

Spectrum from 181128-SM0022.wiff (sample 1) - 181128-SM0022, Experiment 5, +TOF MS² (50 - 1000) from 5.213 min
Precursor: 553.1 Da, CE: 35.0

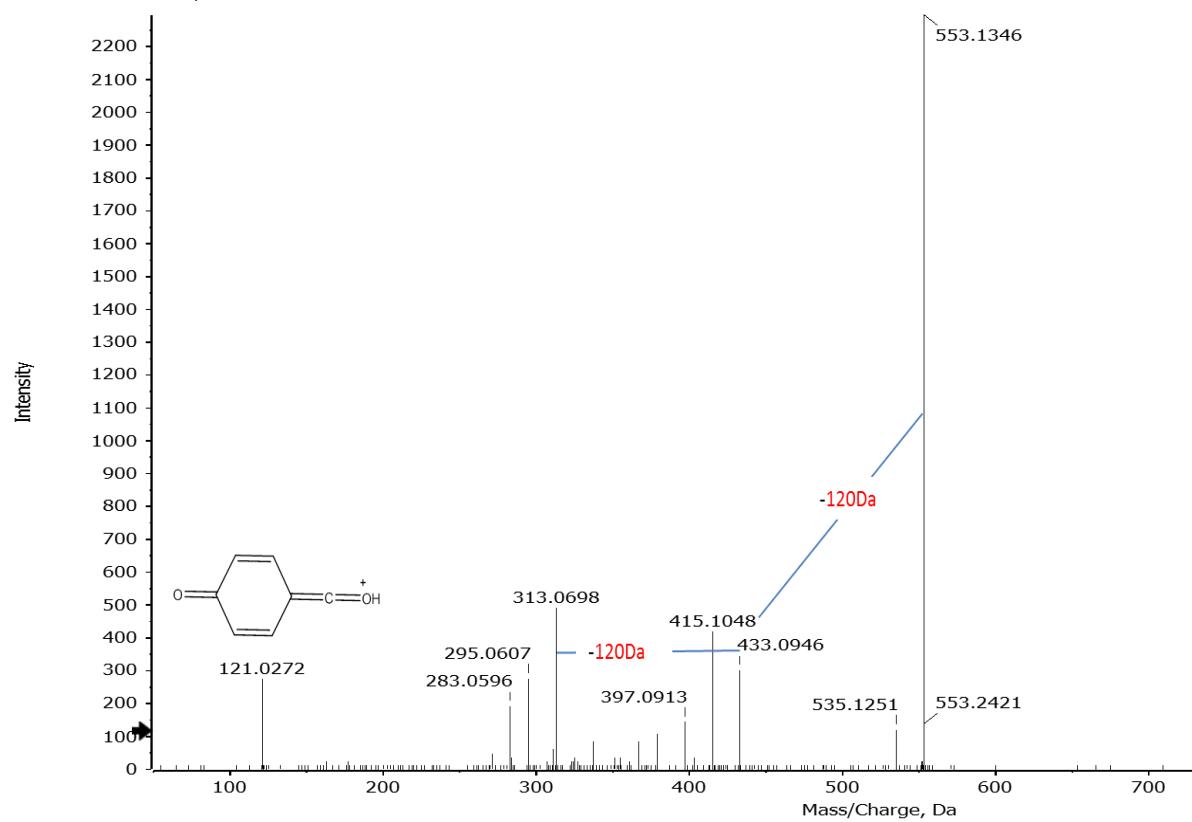


Figure S1. MS/MS spectrum of peak 29: Vitexin-p-hydroxybenzoate.

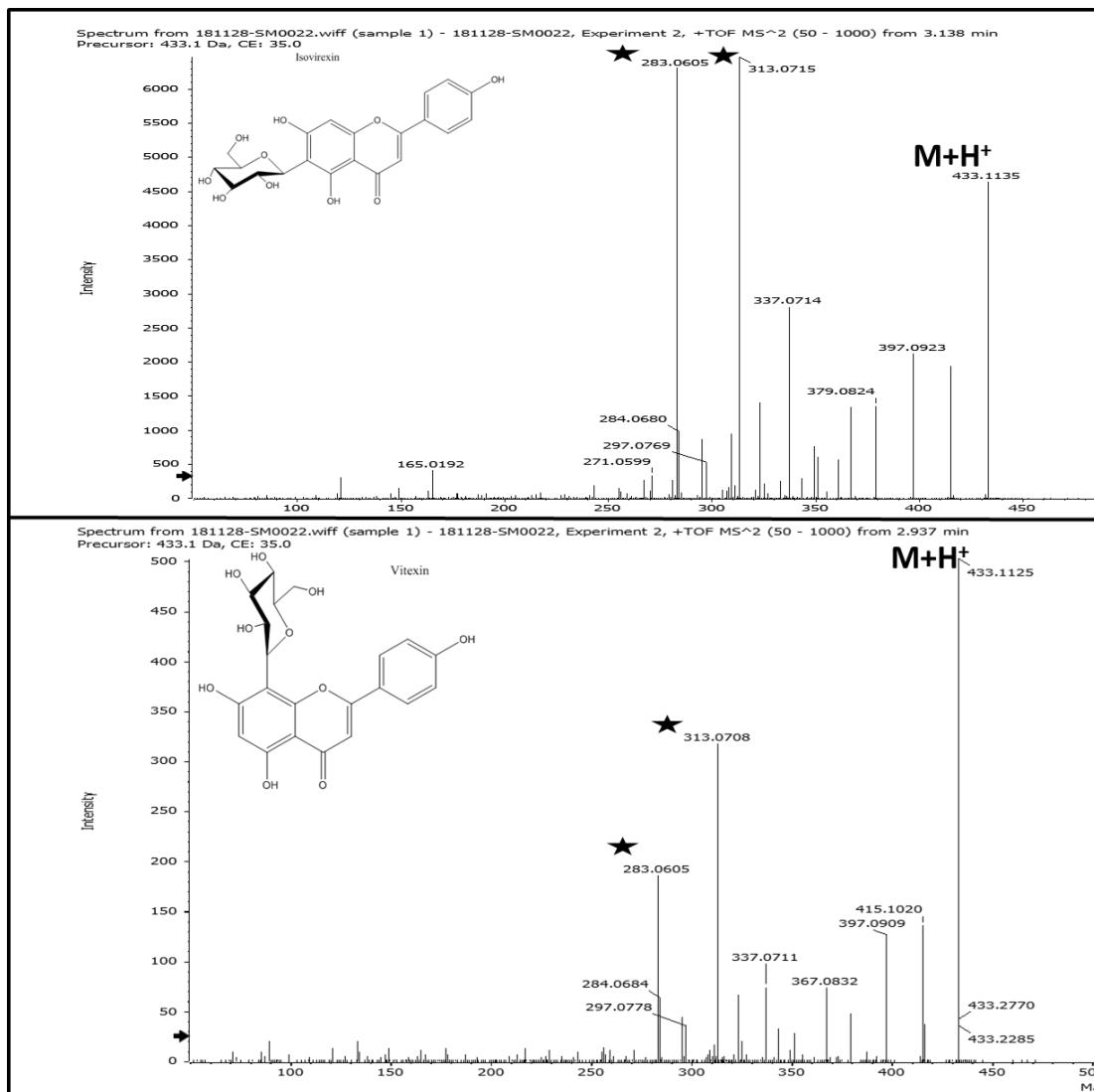
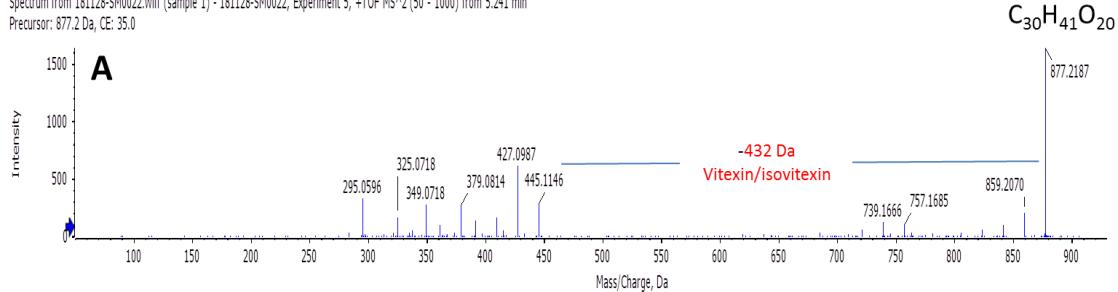


Figure S2. Fragmentation pattern highlighting different fragmentation of the two structural isomer vitexin and isovitaxin based on the intensity of 313 and 283 fragment ions.

