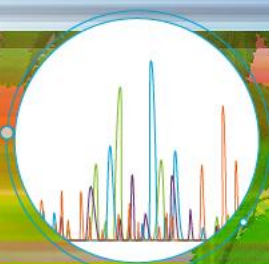




Answers for Science.
Knowledge for Life.™



It's Time to
See Everything
Clearly at
Trace Levels



Chemovar Typing of *Cannabis* Strains with MarkerView® and SCIEX X500R QTOF System

KC Hyland

Food and Environmental Technical Marketing, SCIEX

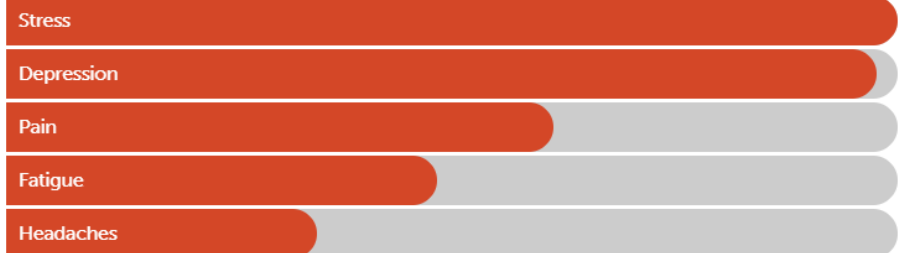
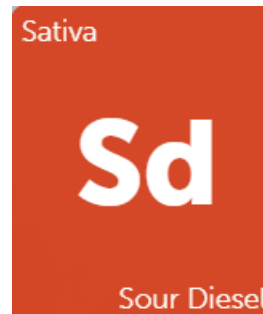
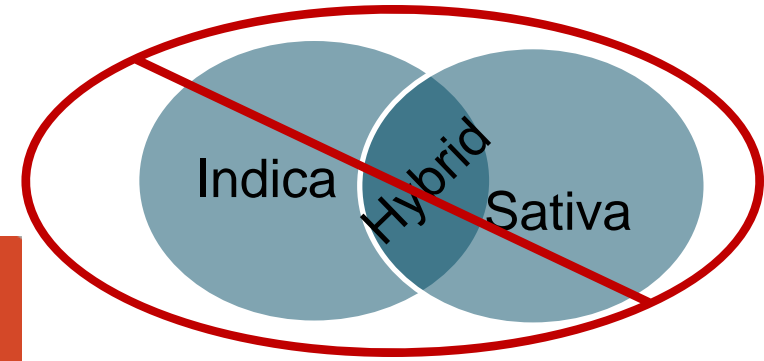
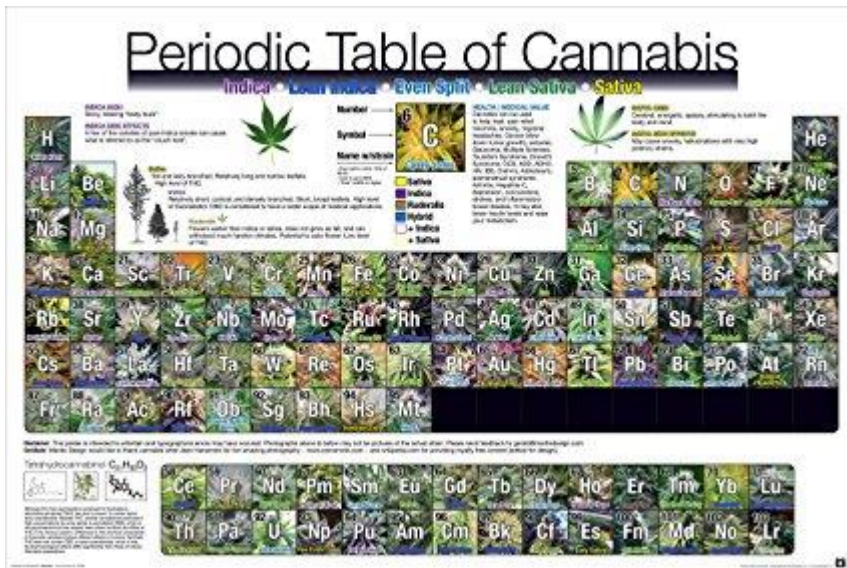
RUO-MKT-11-8252-A



Different Strains for Different Pains

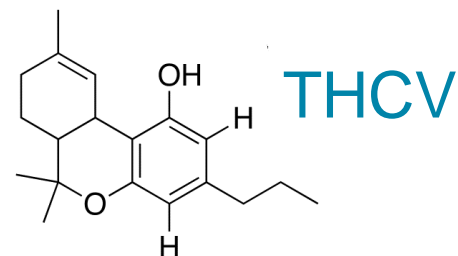
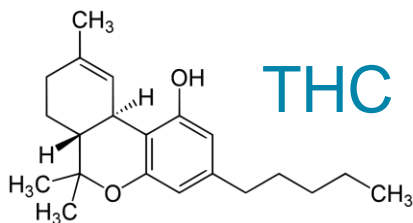
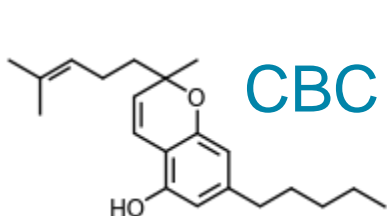
Cannabis strains are consumed for specific desired effects

- Consumers of Cannabis have long asserted the differences between cultivars, or strains, for user experience
- Historical classifications no longer explain the differences between or properties of the hundreds of commercially available Cannabis strains



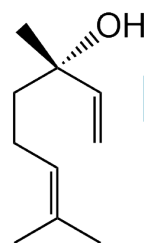
Cannabinoid Profile: Psychotropic, Therapeutic, etc.

- THC, CBD
- 119 individual cannabinoids have been identified in Cannabis

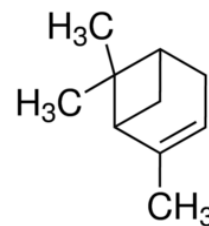


Terpene Profile: Flavor and Aroma

- 200 terpenes have been identified in *Cannabis*
- Unique strains present varying terpene profiles
- Contribute to distinct flavor and aroma
- Both growers and consumers have interest in profiling terpene character



Linalool (floral)



Pinene (pine)



“The Entourage Effect”

WHAT YOU SMELL = HOW YOU'LL FEEL

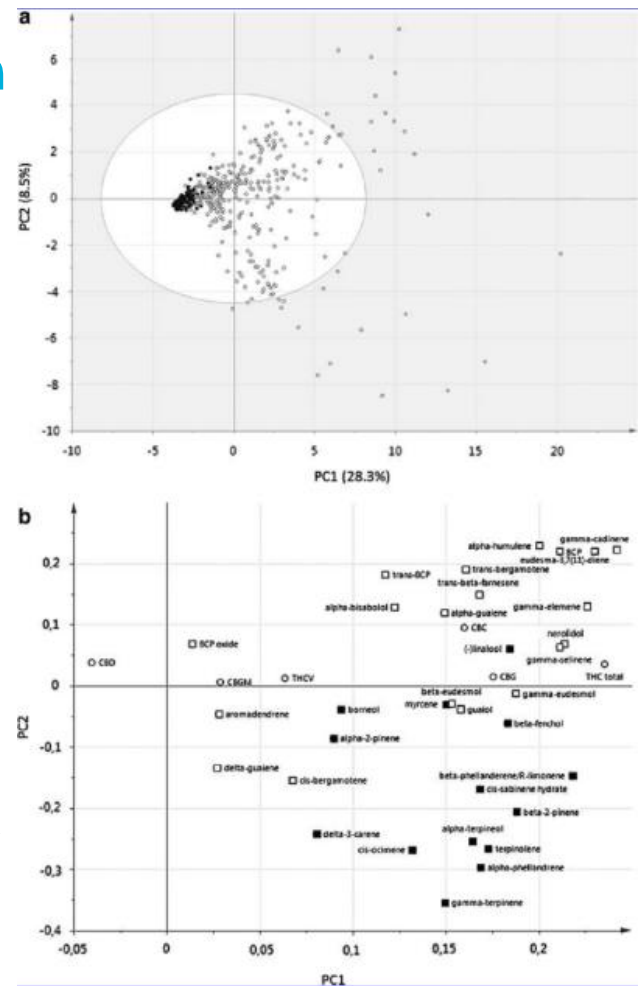
IDENTIFYING COMMON CANNABIS TERPENES

					
TERPENE:	ALPHA-PINENE BETA-PINENE	MYRCENE	LIMONENE	ACARYOPHY- LLENE	LINALOOL
	PINE	MUSKY, EARTHY, CITRUS HINTS	CITRUS	SPICY, WOODY, PEPPERY, CLOVE	FLORAL, CANDY, CITRUS
	FOUND IN Pine, Dill, Parsley, Basil, Rosemary	FOUND IN Mango, Thyme, Lemongrass, Hops	FOUND IN Juniper, Rosemary, Fruit Rinds, Peppermint,	FOUND IN Black Pepper, Clove, Cotton	FOUND IN Lavender
	Alertness, Euphoria, Creativity, Memory Retention	"Couchlock", Sedation, Relaxation, Body High	Elevated Mood, Stress Relief	No noted effects	Anxiety Relief, Sedation
	Asthma, Antiseptic	Antioxidant, Pain, Muscle Tension, Sleeplessness, Anti-Carcinogenic	Gallstones, Gastroprotective, Heartburn, Anti-fungal, Depression	Gastroprotective, Anti-inflammatory, Arthritis, Ulcers	Anti-anxiety, Anti-convulsant, Anti-depressant, Anti-acne
	Jack Herer, Trainwreck, Bubba Kush, Chem Dawg, Super Silver Haze	Pure Kush, El Nino, Himalayan Gold, Skunk #1, White Widow	OG Kush, Super Lemon Haze, Jack the Ripper, Lemon Skunk	Big Bang, Damn Sour, Great White Shark, Ice Dream	G-13, Lavender, Amnesia Haze, LA Confidential

