.184	0.347	0.684	1.361	2.657	4.469	6.07	0.003
<input type="checkbox"/> Value 2	0.184	0.35	0.728	1.365	2.819	4.551	5.814	0.000
<input type="checkbox"/> Value 3	0.202	0.36	0.705	1.363	2.66	4.323	6.046	0.000
<input type="checkbox"/> Value 4	0.174	0.4	0.534	1.362	2.987	4.207	5.563	0.000

http://water.epa.gov/scitech/drinkingwater/labcert/analyticalmethods_ogwdw.cfm

The LCMRL is defined as the lowest spiking concentration at which recovery of between 50 and 150 percent is expected 99 percent of the time by a single analyst. The procedure requires, at a minimum, four replicates at each of seven fortification levels. Four laboratory reagent blanks should also be included. All must be processed through the entire method procedure

Target & non targeted compounds EPA 537 plus.



PRM

EPA 537 PFCA's,
and PFSA'S target
list

LCMRL equal or better than high end - mid range triple
quads – background contamination is the limiting factor.

	Critical level	DL	LCMRL
PFBS	0.077	0.12	<0.5
PFDA	0.18	<0.5	<0.5
PFDoA	0.14	0.29	<0.5
PFHpA		0.35	0.97
PFHxA	0.16	0.27	<0.5
PFHxS		0.52	0.77
PFNA	0.14	0.26	<0.5
PFOA		0.36	0.5
PFOS	0.14	0.21	<0.5
PFTA		0.48	0.71
PFTrDA	0.18	0.32	<0.5
PFuNA		0.31	0.72

Stock standard contained other compounds
not part of EPA 537 target list which were
identified and quantified using Full-MS

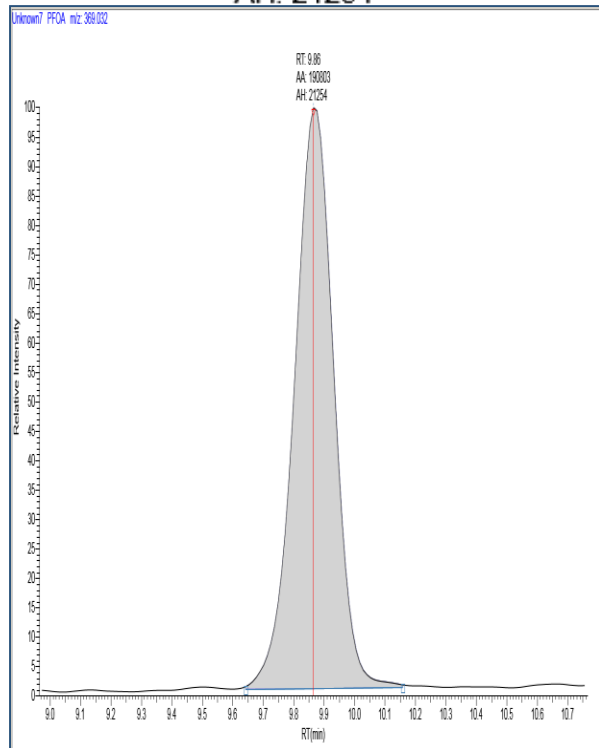
Full Scan

	Critical level	DL	LCMRL
PFBS	0.15	0.2	<0.5
PFDA	0.15	0.26	<0.5
PFDoA		0.47	0.73
PFHpA	0.09	0.15	<0.5
PFHxA	0.13	0.19	<0.5
PFHxS		1.7	2.4
PFNA	0.11	0.17	<0.5
PFOA		0.22	0.5
PFOS		0.26	0.5
PFTA	0.15	0.2	<0.5
PFTrDA		0.31	0.55
PFuNA		0.38	1
PFBA		0.19	0.64
PFODA		0.55	1
PFDS	0.13	0.19	<0.5
PFHxDA		0.12	0.5
PFPA	0.18	0.19	<0.5

A 2.5ppt standard of PFOA. Excellent quantitation and sensitivity is obtained with HRAM in comparison to QQQ analysis.