Spectrum from 181128-SM0022.wiff (sample 1) - 181128-SM0022, Experiment 5, +TOF MS² (50 - 1000) from 5.241 min
Precursor: 877.2 Da, CE: 35.0



Spectrum from 181128-SM0022.wiff (sample 1) - 181128-SM0022, Experiment 4, +TOF MS² (50 - 1000) from 5.292 min
Precursor: 877.2 Da, CE: 35.0

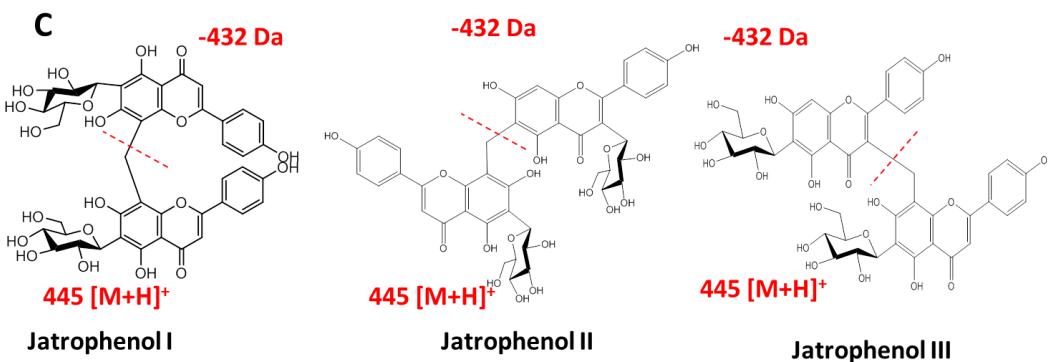
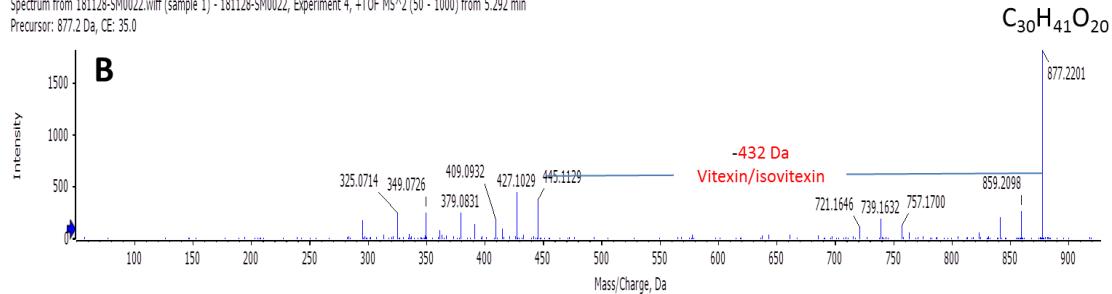


Figure S3. MS/MS spectrum of peaks 30 and 32: Jatrophenol I/II/III.

Spectrum from 181128-SM0022.wiff (sample 1) - 181128-SM0022, Experiment 8, +TOF MS² (50 - 1000) from 3.706 min
Precursor: 560.2 Da, CE: 35.0

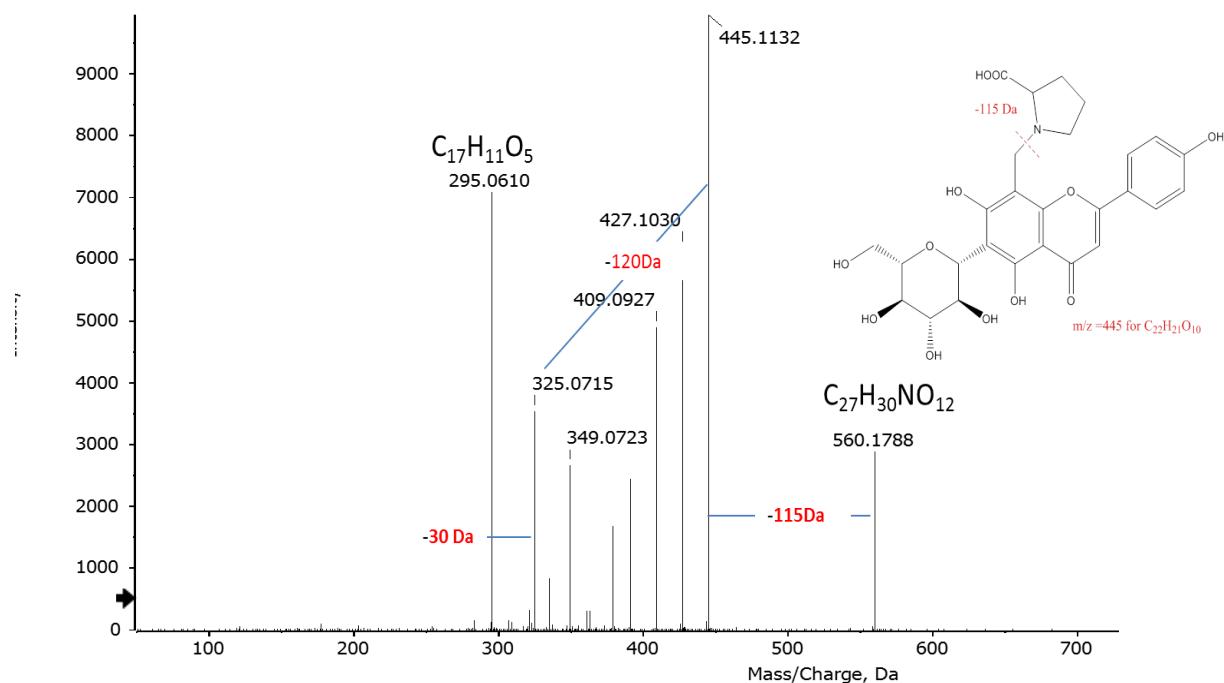


Figure S4. MS/MS spectrum of peak 35: Proline methylisovitexin.