Cultivars vs Chemovars

Cannabis strains are cultivated for specific profiles and characteristics

- The concept of chemovars- **a chemistry-based, phenotypical fingerprint rather than a horticultural cultivar-** has been proposed and gained popularity in the scientific community.
- Scientific studies are yet to identify the **biochemical markers that can sufficiently explain differences between cannabis varieties.**
- Hazekamp *et al.* applied a targeted detection of 44 major terpenes and cannabinoids followed by **Multivariate Data Analysis to identify the cannabis constituents** that may act as markers for distinction between Indica and Sativa.



Overview

- High resolution mass spec workflow described for the exploration of chemovar profiling for several Cannabis strains
- A nontargeted approach which does not try to target a “short-list” of cannabinoids or terpenes
- X500R QTOF System, SWATH® Data Independent Acquisition, SCIEX OS and MarkerView™ software platforms, SCIEX All-in-One plus NIST MSMS library

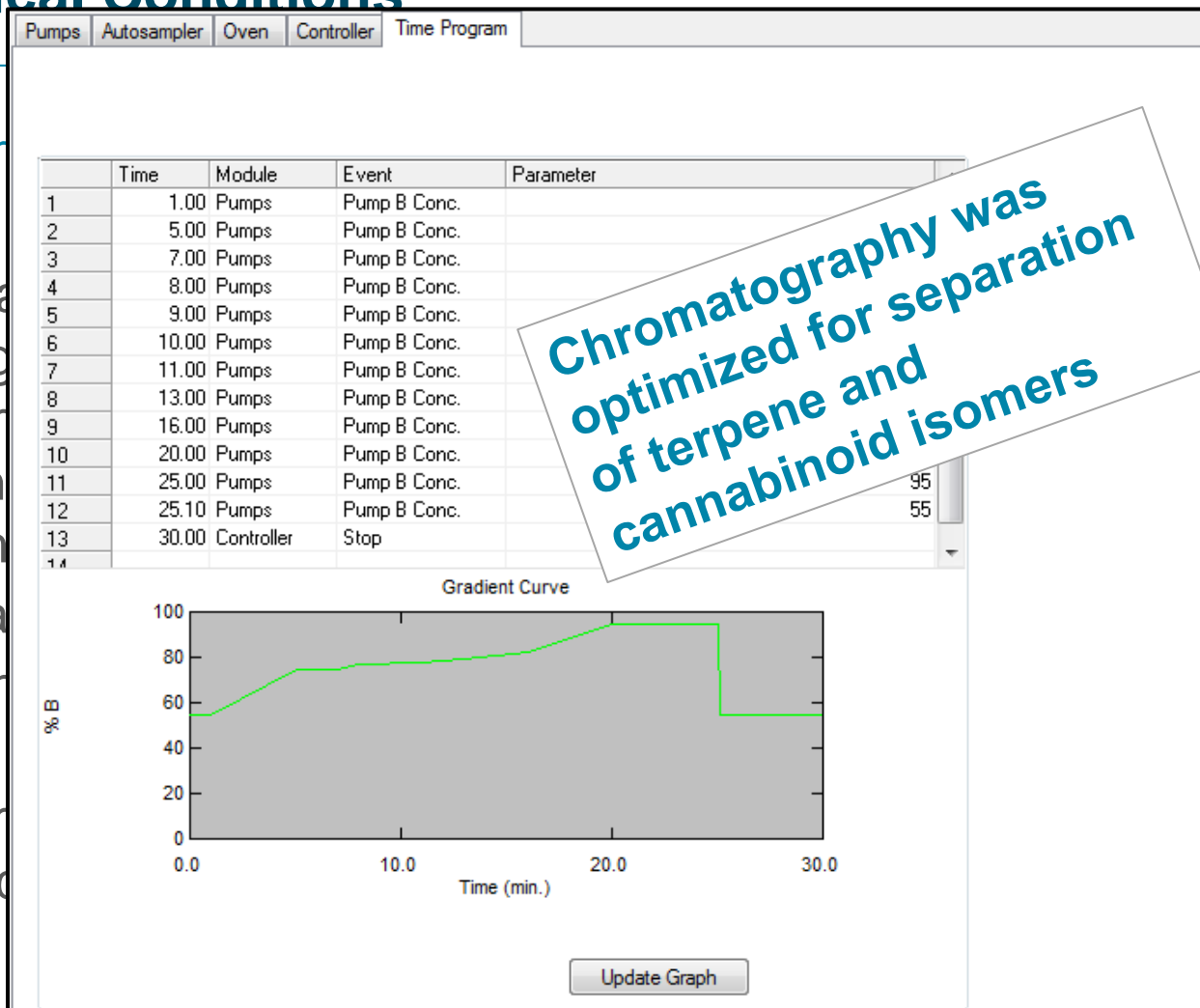


Answers for Science.
Knowledge for Life.™

Analytical Conditions

HPLC Conditions

- SCIEX
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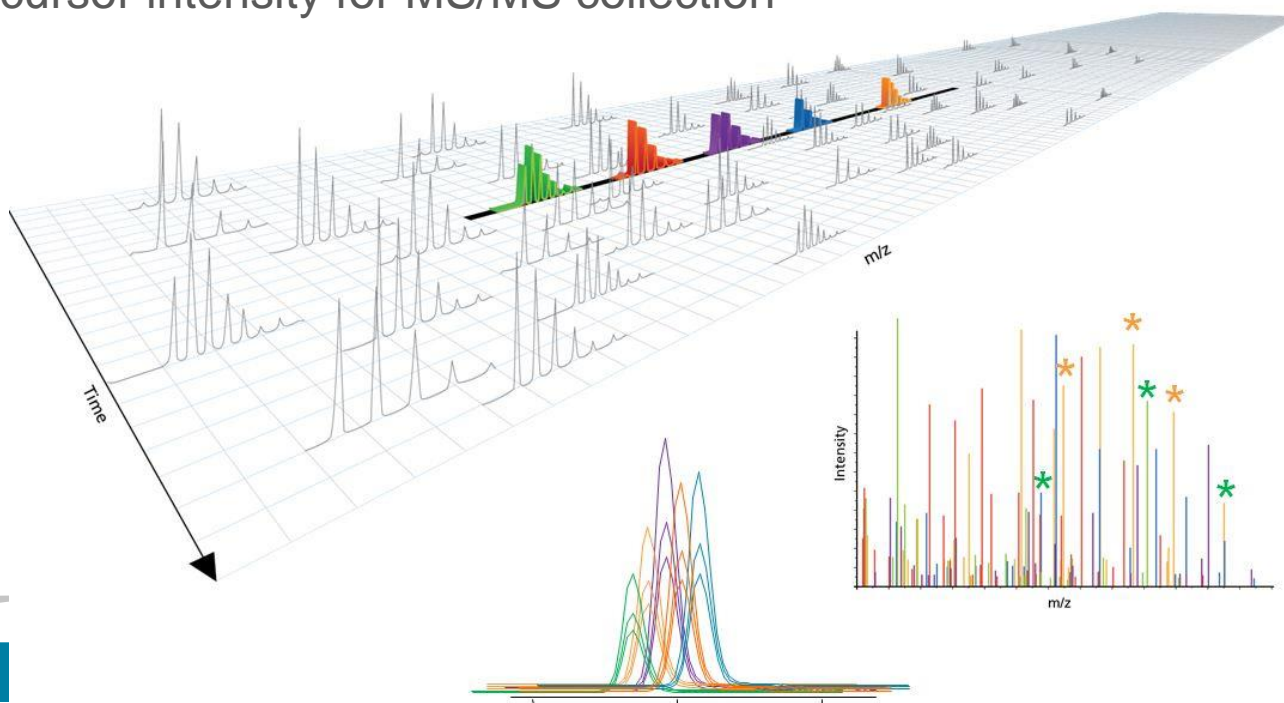
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SWATH® Acquisition

- SWATH = Data Independent Acquisition (DIA)
 - For each cycle, the instrument focuses on a mass window of Q1 precursors
 - Acquires MS/MS data from **all** precursors detected within that window
 - This mass window is then stepped across the **entire** mass range, systematically collecting MS/MS data from every mass and from all detected precursors
 - Unlike IDA (Information Dependent Acquisition), there is no dependence on precursor intensity for MS/MS collection