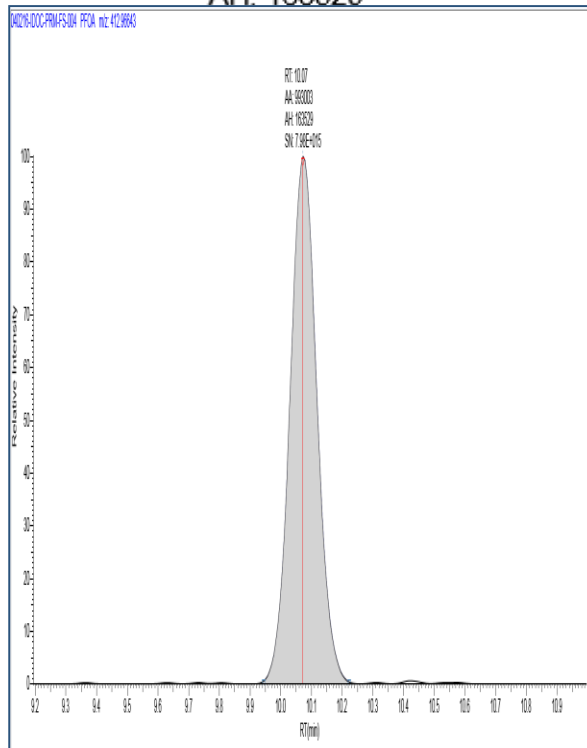


RT: 9.86
AA: 190803
AH: 21254



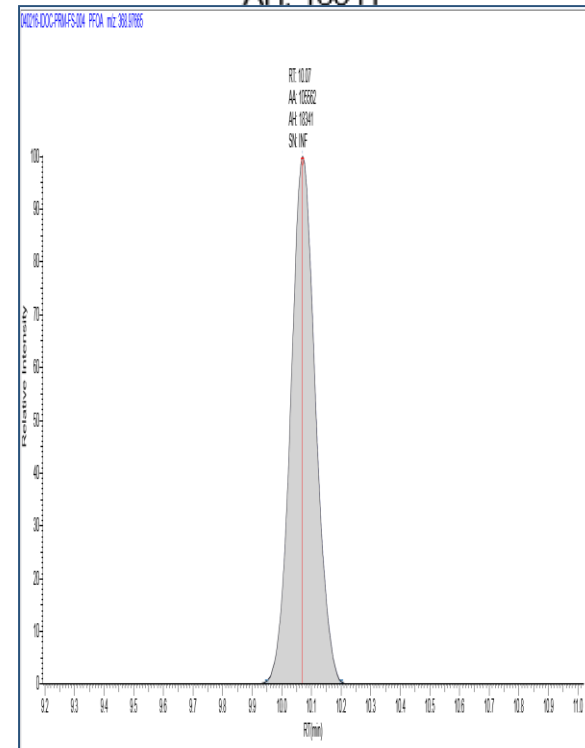
a) SRM Analysis-QQQ

RT: 10.07
AA: 993003
AH: 163529



b) HRAM Full Scan

RT: 10.07
AA: 105562
AH: 18341





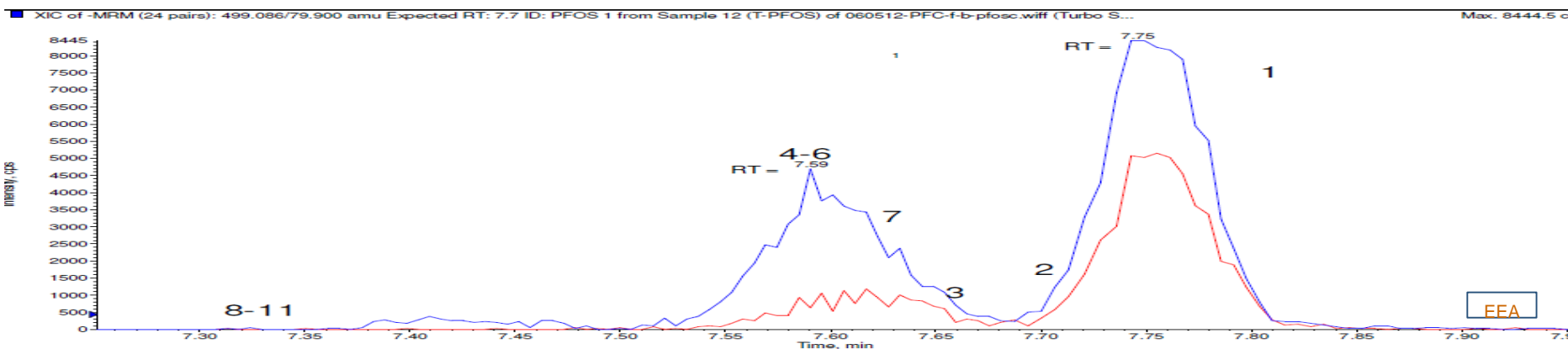
c) HRAM PRM

PFOS quantification is challenging: Showing a technical grade standard



Isomer 1 2 3 4 5 6 7 8 9 10 11

				MS/MS relative response factors									
	m/z 499	m/z 99	100	117	97	49	39	43	78	10	0	0	19
	m/z 499	m/z 80	100	0	78	135	241	142	123	113	118	220	90



1) $\text{CF}_3\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{SO}_3$ 2) $\text{CF}_3\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{SO}_3$ 3) $\text{CF}_3\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{SO}_3$ 4) $\text{CF}_3\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{SO}_3$

CF_3

CF_3

CF_3

5) $\text{CF}_3\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{SO}_3$

CF_3

6) $\text{CF}_3\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{SO}_3$

CF_3

7) $\text{CF}_3\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{SO}_3$

CF_3

8) $(\text{CF}_3)_3\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{SO}_3$

9) $\text{CF}_3\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{SO}_3$

CF_3

CF_3

10) $\text{CF}_3\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{SO}_3$

CF_3CF_3

11) $\text{CF}_3\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{CF}_2\text{SO}_3$

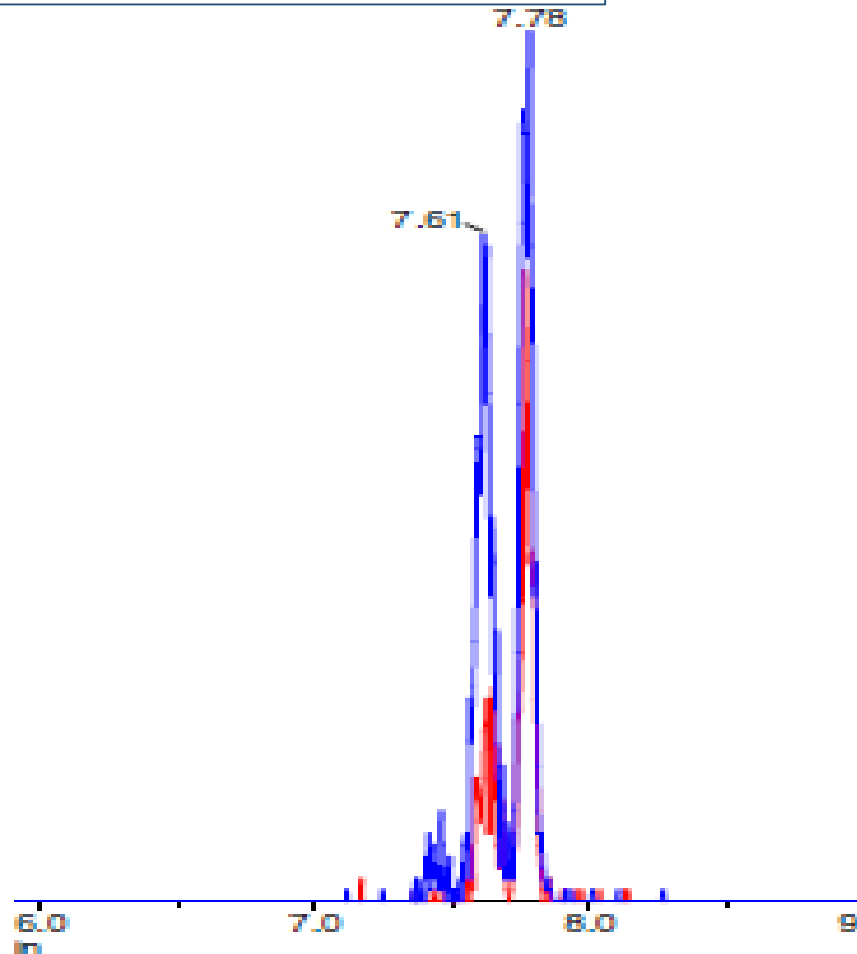
CF_3

CF_3

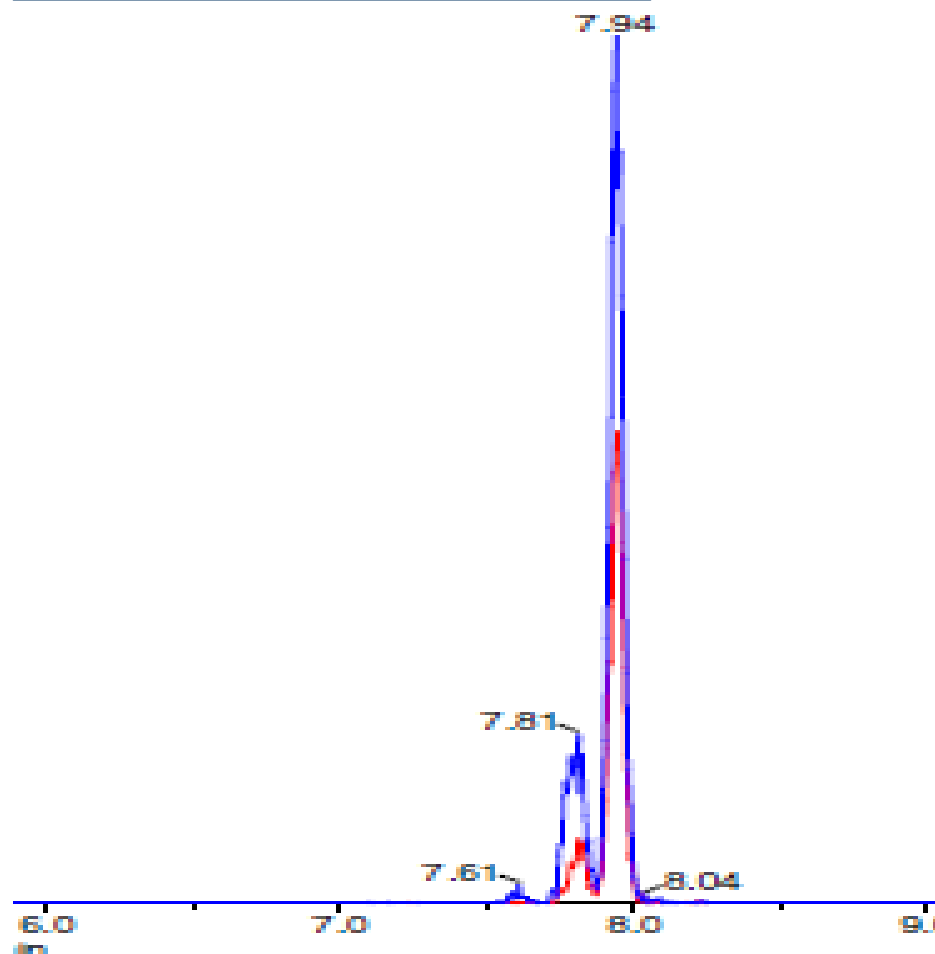
Samples from different locations can have different branch ratios