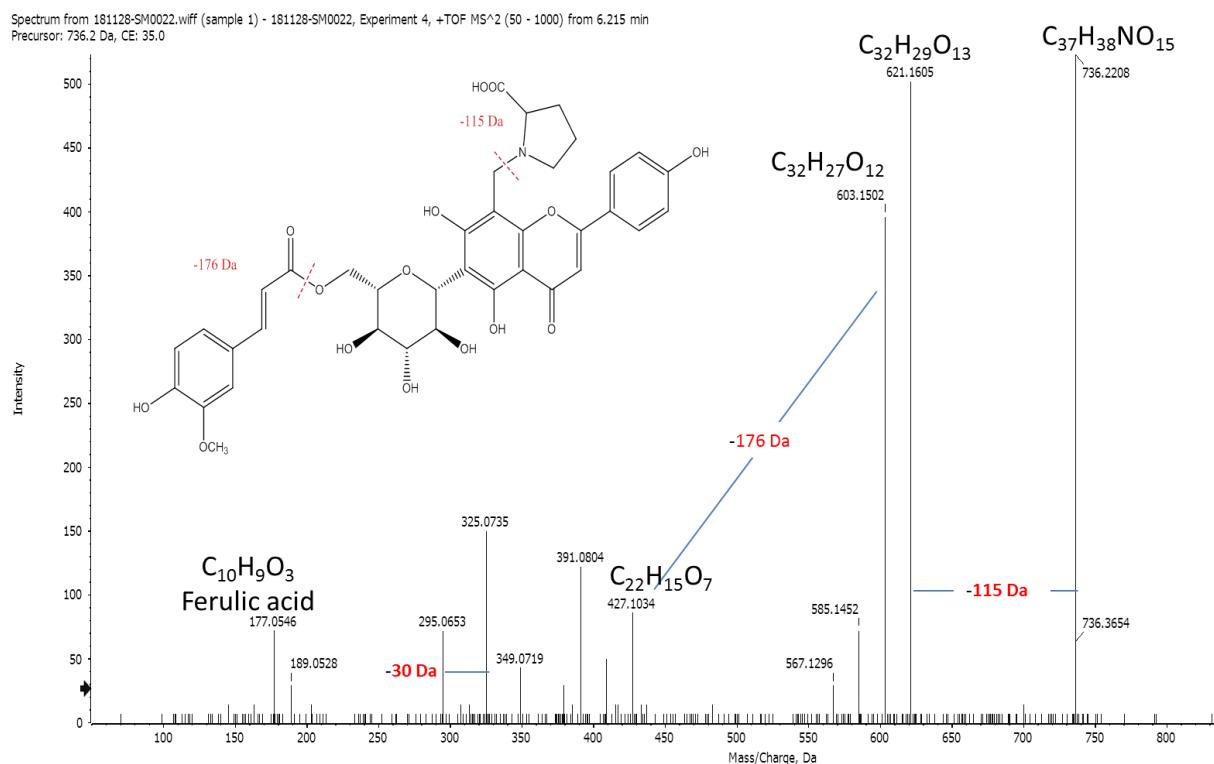


Figure S5. MS/MS spectrum of peak 35: Methylisovitexin proline ferulate.

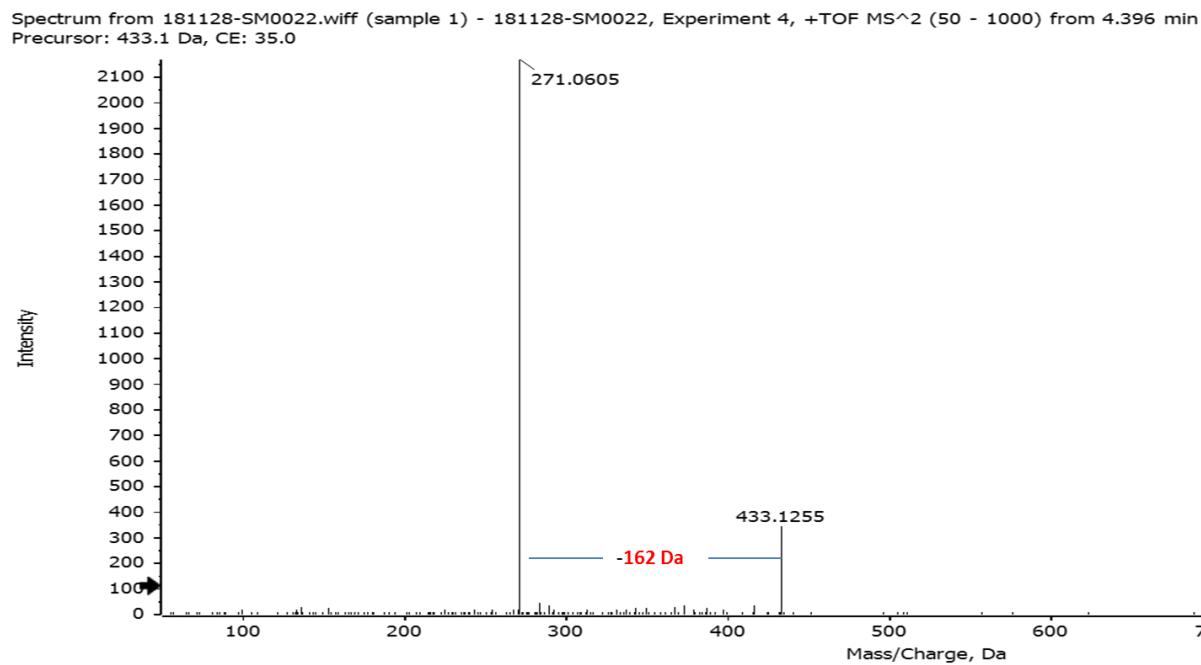


Figure S6. MS/MS spectrum of peak 26: Apigenin-O-hexoside.

Spectrum from 181128-SM0022.wiff (sample 1) - 181128-SM0022, Experiment 9, +TOF MS² (50 - 1000) from 4.253 min
Precursor: 579.2 Da, CE: 35.0