Variable Window SWATH

Method duration: 21 min

Total scan time: 1.763727 sec

Estimated cycles: 714

Source and Gas Parameters

Ion source gas 1: 60 psi
Ion source gas 2: 60 psi
Curtain gas: 35
CAD gas: 11
Temperature: 500 °C

Experiment

SWATH

Polarity: Positive
Spray voltage: 5500 V

TOF MS

TOF start mass: 40 Da
TOF stop mass: 1000 Da
Accumulation time: 0.06 s
Declustering potential: 80 V
DP spread: 0 V
Collision energy: 10 V
CE spread: 0 V

TOF MSMS

TOF start mass: 40 Da
TOF stop mass: 1000 Da
Accumulation time: 0.03 s
Charge state: 1
Dynamic collision energy: ☐
Enhance dynamic range: ☒

Mass Table

[Autofill SWATH windows...](#)

	Precursor ion start mass (Da)	Precursor ion stop mass (Da)	Declustering potential (V)	DP spread (V)	Collision energy (V)	CE spread (V)
1	39.5000	122.1000	80	0	35	15
2	121.1000	141.9000	80	0	35	15
3	140.9000	156.3000	80	0	35	15
4	155.3000	170.7000	80	0	35	15
5	169.7000	184.2000	80	0	35	15
6	183.2000	200.4000	80	0	35	15
7	199.4000	216.6000	80	0	35	15
8	215.6000	233.2000	80	0	35	15
9	232.2000	249.9000	80	0	35	15
10	248.9000	267.9000	80	0	35	15
11	266.9000	286.3000	80	0	35	15
12	285.3000	303.9000	80	0	35	15
13	302.9000	320.1000	80	0	35	15
14	319.1000	337.6000	80	0	35	15
15	336.6000	353.8000	80	0	35	15
16	352.8000	370.5000	80	0	35	15
17	369.5000	386.2000	80	0	35	15

- Narrower Q1 isolation windows → increased specificity, but more windows needed to cover the m/z range
 - Need to balance m/z coverage, with impact to cycle time
- Optimizing windows of varying width based on m/z for enhancement of specificity by narrowing windows where most ion masses occur
 - Allows for increased mass range to be covered while keeping number of windows (and cycle time) down

SCIEX All-in-One High Resolution MS/MS and NIST'17 MS/MS Mass Spectral Libraries

Enhanced compound coverage across compound classes

The flexibility of the multiple SCIEX software platforms provide scientists a fast way to analyze large batches of MS/MS data for accurate and efficient MS/MS library searching, data mining, and compound database management. In combination with the National Institute of Technology (NIST) MS/MS Spectral Library we have assembled a comprehensive high resolution, accurate mass MS/MS spectral library bundle containing 19,143 compound entries.

Features of the SCIEX All-in-One High Resolution MS/MS Spectral Library

- Includes a SCIEX proprietary 3900 analyte library created using certified reference materials, including compounds commonly tested for in forensics, food, environmental and metabolomics samples.
- The NIST '17 MS/MS Library bundle adds a comprehensive range of different molecules (13,808 small molecules and 1,435 biologically relevant peptides) for enhanced coverage.
- Contains spectra for both positive and negative ionization for compounds that ionize in both polarities.



Advantages of the SCIEX All-in-One MS/MS Spectral Library

- Use the integrated MS and MS/MS information to build methods without the need to infuse standards and optimize conditions for a given compound.
- Easily create processing methods for a TOF-MS-IDA-MS/MS workflow or SWATH® Acquisition for use on TripleTOF® and X-Series QTOF Systems.
- Quickly setup XIC tables for quantitation and identification with SCIEX OS Software or MasterView™ software. Build customized libraries by simply selecting only the compounds of interest using the LibraryView™ Software.

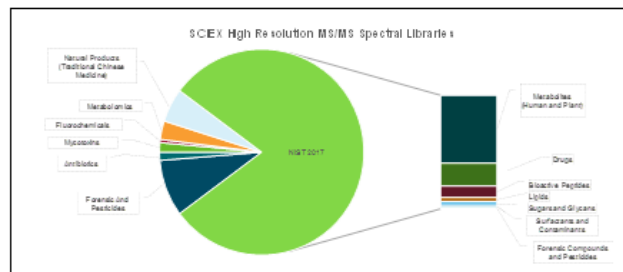


Figure 1. Gain Comprehensive Compound Coverage using the SCIEX All-In-One High Resolution MS/MS Spectral Library bundle containing over 19000 compounds. The inclusion of the NIST '17 MS/MS library increases compound coverage all the way from human and plant Metabolites, to additional Forensic Compounds and Pesticides contained in the proprietary SCIEX MS/MS Spectral Libraries.

This comprehensive library, bundled with the NIST '17 MS/MS Library, provides spectra for over **19000 compounds** including pesticides, pharmaceuticals and personal care products (PPCPs), and natural products found in foods and traditional medicines.

Data Processing Workflow: Nontargeted Approach

Statistical Tools to Identify: Which Features Are Distinctive For Strain Classification?

MarkerView™ software to identify important features using PCA



Build Peaks of Interest list from the distinguishing features identified



Import Peaks of Interest list into Analytics



Search MSMS libraries for first-pass identification of the Peaks of Interest

Identify Those Features!

Choose a probable formula from the formula finder based on HR-AM TOF MS data (mass error, elemental composition, hit count)



Start ChemSpider session to open the ChemSpider list of hits with that formula



ChemSpider database lists predicted fragments from each structure in the "hit list"

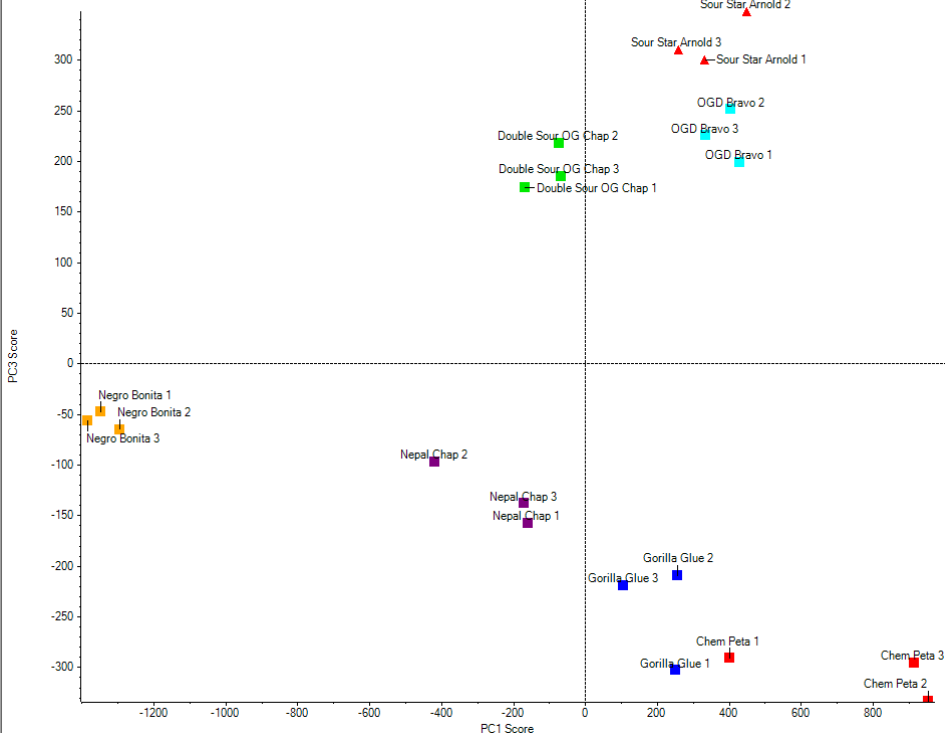


Choose a candidate structure based on the fit of the collected MSMS spectrum to the predicted fragmentation (mass error, number of matched fragment peaks, does the fragment make sense)