Field Sample



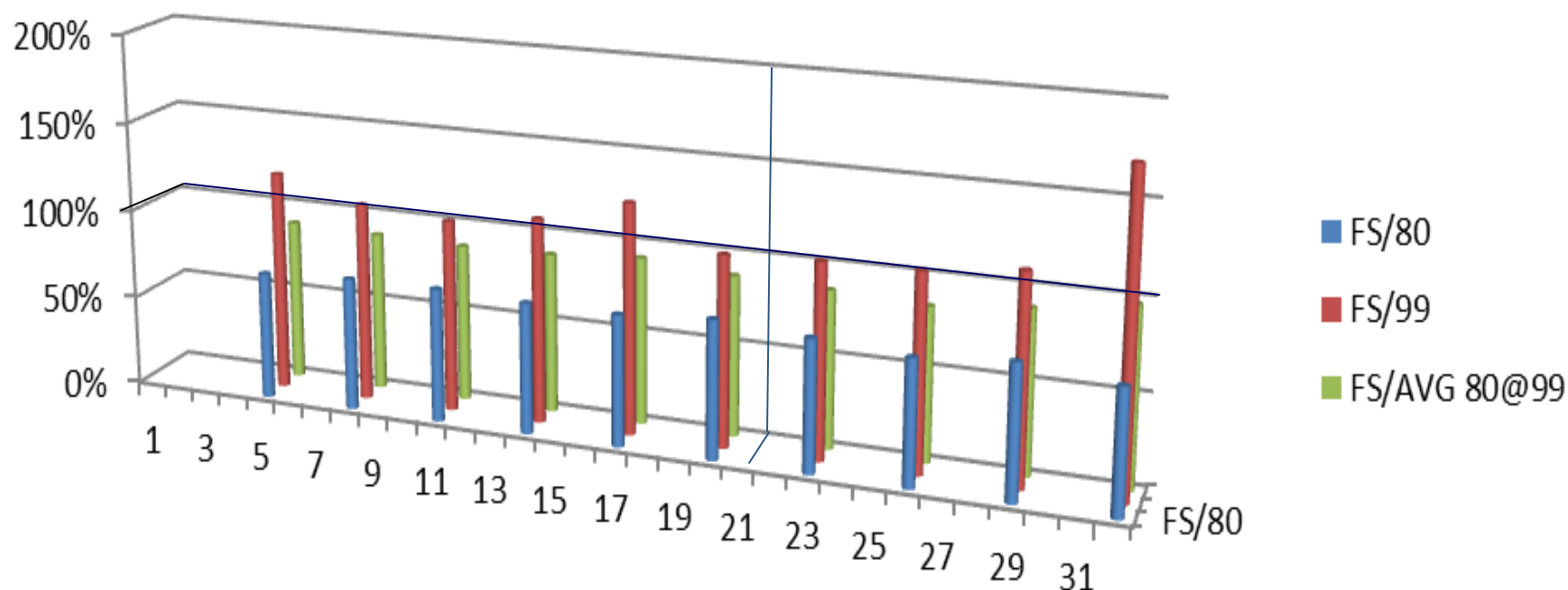
Std PFOS Branched



Fs scan covers all of the branches and looks to be more reliable for PFOS quantitation.



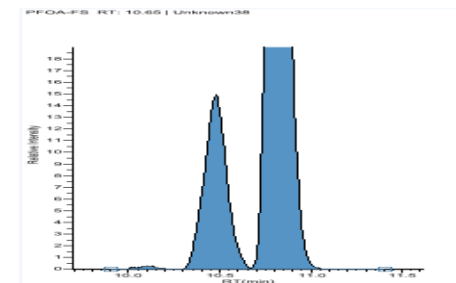
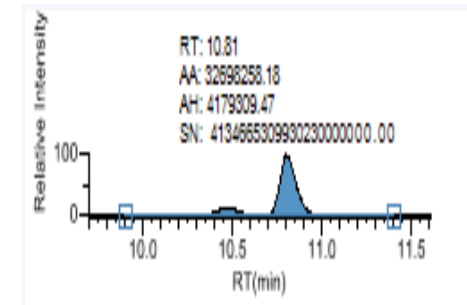
10 samples - conc. 4 - 30ppt



Linear PFOS used for calibration



Technical Advisory- Laboratory Analysis of Drinking Water Samples for Perfluorooctanoic Acid (PFOA) Using EPA Method 537 Rev. 1.1



September 2016

Office of Water (MS-140)

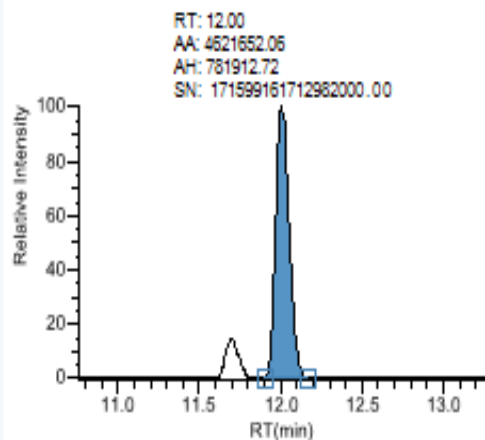
EPA 815-B-16-021

Till around 1970 PFOA was also produced by Electrochemical fluorination (ECF) process creating branched isomers which can still be detected occasionally so it is important to also integrate the branch isomers.