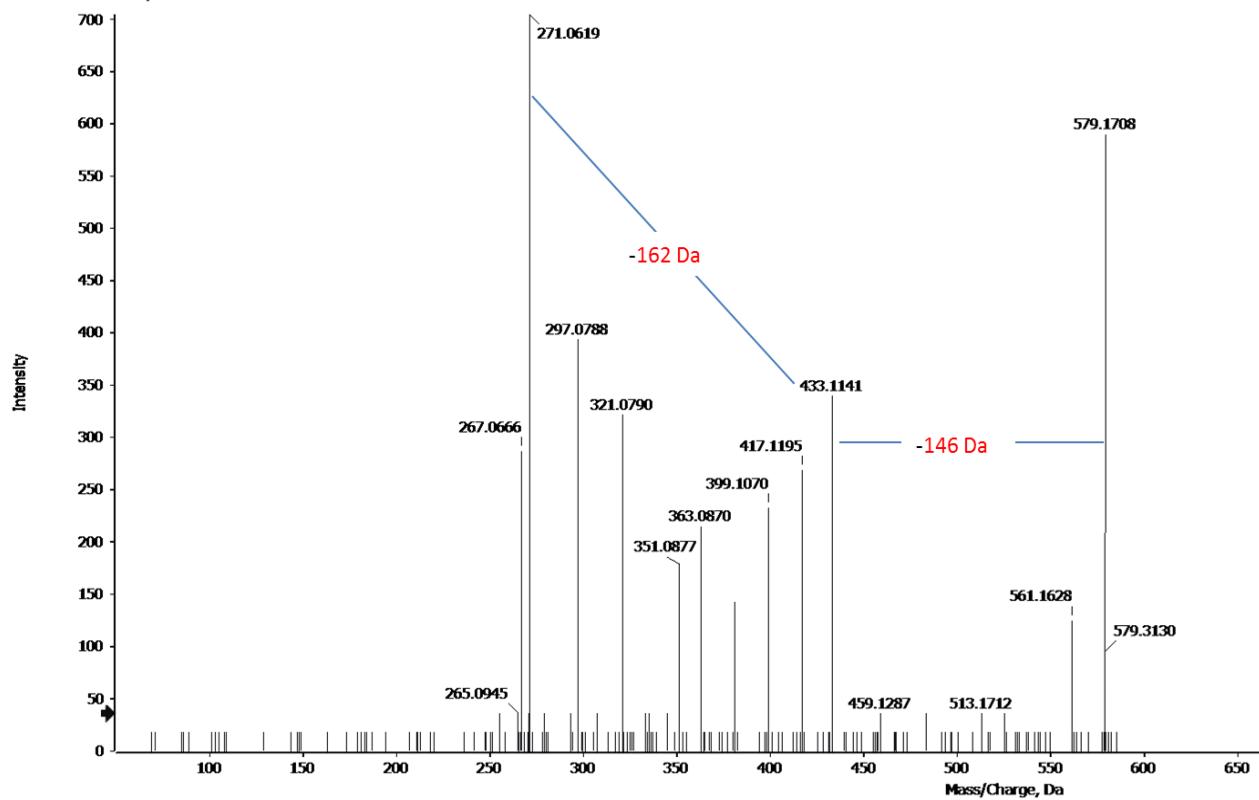


Figure S7. MS/MS spectrum of peak 25: Apigenin-O-hexoside-O-rhamnoside.

Spectrum from 181128-SM0022.wiff (sample 1) - 181128-SM0022, Experiment 7, +TOF MS² (50 - 1000) from 9.543 min
Precursor: 722.5 Da, CE: 35.0

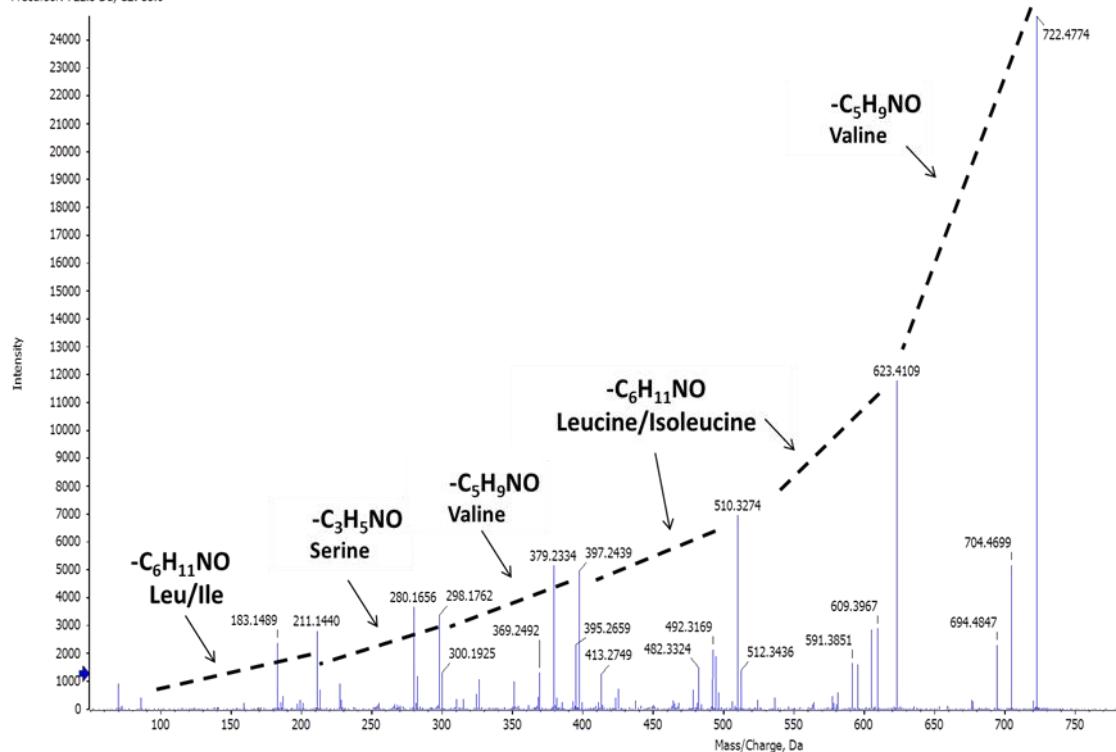


Figure S8. MS/MS spectrum of peak 43: A cycloheptapeptide.

Spectrum from 181128-SM0022.wiff (sample 1) - 181128-SM0022, Experiment 3, +TOF MS² (50 - 1000) from 9.591 min
Precursor: 809.5 Da, CE: 35.0

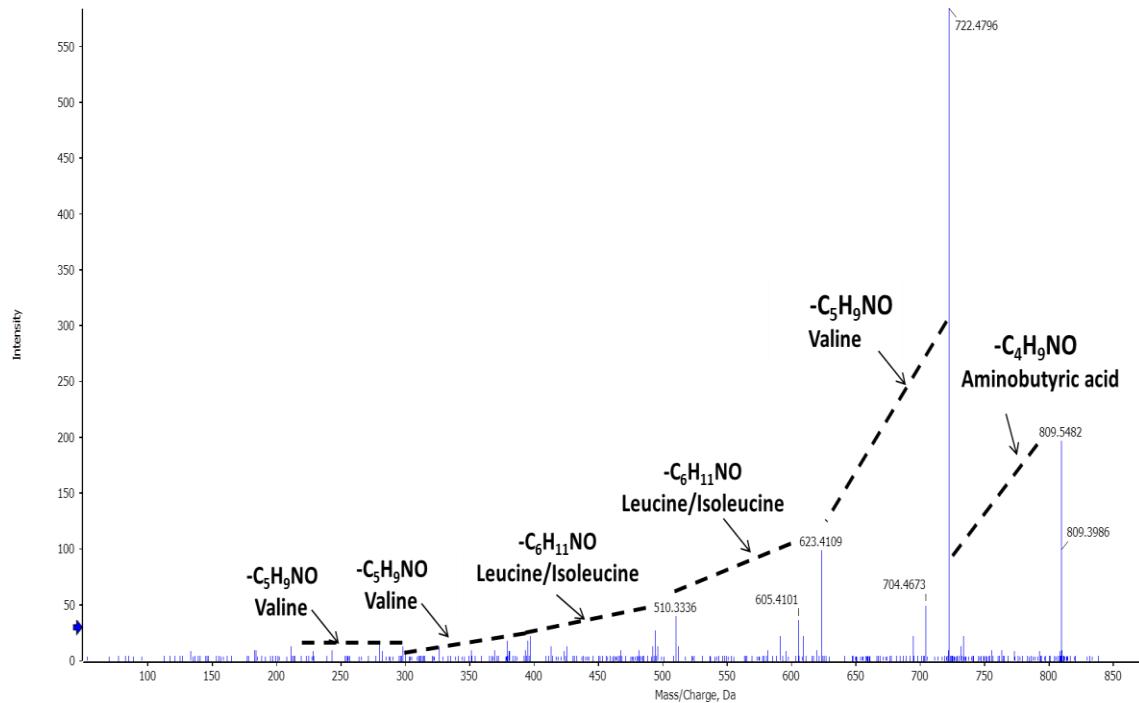


Figure S9. MS/MS spectrum of peak 45: A cyclooctapeptide.