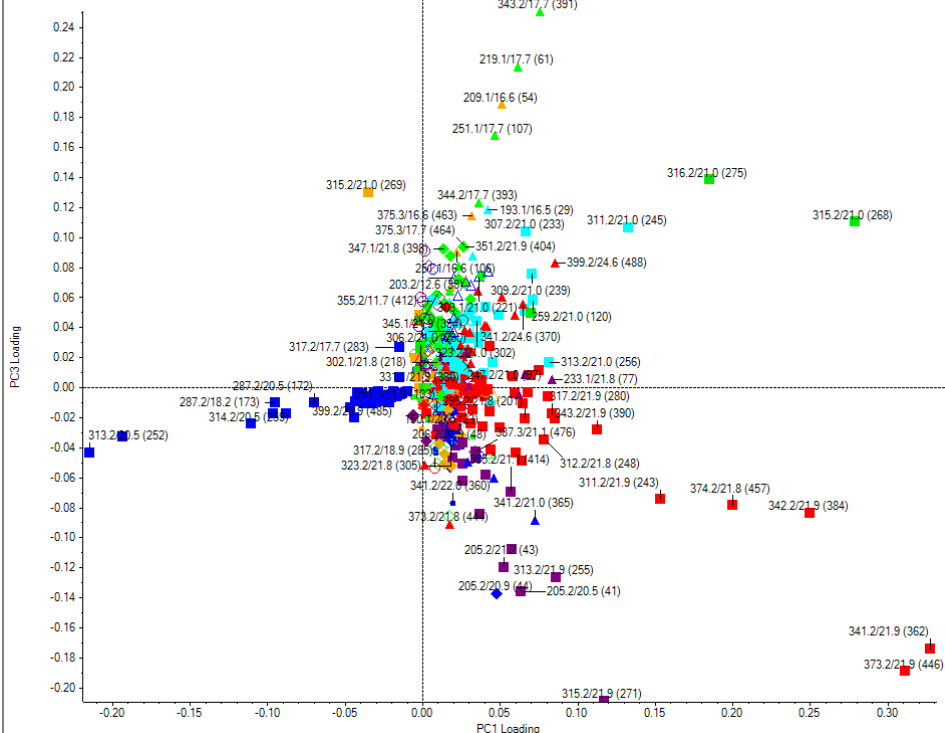
Step 1: Load up Data into MarkerView

PC1 v PC3, Unsupervised PCA

Scores for PC1 (54.7 %) versus PC3 (7.0 %), Pareto



Loadings for PC1 (54.7 %) versus PC3 (7.0 %), Pareto



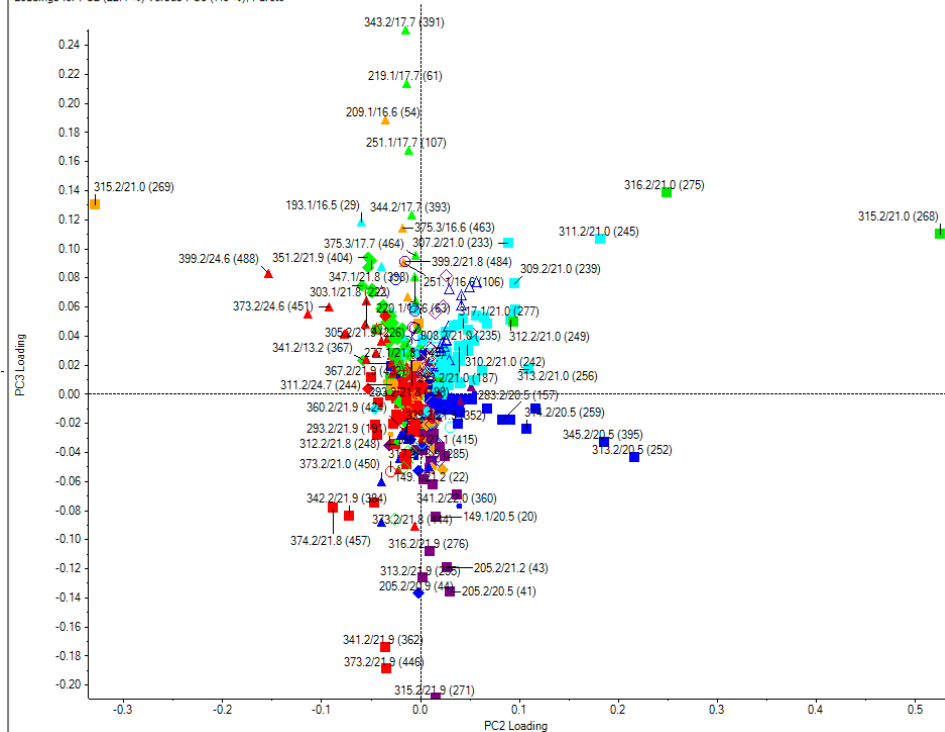
Step 1: Load up Data into MarkerView

PC2 v PC3, Unsupervised PCA, Data Normalized (MLR method)

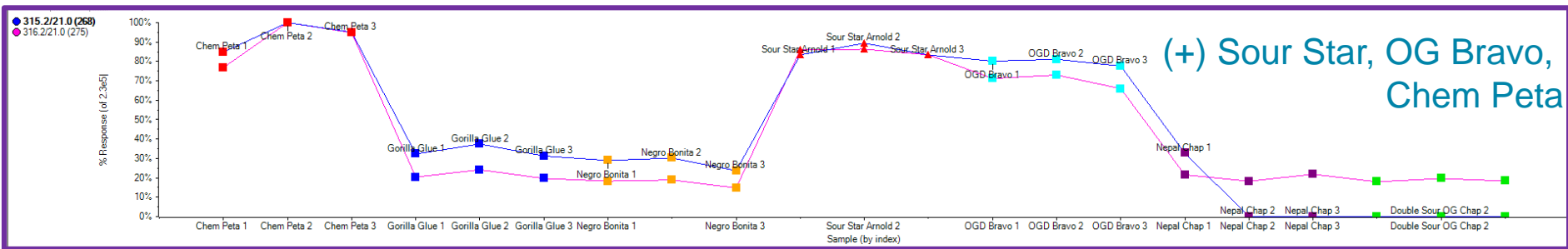
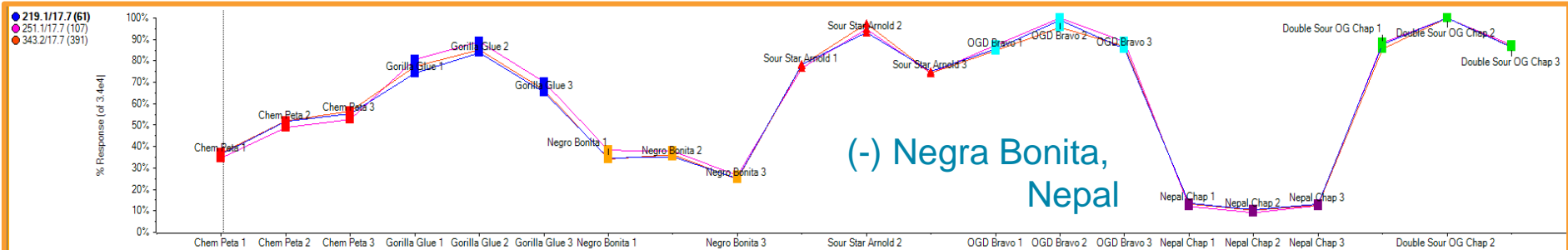
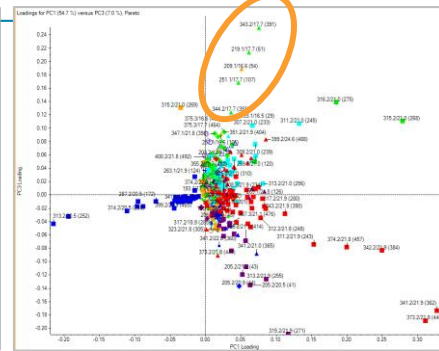
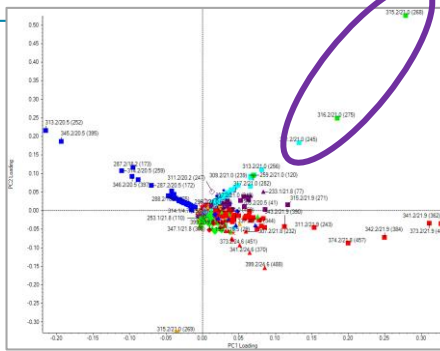
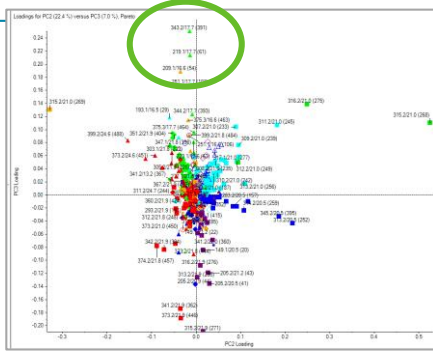
Scores for PC2 (22.4 %) versus PC3 (7.0 %), Pareto



Loadings for PC2 (22.4 %) versus PC3 (7.0 %), Pareto



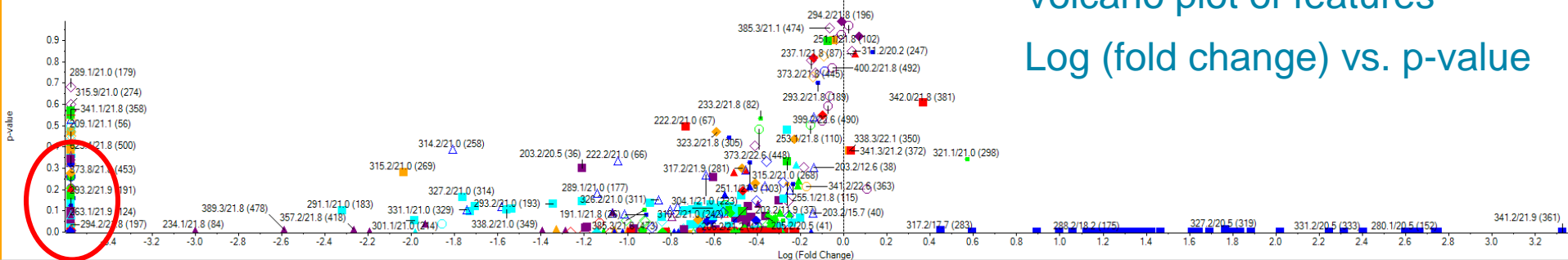
Step 2: Find Distinguishing Features → Peaks of Interest