Full Scan 70000 resolution

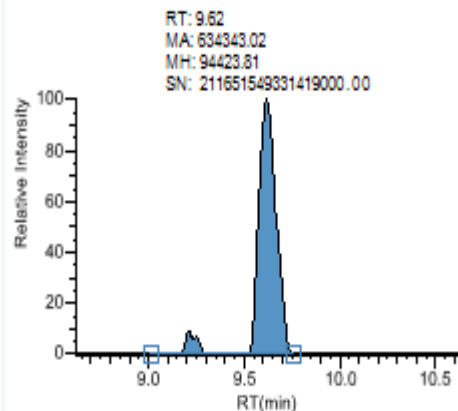


PFNA-FS RT: 12.00 | 091416-034



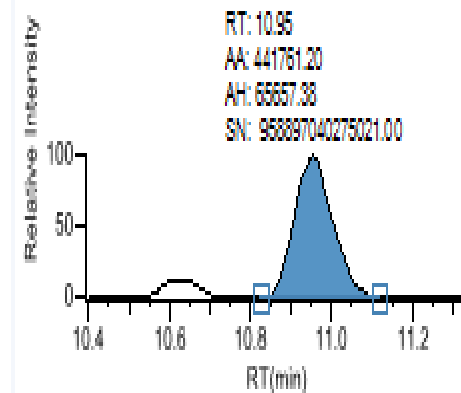
PFNA

PFHFA-FS RT: 9.62 | 091416-032



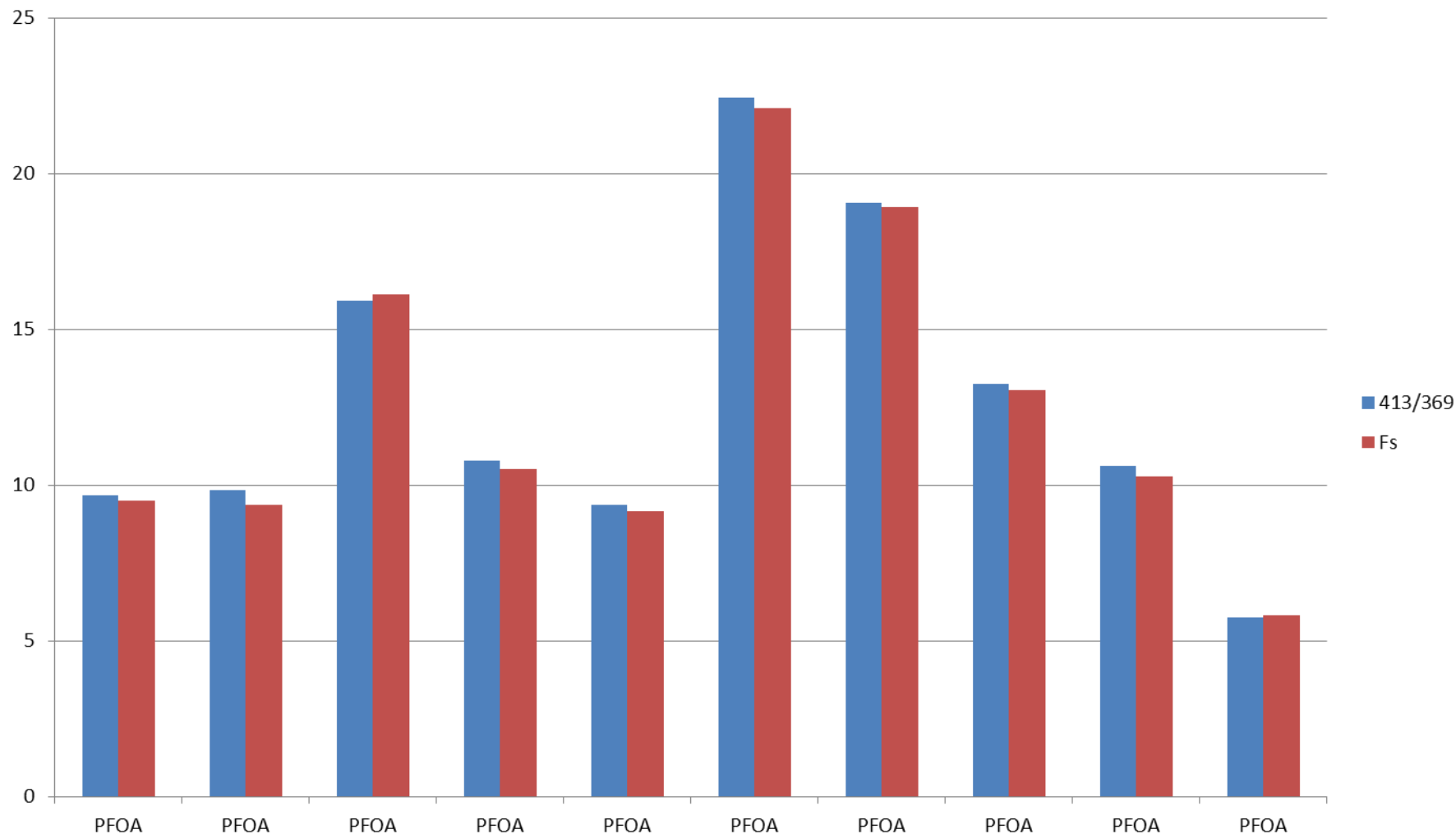
PFHpA

PFOA RT: 10.95 | 091416-034

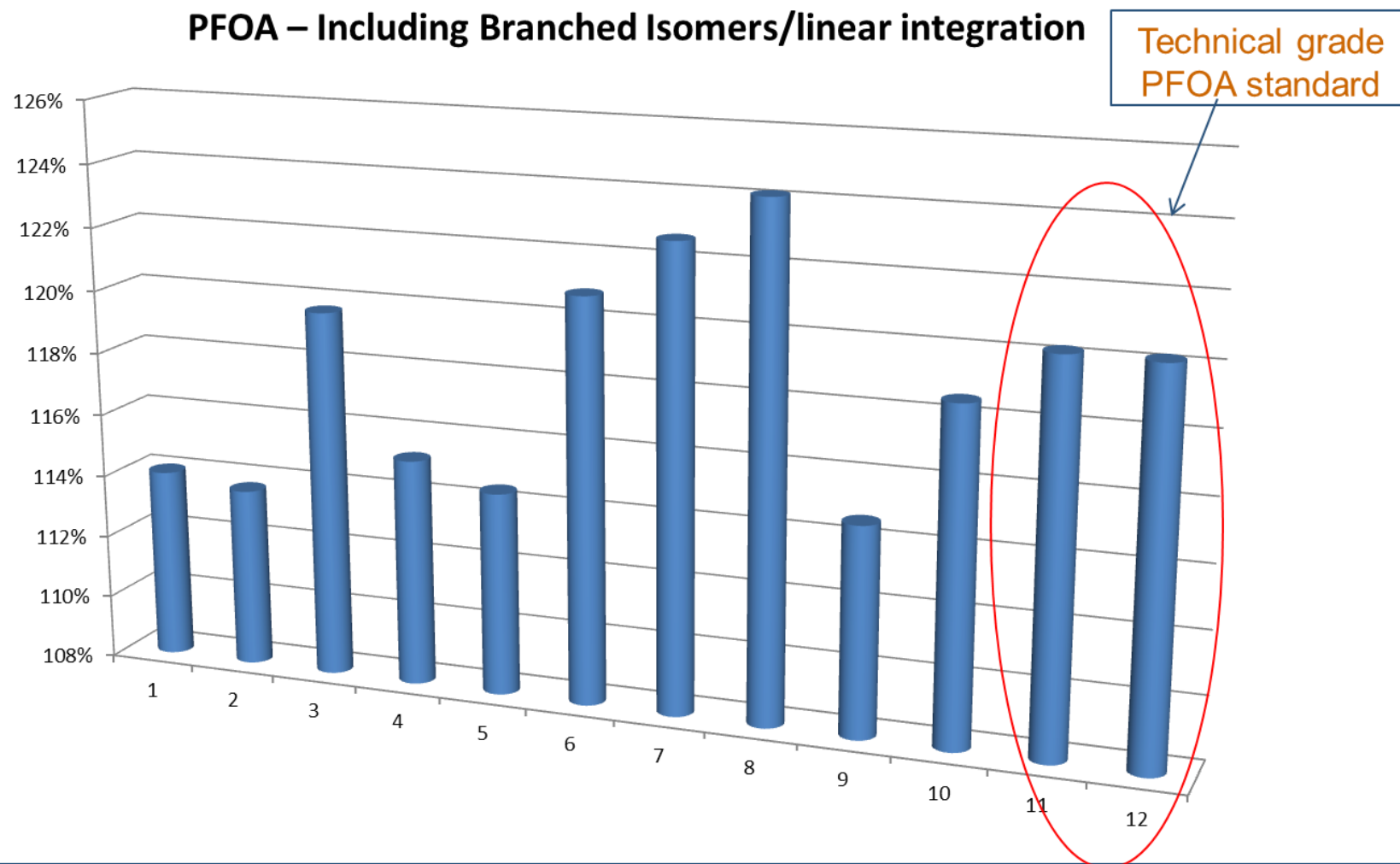


PFOA

FS and 413/369 compares well in real field samples having branched PFOA - ppt



Including branched isomers when present about 20% difference in a technical grade