Spectrum from 181128-SM0022.wiff (sample 1) - 181128-SM0022, Experiment 8, +TOF MS² (50 - 1000) from 9.616 min
Precursor: 767.5 Da, CE: 35.0

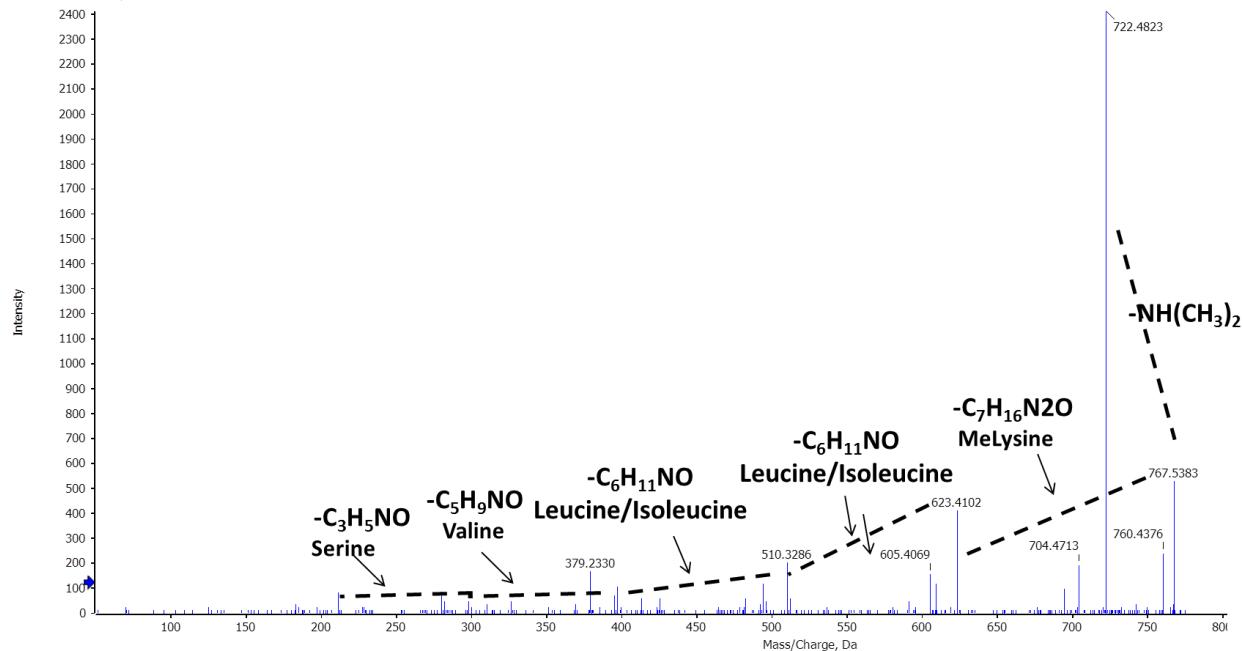


Figure S10. MS/MS spectrum of peak 46: A cycloheptapeptide.

Spectrum from 181128-SM0022.wiff (sample 1) - 181128-SM0022, Experiment 6, +TOF MS² (50 - 1000) from 10.554 min
Precursor: 668.4 Da, CE: 46.5

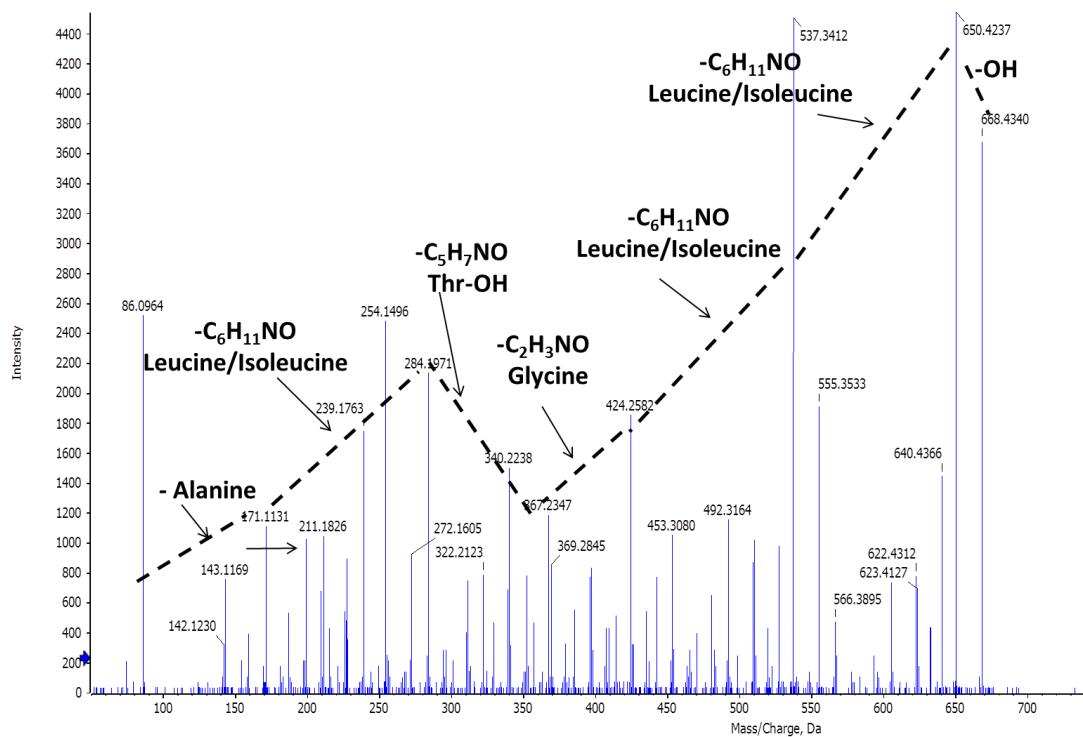


Figure S11. MS/MS spectrum of peak 46: A cycloheptapeptide.

Spectrum from 181128-SM0022.wiff (sample 1) - 181128-SM0022, Experiment 2, +TOF MS² (50 - 1000) from 11.364 min
Precursor: 301.2 Da, CE: 35.0

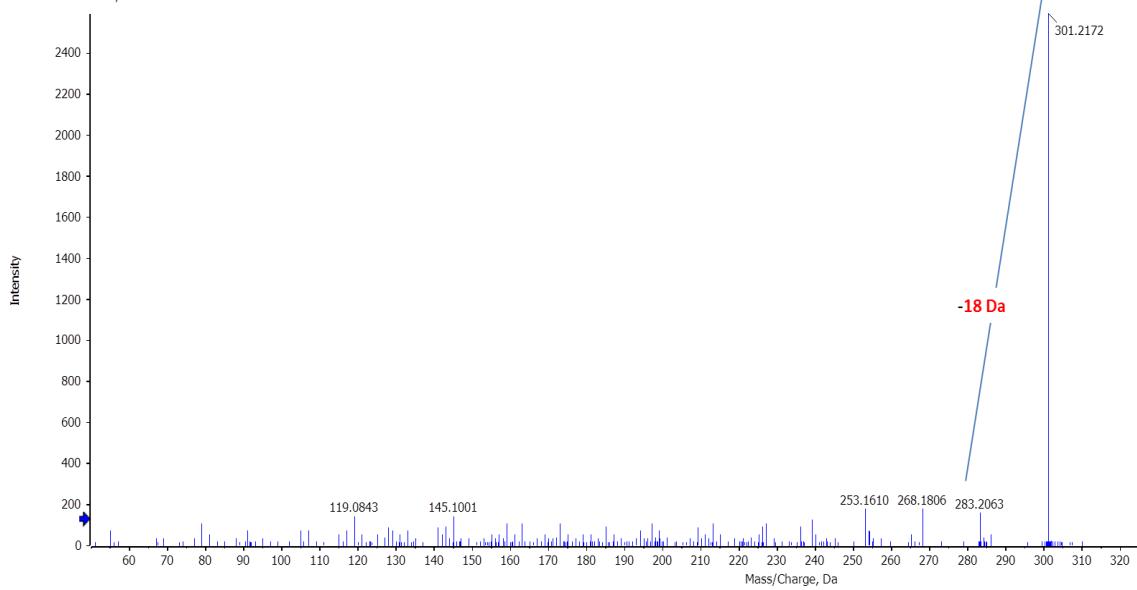


Figure S12. MS/MS spectrum of peak 59: Spruceanol.