Step 2: Find Distinguishing Features → Peaks of Interest

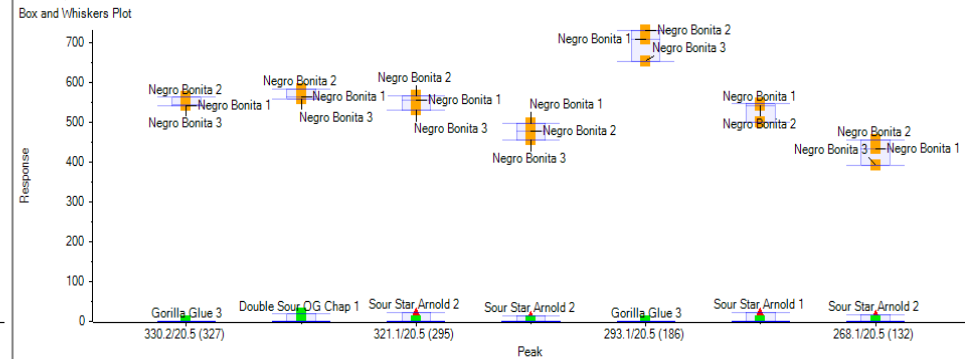
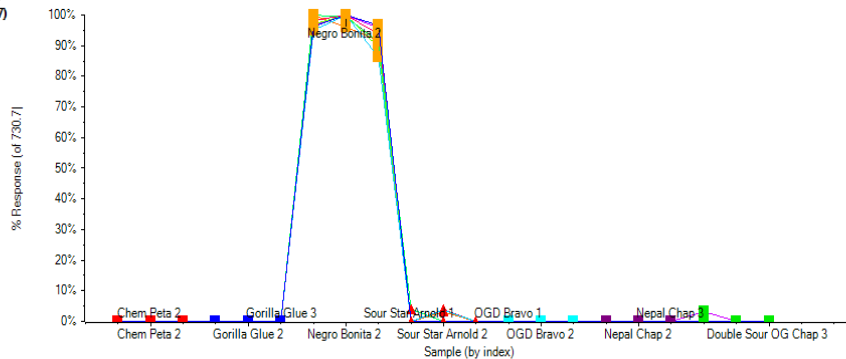
Perform t-Test

Log (Fold Change) versus p-value for Negro Bonita to (All Others)



Lowest p-value and greatest fold change
Features which are most distinguishing between the two groups compared in the t-Test

● 330.2/20.5 (327)
● 325.1/20.5 (308)
● 321.1/20.5 (295)
● 278.1/20.5 (146)
● 293.1/20.5 (186)
● 233.1/20.5 (78)
● 268.1/20.5 (132)



Peaks of Interest



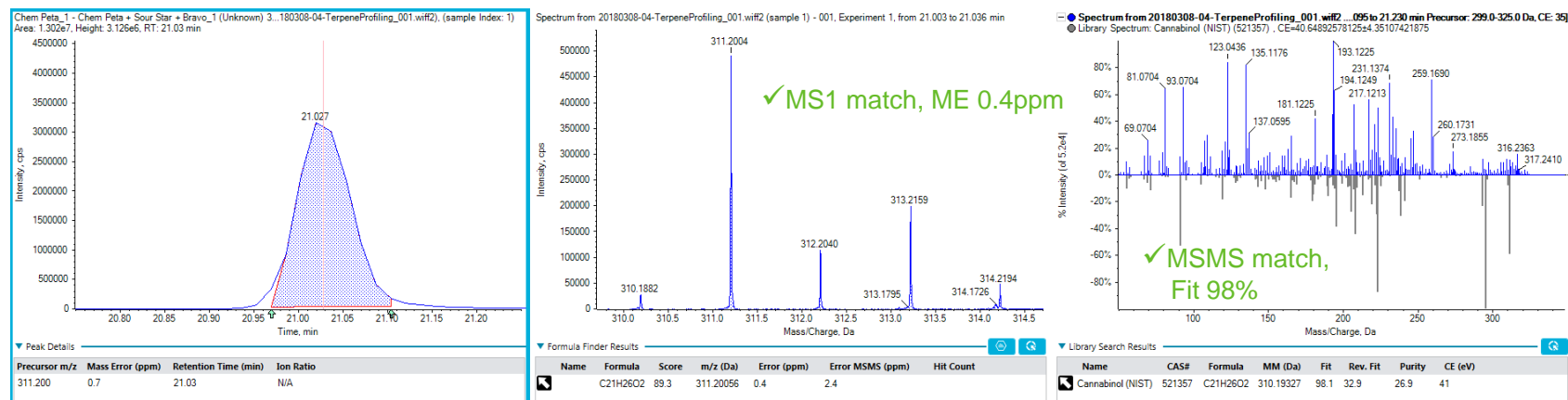
Peak of Interest	<i>m/z</i>	RT
1 (-) Negro Bonita_1	341.2107	21.86
2 (-) Negro Bonita_2	341.2109	21
3 (-) Negro Bonita_3	373.2363	21.86
4 (-) Nepal_1	219.1014	17.67
5 (-) Nepal_2	251.1277	17.66
6 (-) Nepal_3	343.2266	17.67
7 (+) Chem Peta + Sour Star + Bravo_1	311.2002	21
8 (+) Chem Peta + Sour Star + Bravo_2	315.2309	20.99
9 (+) Chem Peta + Sour Star + Bravo_3	316.235	21
10 (+) Negro Bonita_1	313.1794	20.52
11 (+) Negro Bonita_2	345.2057	20.52
12 (+) Sour Star + Double Sour_1	375.2528	16.56

Step 3: Suspect Screening

Some Peaks of Interest Identified by MSMS Library Matches

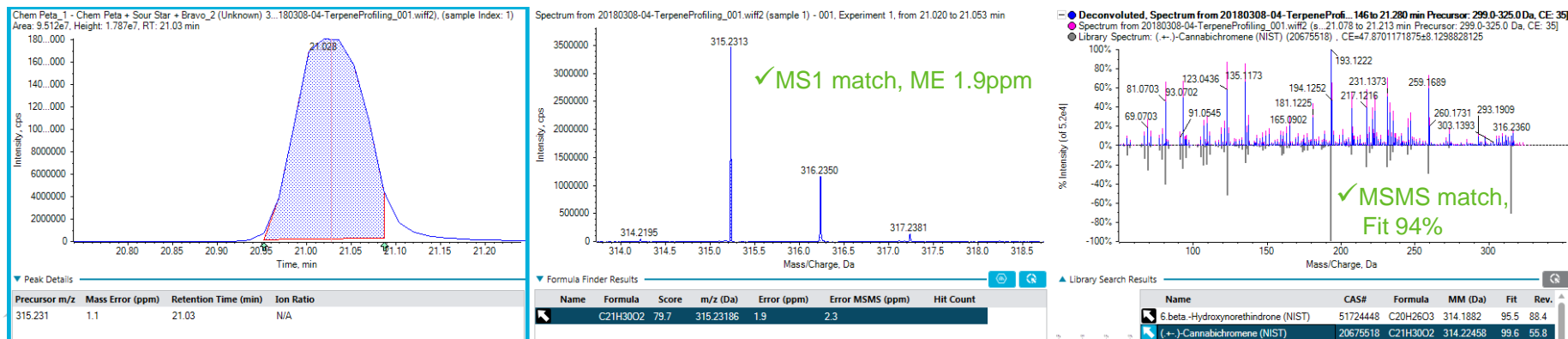
Peak of Interest #7: (+) in Chem Peta, Sour Star, OG Bravo (m/z 311.2003)

- NIST Library Match for Cannabinol (CBN)
- A non-psychoactive cannabinoid usually found only in trace levels



Peak of Interest #8: (+) in Chem Peta, Sour Star, OG Bravo (m/z 315.2313)

- NIST Library Match for Cannabichromene (CBC)
- May have anti-inflammatory, anti-viral, antifungal properties
- Contribute to the analgesic effects



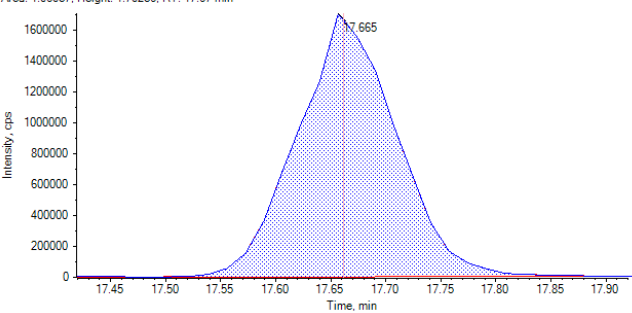
Step 3: Suspect Screening

Some Peaks of Interest Identified by MSMS Library Matches

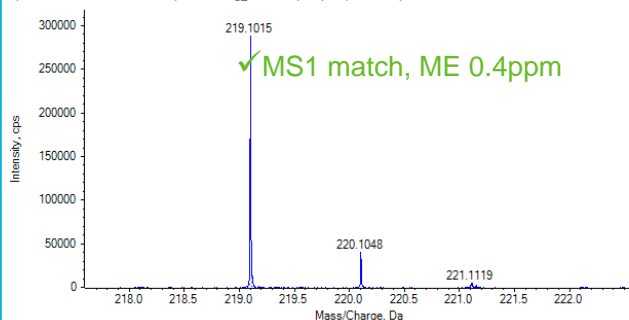
Peak of Interest #4: (-) in Nepal (m/z 219.1015)