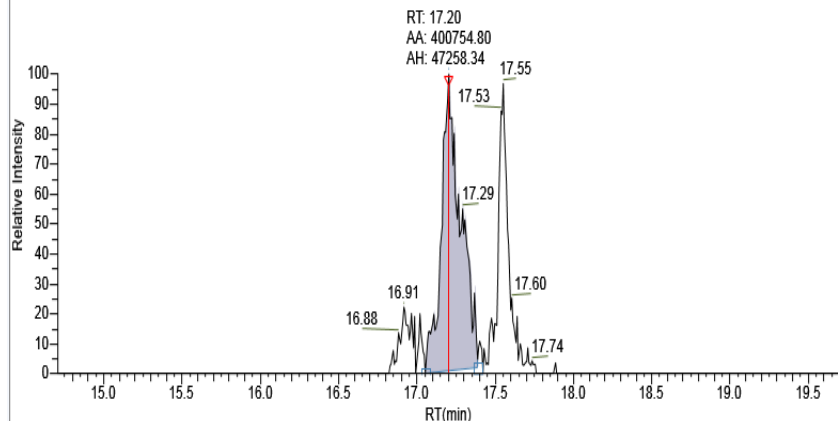


A UCMR3 sample shown having a trace hit for non-targeted known compound: PFDS



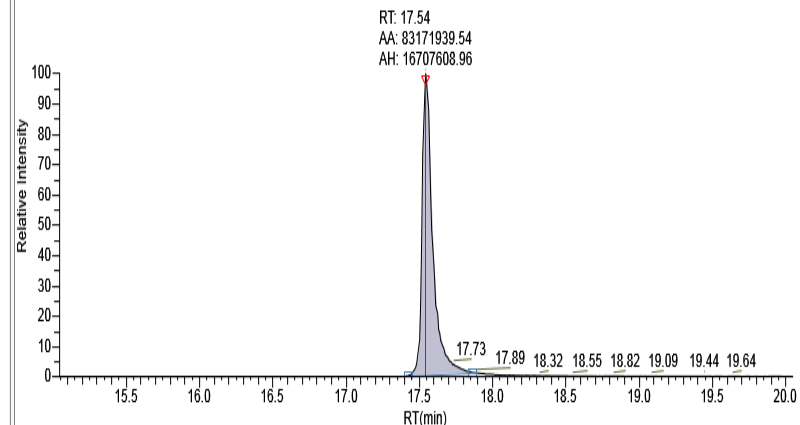
Sample

201508080116 L-PFDS NL: 4.77E4 m/z: 598.92 - 598.93
F: FTMS - p ESI Full ms [100.00-1100.00]

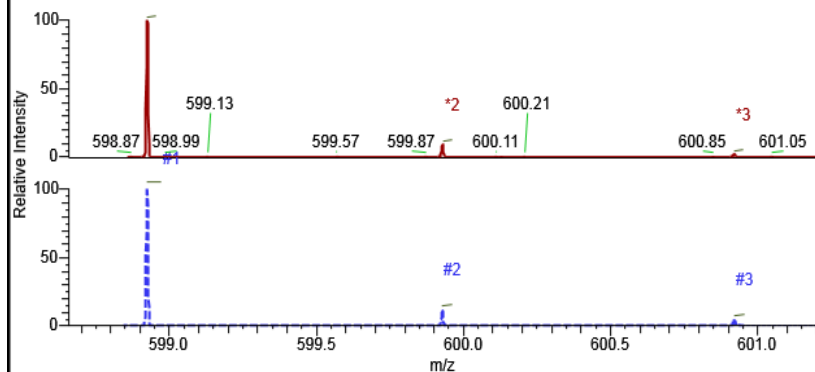


80 ppt STD

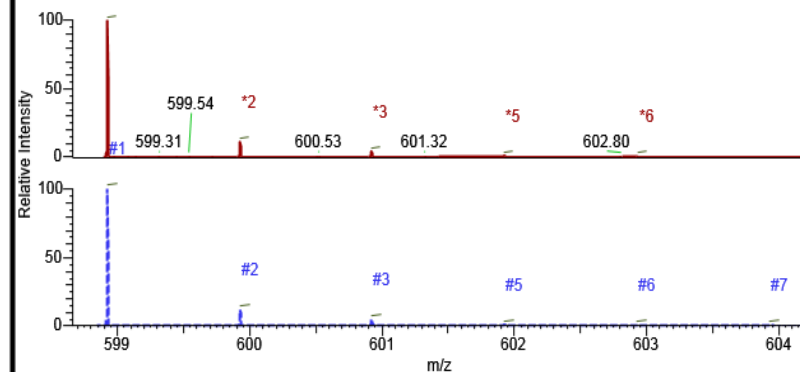
STD NaPFDS NL: 1.68E7 m/z: 598.92 - 598.93
F: FTMS - p ESI Full ms [100.00-1100.00]



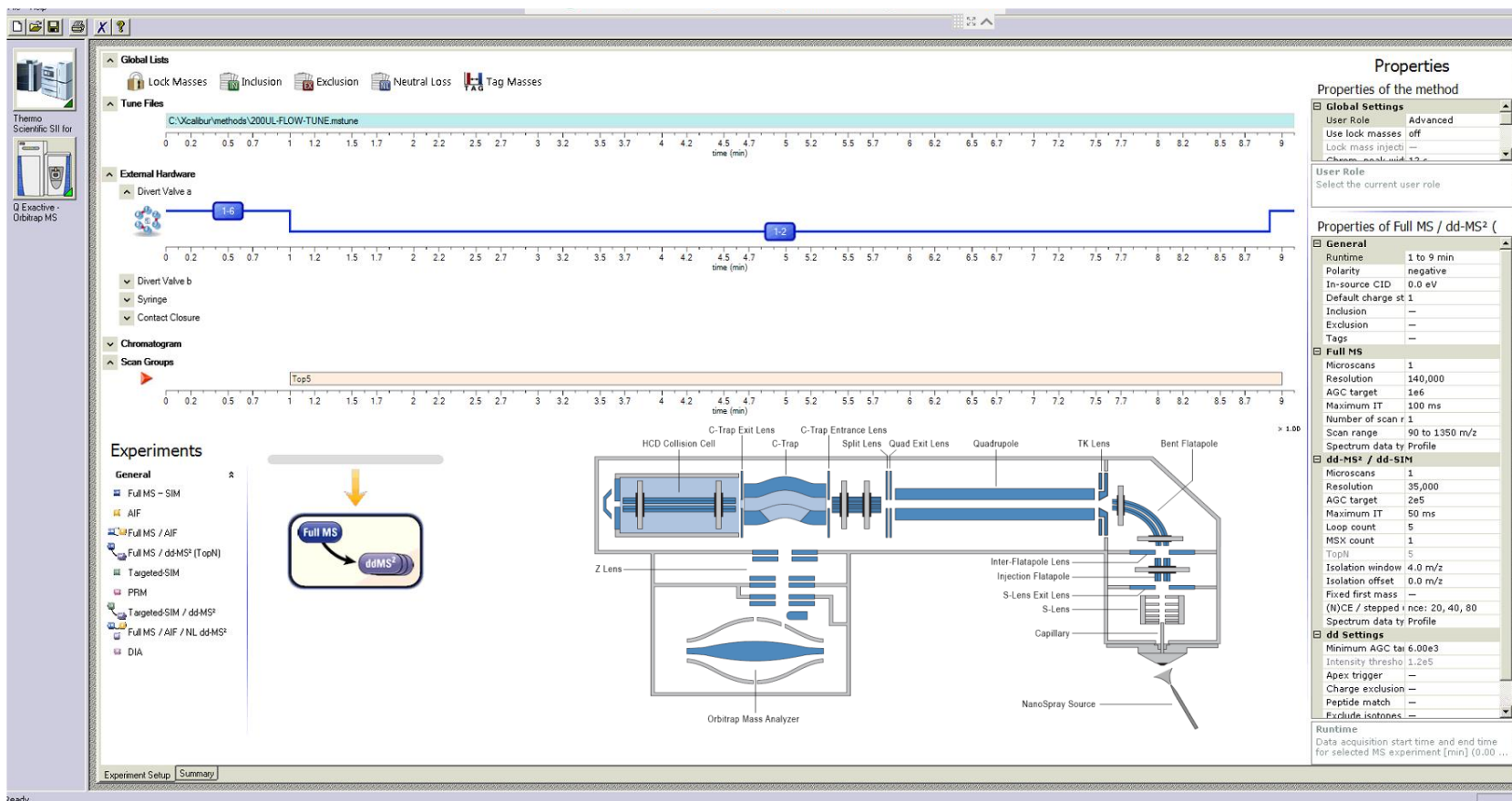
201508080116
F: FTMS - p ESI Full ms [100.00-1100.00]