Spectrum from 181128-SM0022.wiff (sample 1) - 181128-SM0022, Experiment 3, +TOF MS² (50 - 1000) from 11.952 min
Precursor: 275.2 Da, CE: 35.0

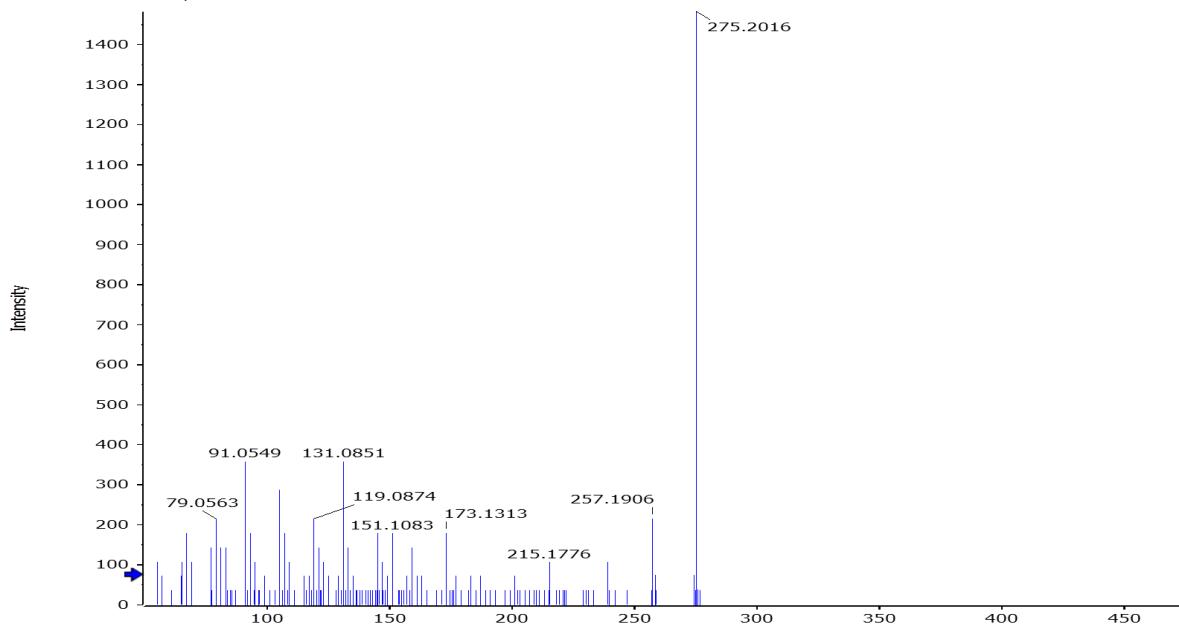


Figure S13. MS/MS spectrum of peak 61.

Spectrum from 181128-SM0022.wiff (sample 1) - 181128-SM0022, Experiment 2, +TOF MS² (50 - 1000) from 12.420 min
Precursor: 411.2 Da, CE: 35.0

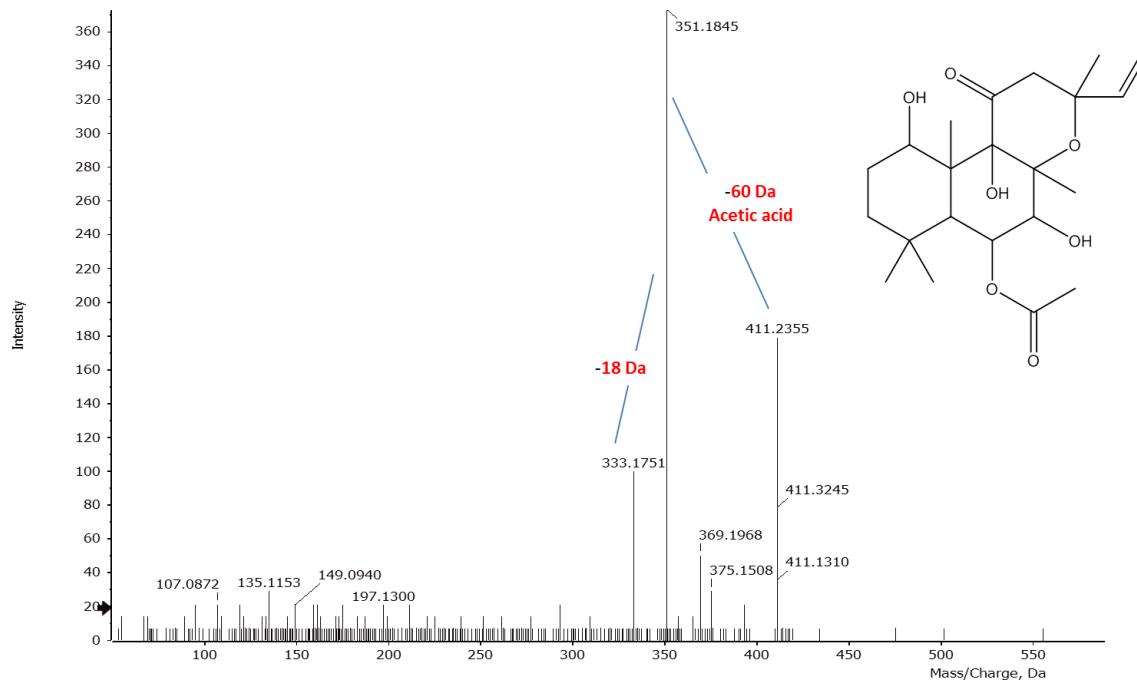


Figure S14. MS/MS for peak 67: Isoforskolin.

Spectrum from 181128-SM0022.wiff (sample 1) - 181128-SM0022, Experiment 3, +TOF MS^2 (50 - 1000) from 20.410 min
Precursor: 637.3 Da, CE: 35.0