- NIST Library Match for Xanthorrhizol
- A sesquiterpenoid which exhibits natural antibacterial, antifungal activity

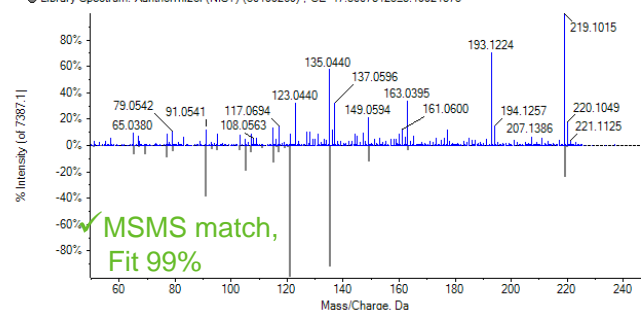
Gorilla Glue Chap. 1 - (-) Nepal_1 (Unknown) 219.0914 - 219.0180308-07-TerpeneProfiling_004.wiff2). (sample Index: 1)
Area: 1.060e7, Height: 1.702e6, RT: 17.67 min



Spectrum from 20180308-07-TerpeneProfiling_004.wiff2 (sample 1) - 004, Experiment 1, from 17.657 to 17.690 min



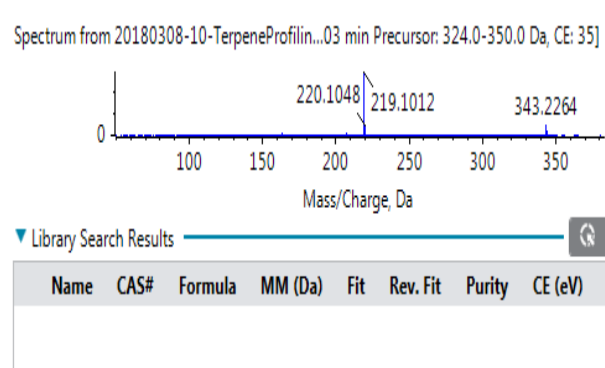
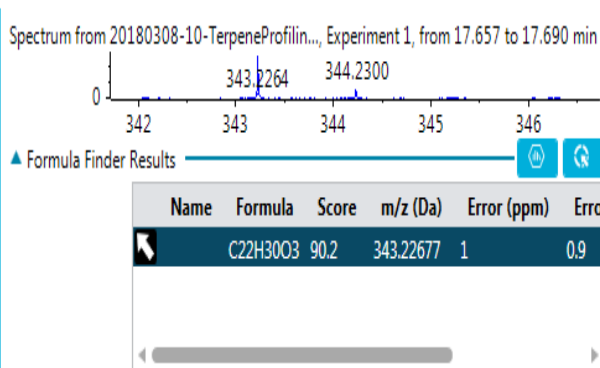
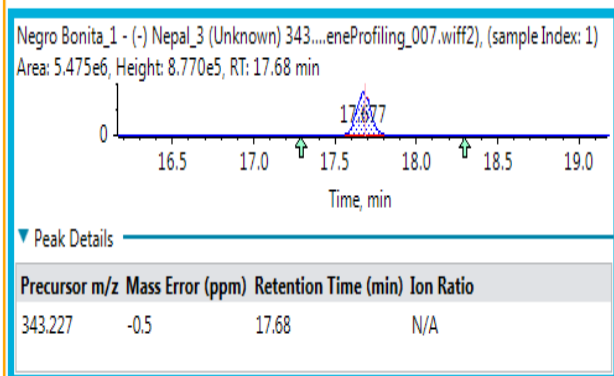
■ Spectrum from 20180308-07-TerpeneProfiling_004.wiff2 ...813 to 18.116 min Precursor: 199.0-225.0 Da, CE: 35
● Library Spectrum: Xanthorrhizol (NIST) (30199269) , CE=47.80078125±8.19921875



...but some needed some more digging to ID

Peak of Interest #6: (-) in Nepal (m/z 343.2266)

Index	Sample Name	Component Name	Precursor Mass	Area Ratio of...	Mass Error...	Library Confidence	Found At Mass	Mass Error (pp...	Library Hit	Library Score	Formula Finder Results	Formula Finder Sc...
6	MeOH Blank	(-) Nepal_3	343.227	N/A	■	■	N/A	N/A		N/A		N/A
439	Chem Peta_1	(-) Nepal_3	343.227	N/A	✓	●	343.2268	0.5	No Match	0.0	C22H30O3	99.125
872	Gorilla Glue Chap_1	(-) Nepal_3	343.227	N/A	✓	●	343.2265	-0.3	No Match	0.0	C22H30O3	87.331
▶ 1305	Negro Bonita_1	(-) Nepal_3	343.227	N/A	✓	●	343.2264	-0.5	No Match	0.0	C22H30O3	90.203
1738	Sour Star Arnold_1	(-) Nepal_3	343.227	N/A	✓	●	343.2266	0.0	No Match	0.0	C22H30O3	95.001
2171	OGD Bravo_1	(-) Nepal_3	343.227	N/A	✓	●	343.2265	-0.3	No Match	0.0	C22H30O3	88.962
2604	Nepal Chap_1	(-) Nepal_3	343.227	N/A	✓	●	343.2267	0.4	No Match	0.0	C22H30O3	97.504
3037	Double Sour OG Chap_1	(-) Nepal_3	343.227	N/A	✓	●	343.2266	-0.1	No Match	0.0	C22H30O3	93.956



Peak of Interest #6: $C_{22}H_{30}O_3$

No MSMS library match

Empirical Formula: C₂₂H₃₀O₃

ChemSpider Search with Predicted MSMS Comparison

ChemSpider results for: C₂₂H₃₀O₃

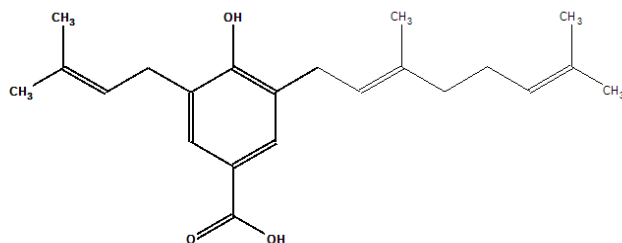
1-40 of 526

CSID	Common Name	Molecular Weight
166817	Siccanin	342.4718
18023	Megestrol	342.4718
62152	Trimegestone	342.4718
92091	Spirolactone intermediate	342.4718
28184844	5-Isopropenyl-2-methyl-2-cyclohexene-1-carboxylic anhydride	342.4718
64512	endrisone	342.4718
248321	4,4,6a,9-Tetramethyl-1,2,3,4,4a,5,6,6a,11b,13b-decahydrobenzo[a]furo[2,3,4-mn]xanthen-11-ol	342.4718
60209	340308D18M	342.4718
4534900	2-Hydroxy-6-[(8E,11E)-8,11,14-pentadecatrien-1-yl]benzoic acid	342.4718
197094	4P9MHB40VF	342.4718
14392179	DWA2JG4TUB	342.4718
8050818	anacardic acid	342.4718
548039	10,13-Dimethyl-1,6,7,8,9,10,11,12,13,14,15,16-dodecahydro-3'H-spiro[cyclopenta[a]phenanthrene-17,2'-furan]-3,5'(2H,4'H)-dione	342.4718
9511768	3OG14VJA88	342.4718
21675312	3-Hexyl-4,8-dimethyl-7-[(3-methyl-2-buten-1-yl)oxy]-2H-chromen-2-one	342.4718
8535482	myrsinoic acid A	342.4718
3100845	1,1'-[Oxybis(2,1-ethanediylloxy)]bis(2,3,5-trimethylbenzene)	342.4718
198081	1WDZ80D40Y	342.4718
64914	(4aS,6aS,11bR,13aS,13bS)-4,4,6a,9-Tetramethyl-1,2,3,4,4a,5,6,6a,11b,13b-decahydrobenzo[a]furo[2,3,4-mn]xanthen-11-ol	342.4718
135019	(2S)-2-[(8S,9S,10R,13S,14S,17R)-10,13-Dimethyl-3-oxo-6,7,8,9,10,11,12,13,14,15,16,17-dodecahydro-3H-cyclopenta[a]phenanthren-17-yl]propanoic acid	342.4718
3360053	1,1'-[Oxybis(2,1-ethanediylloxy)]bis(2,4,6-trimethylbenzene)	342.4718
2667466	3-Oxoandrosta-1,4-dien-16-yl propionate	342.4718
140121	(17beta)-6-Methylene-3-oxoandrosta-4-en-17-yl acetate	342.4718
217557	16-Methylene-17-oxoandrosta-5-en-3-yl acetate	342.4718
146862	3-oxo-23,24-bisnorchola-1,4-dien-22-oic acid	342.4718
553407	(4aS,6aS,12aR,12bS)-10-Methoxy-4,4,6a,12b-tetramethyl-1,2,3,4,4a,5,6,6a,12a,12b-decahydro-9H-benzo[a]xanthen-9-one	342.4718