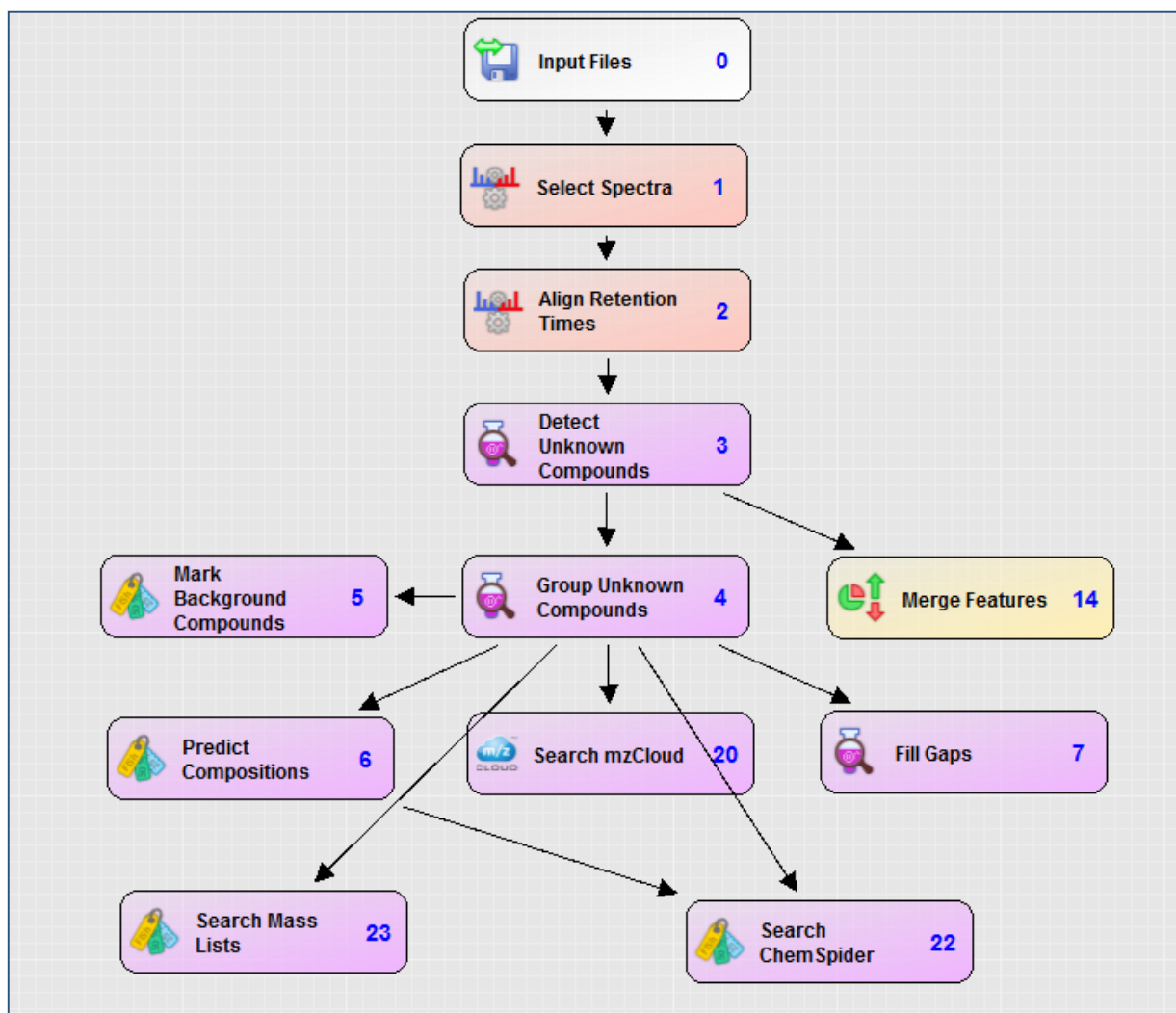
STD
F: FTMS - p ESI Full ms [100.00-1100.00]

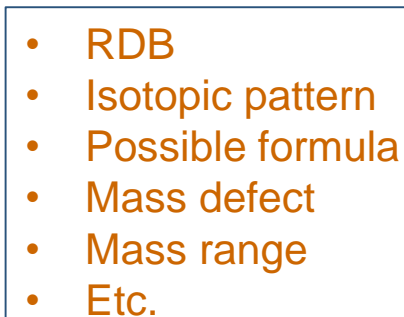


Looking for Unknowns : Contaminated GW in a AFFF site: On-line SPE UHPLC / Fs-ddms2, top 5



Data mining software using “Compound Discoverer”



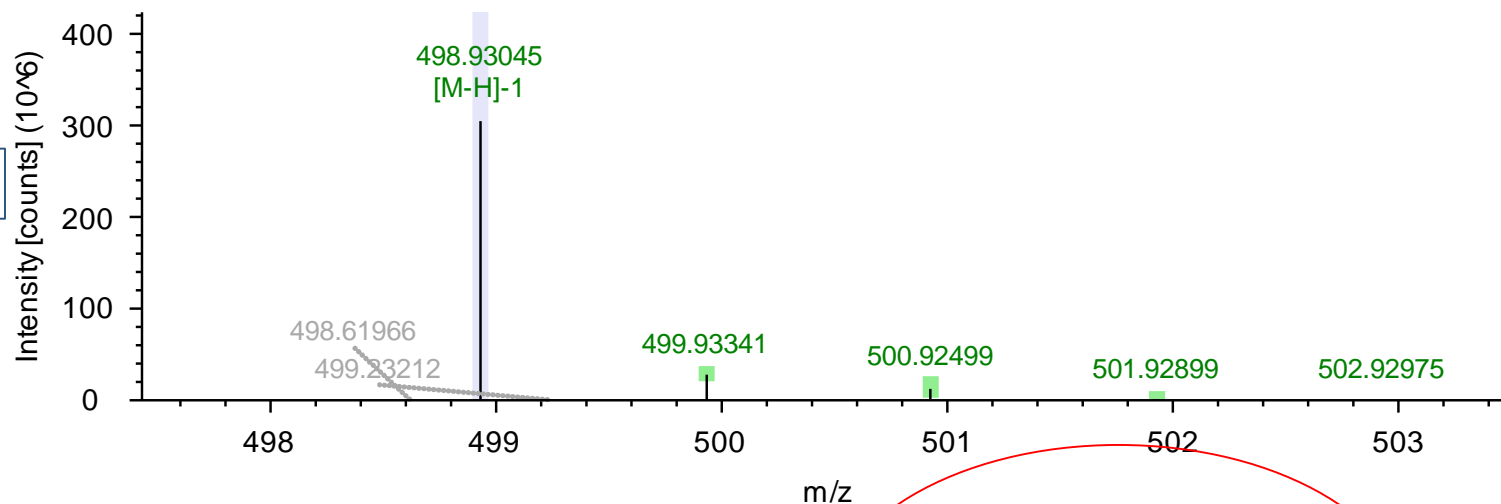


At higher resolutions more trace isotopic patterns can be used for MS scans.