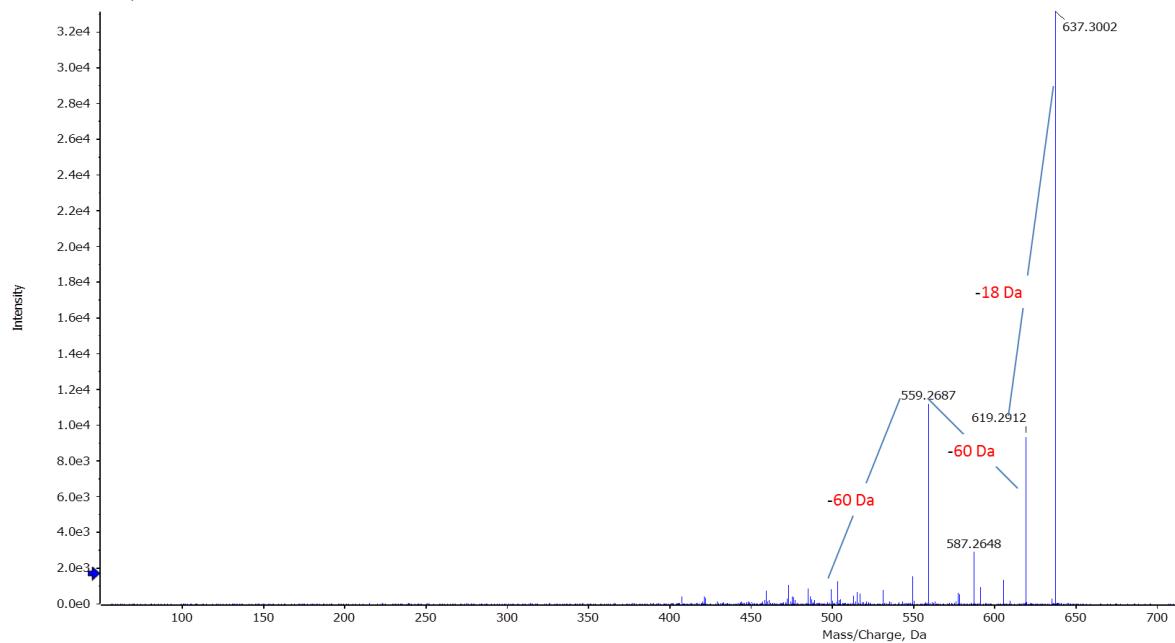


Figure S15. MS/MS for peak 114: Premyrsinol/peditithin derivatives.

Spectrum from 181128-SM0022.wiff (sample 1) - 181128-SM0022, Experiment 6, +TOF MS^2 (50 - 1000) from 21.962 min
Precursor: 665.3 Da, CE: 46.5

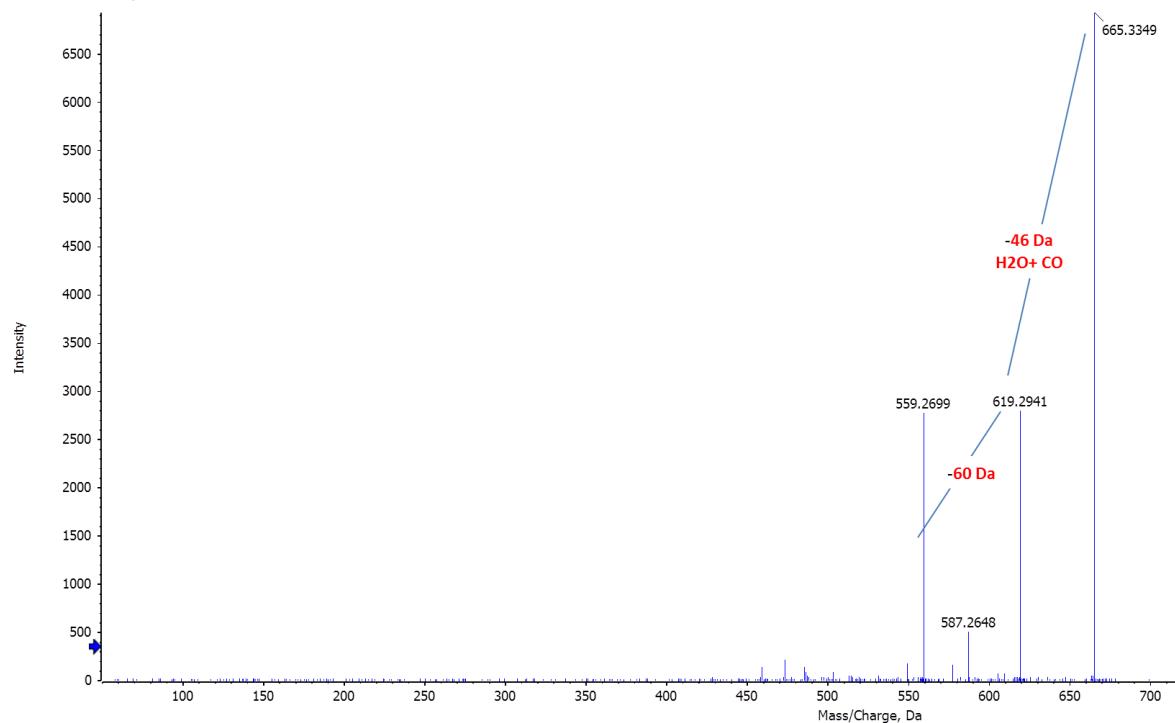


Figure S16. MS/MS of peak 125: Premyrsinol/peditithin derivative.

Spectrum from 181128-SM0022.wiff (sample 1) - 181128-SM0022, Experiment 4, +TOF MS² (50 - 1000) from 13.796 min
Precursor: 557.3 Da, CE: 35.0

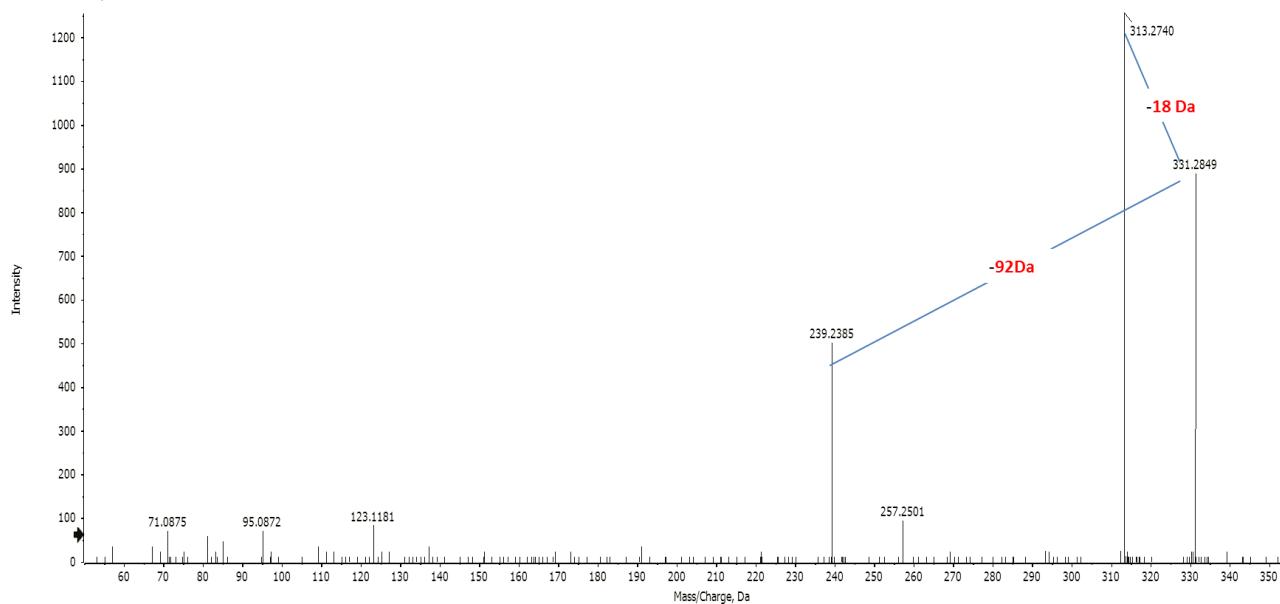


Figure S17. MS/MS of peak 82: Monopalmitin.