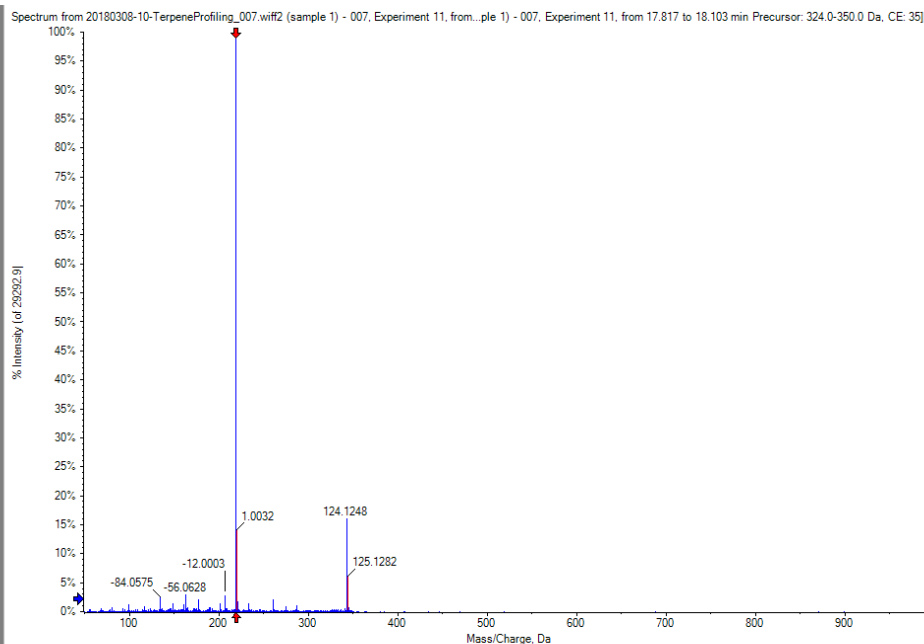
☐ Display all Carbon Atoms

Options...

selected composition: C₂₂H₃₀O₃* (219.1016 Da)



Myrsinoic acid



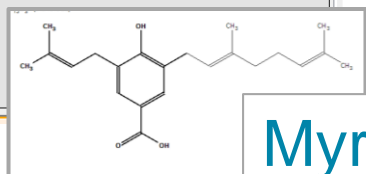
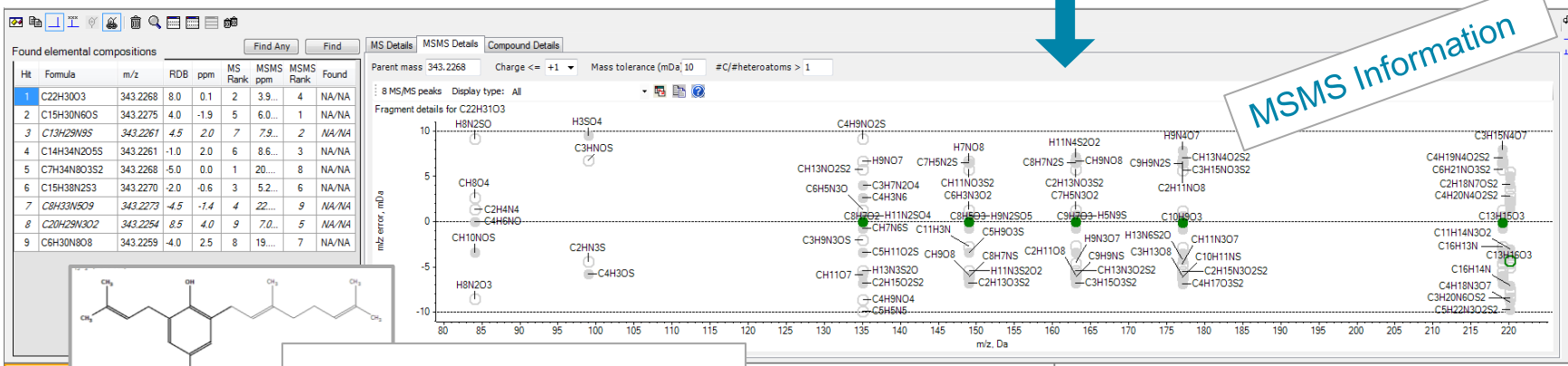
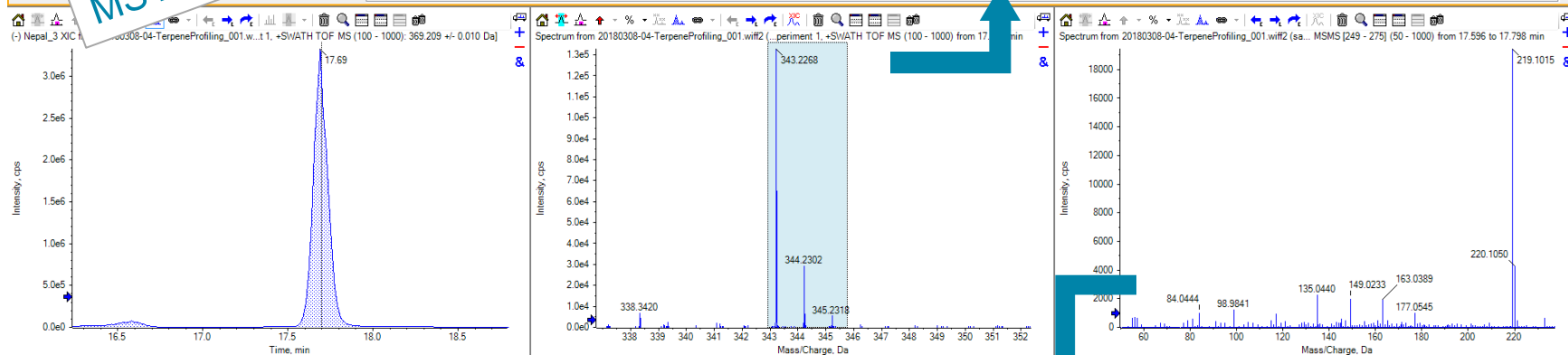
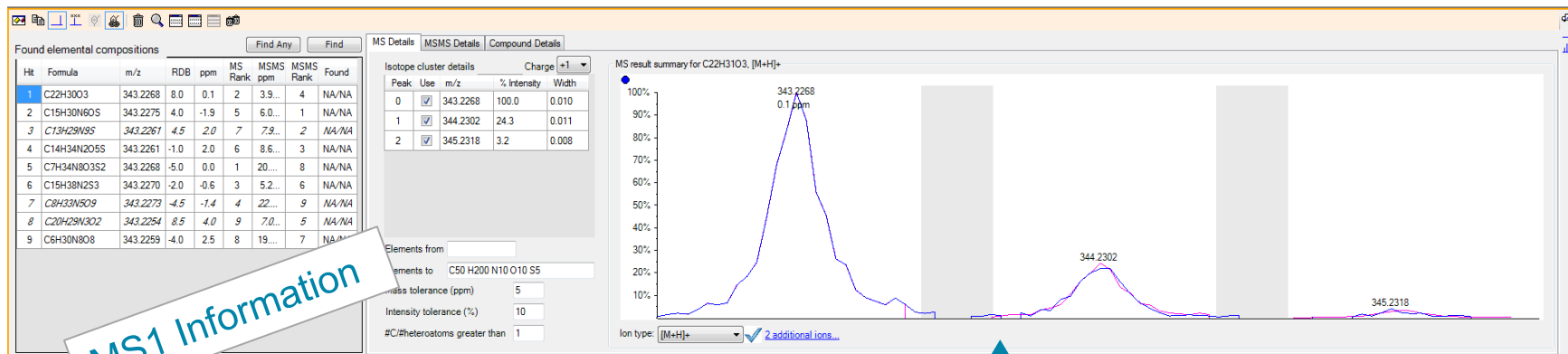
Options...

Mass/Charge	Intensity (%)	Assigned	Error (Da)
135.0441	2.56	<input checked="" type="checkbox"/>	0.036
163.0388	2.88	<input checked="" type="checkbox"/>	0.000
207.1013	2.80	<input checked="" type="checkbox"/>	0.000
219.1012	100.00	<input checked="" type="checkbox"/>	0.000
220.1048	14.09	<input type="checkbox"/>	
343.2264	16.08	<input checked="" type="checkbox"/>	0.000
344.2298	6.14	<input type="checkbox"/>	

Matches: 5 of 7 peaks, 86.0% of total intensity

Select

Cancel



Myrsinoic acid

★ Ranking Confidence Level in Unknown Identification

1. Analytical Standard Comparison
2. Accurate Mass/ Isotope/ Fragments consistent with published data
3. Accurate Mass/ Isotope/ Fragments are consistent with proposed structure, but published spectra are not available
4. Accurate Mass and Isotopes are consistent with proposed structure, but unable to attribute the major fragments to the proposed structure

Schymanski, E. L., Jeon, J., Gulde, R., Fenner, K., Ru, M., Singer, H. P., Hollender, J. (2014) Identifying Small Molecules via High Resolution Mass Spectrometry: Communicating Confidence. 2097–2098.