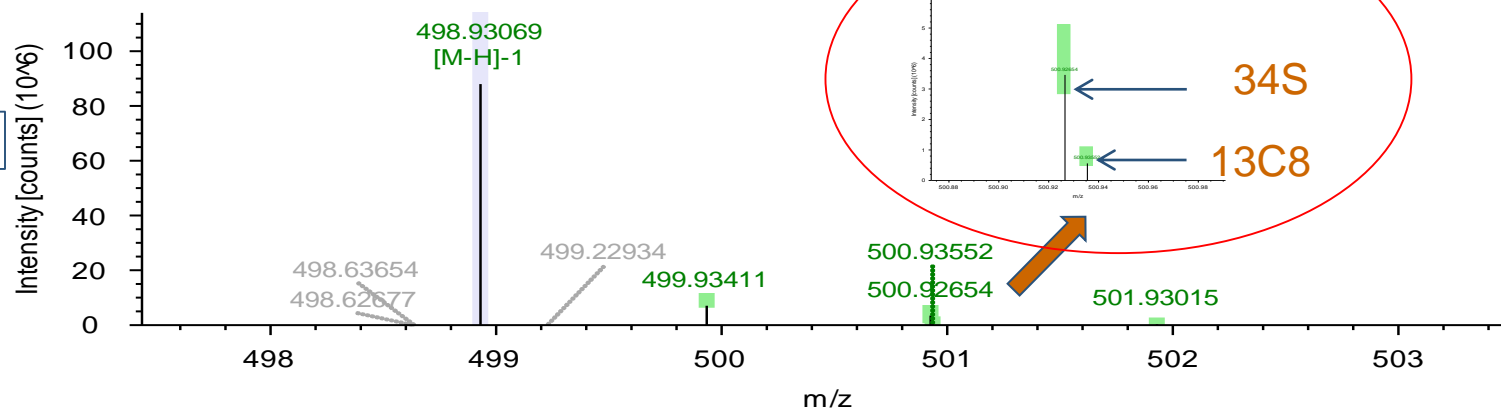


201605240377R, #2094, RT=5.457 min, FTMS (-)
C8 H F17 O3 S as [M-H]-1

70K Res.



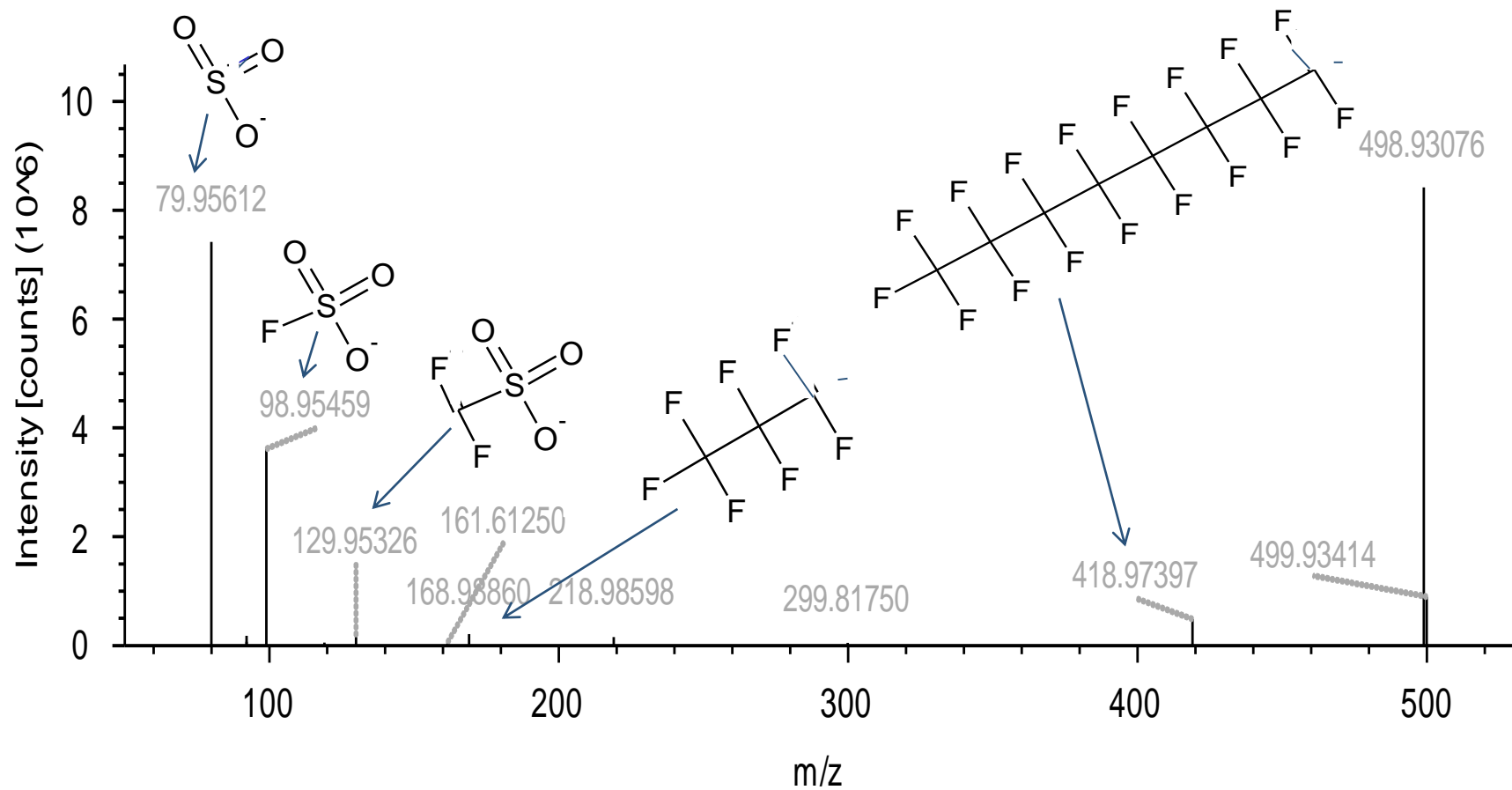
140K Res.



Ms2 Data Shows CmF2m+1- “9 series” and CnF2nSO3- radical “0 series” as expected.



201605240376, #1272, RT=6.094 min, FTMS (-), MS2 (HCD, DDF, 498.93@50.00, z=-1)



The structure of the selected compound can be drawn in “Custom Explanation” using Mass Frontier to check against MS and MS2 collected data



Chromatograms

Group By:

Sample Type (1/1)

Sample (1/1)

Filter By:

Sample Type

Sample

Intensity (counts) (10⁶)

RT [min]

5.451

C6HF11O4S C6 H F11 O4 S MW: 377.94199

File: 201605240383.raw (F10) FTMS (-) MS1

Mass Spectrum

#1111, RT=5.451 min, FTMS (-)

#1115, RT=5.467 min, FTMS (-)

#1118, RT=5.480 min, FTMS (-), MS2 (HCD, DD)

201605240383, #1118, RT=5.480 min, FTMS (-), MS2 (HCD, DDF, 376.94@50.00, z=-1)

C6HF11O4S C6 H F11 O4 S, MW: 377.94199, Area: 331907

FISH Coverage: 3 Direct, 23 Unmatched, 8 Skipped

Intensity (counts) (10³)

m/z

79.95616 O3 S [M+e]-1

130.99167

180.98869 C4 F7 [M+e]-1

230.98608 296.97824 376.95172 377.93854

376.93521 C6 F11 O4 S [M-H]-1

Custom Explanation Editor

Chemical structure editor showing a perfluorinated sulfonic acid derivative.