Spectrum from 181128-SM0022.wiff (sample 1) - 181128-SM0022, Experiment 15, +TOF MS² (50 - 1000) from 14.082 min
Precursor: 467.3 Da, CE: 35.0

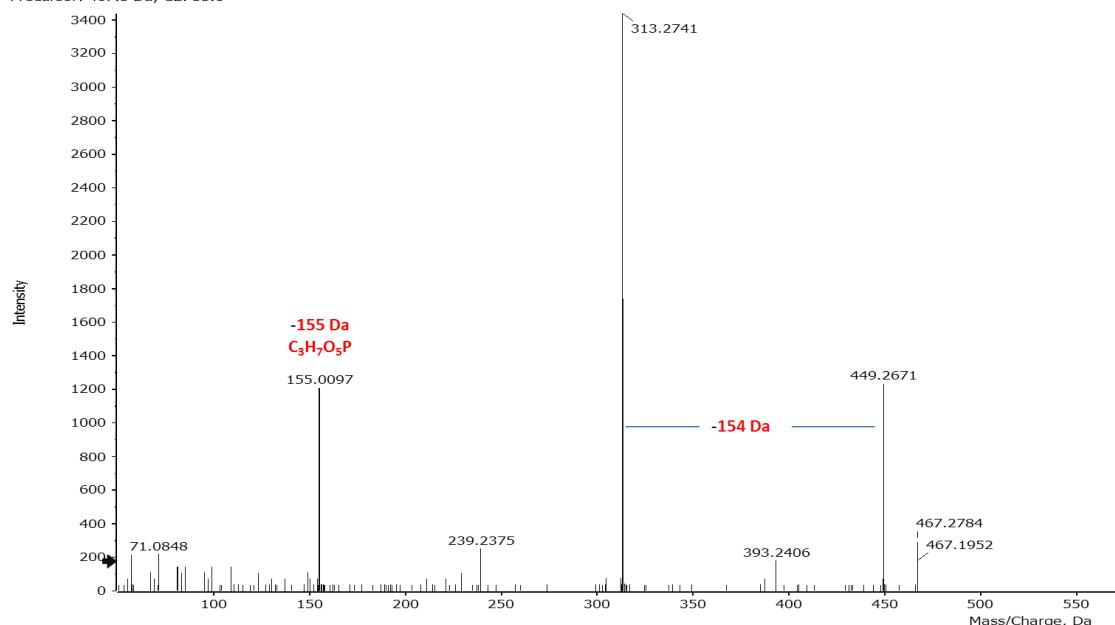


Figure S18. MS/MS of peak 84: Phosphatidic acid (10:0/9:0).

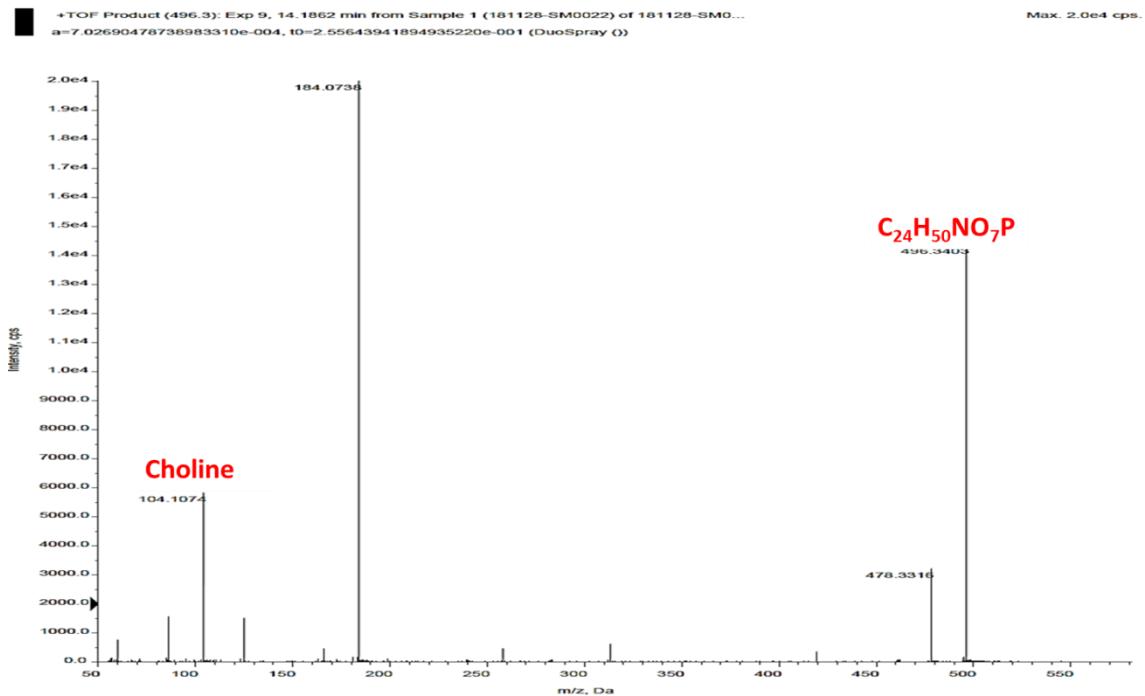


Figure S19. MS/MS of peak 86: Lysophosphatidylcholine (16:0/0:0).

Table S1. Analysis of high resolution MS/MS Q-TOF fragments for newly identified cyclic peptides.

Peak No.	<i>m/z</i>	Calculated formula	MS data <i>m/z</i> calculated formula	Neutral loss	Corresponding amino acid
43/45	722.4774	$C_{36}H_{64}N_7O_8$	623.4151 $C_{31}H_{55}N_6O_7$	-99 Da	Val
			510.3274 $C_{25}H_{44}N_5O_6$	-113 Da	Leu/Ile
			397.2439 $C_{19}H_{33}N_4O_5$	-113 Da	Leu/Ile
			298.1762 $C_{14}H_{24}N_3O_4$	-99 Da	Val
			211.1440 $C_{11}H_{19}N_2O_2$	-87 Da	Ser
46	809.5482	$C_{40}H_{73}N_8O_9$	722.4796 $C_{36}H_{64}N_7O_8$	-87 Da	ABA
			623.4109 $C_{31}H_{55}N_6O_7$	-99 Da	Val
			510.3336 $C_{25}H_{44}N_5O_6$	-113 Da	Leu/Ile
			397.2439 $C_{19}H_{33}N_4O_5$	-113 Da	Leu/Ile
			298.1762 $C_{14}H_{24}N_3O_4$	-99 Da	Val
47	767.5383	$C_{38}H_{71}N_8O_8$	211.1436 $C_{11}H_{19}N_2O_2$	-87 Da	Ser
			623.4102 $C_{31}H_{55}N_6O_7$	-144 Da	MeLys
			510.3286 $C_{25}H_{44}N_5O_6$	-113 Da	Leu/Ile
			397.2445 $C_{19}H_{33}N_4O_5$	-113 Da	Leu/Ile
			298.1805 $C_{14}H_{24}N_3O_4$	-99 Da	Val
55	668.4340	$C_{32}H_{58}N_7O_8$	211.1434 $C_{11}H_{19}N_2O_2$	-87 Da	Ser
			555.3528 $C_{26}H_{47}N_6O_7$	-113 Da	Leu/Ile
			442.2628 $C_{20}H_{36}N_5O_6$	-113 Da	Leu/Ile
			385.2413 $C_{18}H_{33}N_4O_5$	-57 Da	Gly
			284.1949 $C_{14}H_{24}N_3O_4$	-101 Da	Thr
			171.1119 $C_8H_{15}N_2O_2$	-113 Da	Lec/Ile
			86.0964 $C_5H_{12}N$	-85 Da	Ala

ABA : amino butyric acid, Ala : alanine, Gly : glycine, Ile : isoleucine, Leu: leucine, Lys : lysine, Ser : serine, Thr : threonine, Val : valine. Isoleucine and Leucine cannot be differentiated based on their high resolution mass.