★ Ranking Confidence Level in Unknown Identification

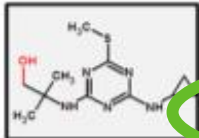
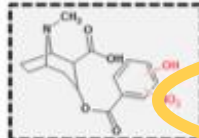
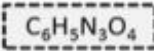
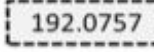
Example	Identification confidence	Minimum data requirements
	Level 1: Confirmed structure by reference standard	MS, MS ² , RT, Reference Std.
	Level 2: Probable structure a) by library spectrum match b) by diagnostic evidence	MS, MS ² , Library MS ² MS, MS ² , Exp. data
	Level 3: Tentative candidate(s) structure, substituent, class	MS, MS ² , Exp. data
	Level 4: Unequivocal molecular formula	MS isotope/adduct
	Level 5: Exact mass of interest	MS

Figure 1. Proposed identification confidence levels in high resolution mass spectrometric analysis. Note: MS² is intended to also represent any form of MS fragmentation (e.g., MSⁿ, MS^m).

Schymanski *et al.* describes levels of identification criteria for nontargeted screening. With a library hit from a suspect screen, you can get as high as level 2 confidence (no reference standard, but good MS1 and MS2 matches). Without a library match, just your work on in silico fragment prediction of structures etc, you may only get as high as level 3 match.

Level 4 Identifications: Empirical formulae



- Peak of Interest #1: $C_{22}H_{28}O_3$ (492 structures in ChemSpider)
- Peak of Interest #5: $C_{14}H_{18}O_4$ (3,022 structures in ChemSpider)
- Peak of Interest #10: $C_{20}H_{24}O_3$ (16 structures in ChemSpider)
- Peak of Interest #11: $C_{21}H_{28}O_4$ (16 structures in ChemSpider)

Hmmm.... Why bother with the statistical analysis?

Can you just start with the SWATH data and the SUSPECT SCREEN?

765 of 3464 rows Filters: 3 ☒ Qualify for Rules Filters

Index	Sample Name	Component Name	Precursor Mass	Area Ratio...	Mass Error...	Library Confi...	Found At Mass	Mass Error (...)	Library Hit	Library Score	Formula Finder Results	Formula Finder...
755	Chem Peta_1	357.2420 / 21.83 [M+H] ⁺	357.242	N/A		✓	357.2420	N/A	3.beta.-Hydroxy-5-cholenoic a...	100.0	No formula found	0.000
2487	OGD Bravo_1	357.2420 / 21.83 [M+H] ⁺	357.242	N/A		✓	357.2420	N/A	3.beta.-Hydroxy-5-cholenoic a...	100.0	No formula found	0.000
2192	OGD Bravo_1	136.0616 / 1.90	136.062	N/A		✓	136.0616	N/A	Adenine (NIST)	99.5	C5H5N5	85.840
2321	OGD Bravo_1	317.2471 / 16.55	317.247	667.733		✓	317.2474	N/A	Cannabigerol (NIST)	98.6	C21H32O2	95.408
1281	Gorilla Glue Chap_1	397.3829 / 25.79	397.383	77.424		✓	397.3825	N/A	Monobehenin (NIST)	98.5	C29H48	92.728
1759	Sour Star Arnold_1	136.0616 / 1.90	136.062	N/A		✓	136.0615	N/A	Adenine (NIST)	97.9	C5H5N5	82.204
3187	Double Sour OG Chap_1	317.2471 / 16.55	317.247	757.118		✓	317.2472	N/A	Cannabigerol (NIST)	97.7	C21H32O2	88.288
460	Chem Peta_1	136.0616 / 1.90	136.062	N/A		✓	136.0617	N/A	Adenine (NIST)	97.0	No formula found	0.000
2360	OGD Bravo_1	399.2339 / 19.10	399.234	N/A		✓	399.2338	N/A	Methanesulfonamide, N-3-(9H...	96.6	C16H34N2O9	97.624
2366	OGD Bravo_1	399.2340 / 19.61	399.234	N/A		✓	399.2338	N/A	Methanesulfonamide, N-3-(9H...	96.6	C16H34N2O9	97.624
597	Chem Peta_1	317.2474 / 17.62	317.247	N/A		✓	317.2471	N/A	Cannabigerol (NIST)	95.7	C21H32O2	90.542
3013	Nepal Chap_1	397.3829 / 25.79	397.383	75.450		✓	397.3825	N/A	Monobehenin (NIST)	95.5	C29H48	90.778
1888	Sour Star Arnold_1	317.2471 / 16.55	317.247	497.440		✓	317.2473	N/A	Cannabigerol (NIST)	95.0	C21H32O2	94.419
2754	Nepal Chap_1	317.2471 / 16.55	317.247	381.961		✓	317.2469	N/A	Cannabigerol (NIST)	95.0	C21H32O2	85.415
1022	Gorilla Glue Chap_1	317.2471 / 16.55	317.247	357.408		✓	317.2472	N/A	Cannabigerol (NIST)	94.9	C21H32O2	90.432
1455	Negro Bonita_1	317.2471 / 16.55	317.247	159.548		✓	317.2472	N/A	Cannabigerol (NIST)	94.8	C21H32O2	93.263
2762	Nepal Chap_1	317.2474 / 17.62	317.247	N/A		✓	317.2472	N/A	Cannabigerol (NIST)	94.4	C21H32O2	92.589
589	Chem Peta_1	317.2471 / 16.55	317.247	336.278		✓	317.2471	N/A	Cannabigerol (NIST)	93.7	C21H32O2	89.434
3154	Double Sour OG Chap_1	369.1332 / 12.70	369.133	N/A		✓	369.1334	N/A	Methoxyfenozide (NIST)	92.3	C21H20O6	95.444
1544	Negro Bonita_1	337.1794 / 20.57 [M+CH3OH+H] ⁺	337.179	192.132		✓	337.1795	N/A	Acebutolol (NIST)	90.8	C21H20O2	92.439
3351	Double Sour OG Chap_1	233.1169 / 21.83 [M+H] ⁺	233.117	562.790		✓	233.1171	N/A	2,4-Di-tert-amyIphenol (NIST)	90.8	C7H16N6OS	66.430
1855	Sour Star Arnold_1	369.1332 / 12.70	369.133	N/A		✓	369.1332	N/A	Methoxyfenozide (NIST)	90.3	C21H20O6	96.888
753	Chem Peta_1	233.1169 / 21.83 [M+H] ⁺	233.117	1411.374		✓	233.1169	N/A	2,4-Di-tert-amyIphenol (NIST)	90.2	C14H16O3	87.243
1422	Negro Bonita_1	369.1332 / 12.70	369.133	N/A		✓	369.1333	N/A	Methoxyfenozide (NIST)	90.0	C21H20O6	97.845
609	Chem Peta_1	287.2007 / 18.23	287.201	N/A		✓	287.2004	N/A	Tetrahydrocannabivarin (NIST)	89.3	C19H26O2	91.959
1908	Sour Star Arnold_1	287.2007 / 18.23	287.201	N/A		✓	287.2006	N/A	Tetrahydrocannabivarin (NIST)	88.5	C19H26O2	96.788
2054	Sour Star Arnold_1	357.2420 / 21.83 [M+H] ⁺	357.242	N/A		✓	357.2418	N/A	Ethanethioic acid, S-2-(hexade...	88.5	No formula found	0.000
3233	Double Sour OG Chap_1	341.2110 / 19.69 [M+H] ⁺	341.211	N/A		✓	341.2111	N/A	(-)-Biphenylol (NIST)	88.3	C22H28O2	98.922

- THOUSANDS of hits, often across multiple sample groups
- Do we need all of them to get to the answer we seek???
- We want to CLASSIFY, DISTINGUISH and find DIFFERENCES that matter

Summary, Potential Applications, Potential Implications

- Unique Cannabis chemovars can be distinguished by their molecular signature
 - Strains cluster together and separate easily by PCA, even with no target masses defined
- Trace cannabinoids CBC and CBN identified as upregulated in Sour Star, Chem Peta, OG Bravo
- Myrsinoic Acid identified as a natural product downregulated in Nepal versus other strains
- Xanthorrhizol identified as a sesquiterpenoid present in multiple strains
 - Not one of the terpenes included in most targeted analyses

Summary, Potential Applications, Potential Implications

- Unique Cannabis chemovars can be distinguished by their molecular signature
 - Intellectual Property?
 - New strain behavior prediction?
 - Authenticity testing? Identifying fraudulent strain labelling?
 - Extraction and manufacturing process refinement?
 - Pharmaceutical/therapy design?
 - Identifying novel natural products?
- Food authenticity
- Metabolomic research
- Workflow: Classification of other types of complex samples



Questions?



Answers for Science.
Knowledge for Life.™

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Answers for Science.
Knowledge for Life.™

It's Time to
See Everything
Clearly at
Trace Levels





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