Description

FISH Scoring

Molecular weight:

377.94199

Molecular weight (original):

377.94246

Formula:

C6 H F11 O4 S

Formula (original):

C6 H F11 O4 S

Name:

C6HF11O4S

Comments:

Composition change:

Save

Cancel

Checked	Structure	Name	Formula	Molecular Weight	Comments
<input type="checkbox"/>			C9 H3 F16 O3 P	493.95643	NO MATCH MS2
<input type="checkbox"/>			C9 H2 F16 O2	445.97993	MS2 NOT MATCHES
<input checked="" type="checkbox"/>		C6HF11O4S	C6 H F11 O4 S	377.94199	
<input type="checkbox"/>		C6HF11O3S	C6 H F11 O3 S	361.94707	C4F7O=280.98346, 9
<input type="checkbox"/>		C4HF7O4S	C4 H F7 O4 S	277.94838	4.798

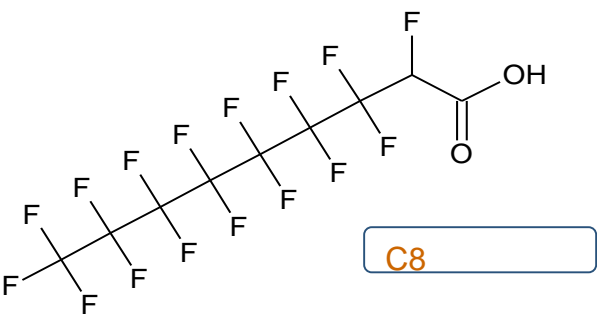
Show Related Tables

[min]	Best Sfit [%]	Max. # MI	# Adducts	Area	Study File ID	FISH Coverage
38		2	1	191959	F2	0.00
54		2	1	108988	F2	0.96
52		4	1	331907	F10	11.54
48		3	1	395253	F10	15.38
54		3	1	49103	F10	

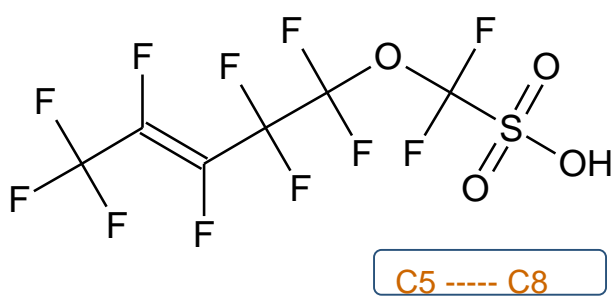
Summary of all PFAS's found for the studied group.



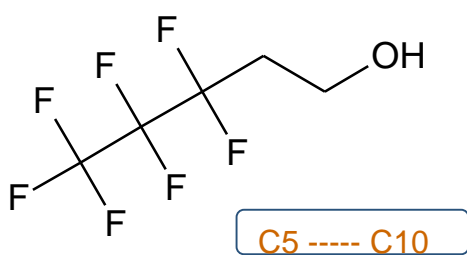
A few identified suspects using prescribed workflow which were missing from the built in library. Some need additional confirmations.



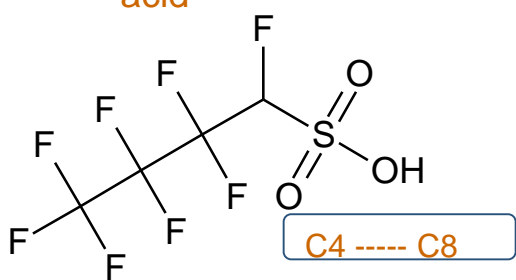
hexadecafluorononanoic acid



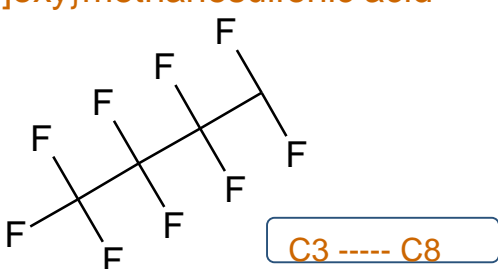
difluoro{[(3E)-1,1,2,2,3,4,5,5,5-nonafluoropent-3-en-1-yl]oxy}methanesulfonic acid



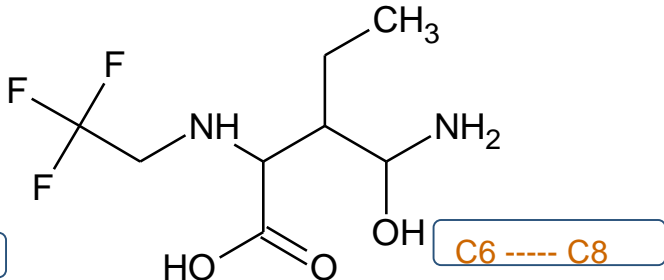
3:2 FTOH



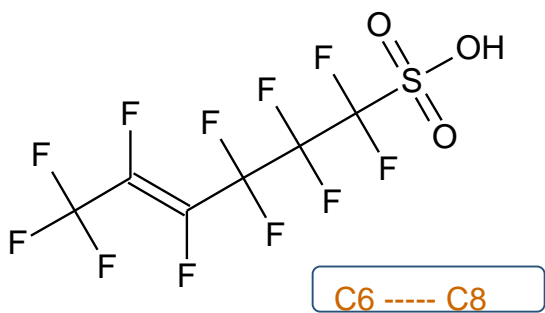
octafluorobutane-1-sulfonic acid



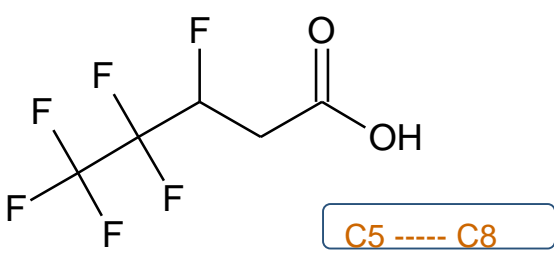
nonafluorobutane



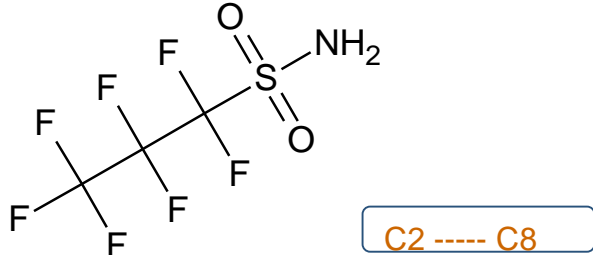
3-[amino(hydroxy)methyl]-2-[(2,2,2-trifluoroethyl)amino]pentanoic acid



undecafluorohex-4-ene-1-sulfonic acid



3:2 FTA



heptafluoropropane-1-sulfonamide

Conclusions



- Q-Exactive HRAM instrumentation in the PRM scan mode can be used for quantitation with performance like a triple quadrupole in SRM mode with added specificity, selectivity and comparable sensitivity.
- Full scan HRAM can likely produce more accurate quantitative data for compounds that contain branched isomers such as PFOS.
- Routine quantitative workflows and non-target analysis can be performed in a single analysis.
- HRAM data processing using Thermo Fisher Scientific Compound Discoverer software can simplify complex data reduction/save time.
- Other techniques may be necessary for further confirmation of suspects/unknowns structures such as MS^n , ^{13}C and ^{19}F NMR, when standards are not commercially available.

Any Questions?



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