

FIGURE 1

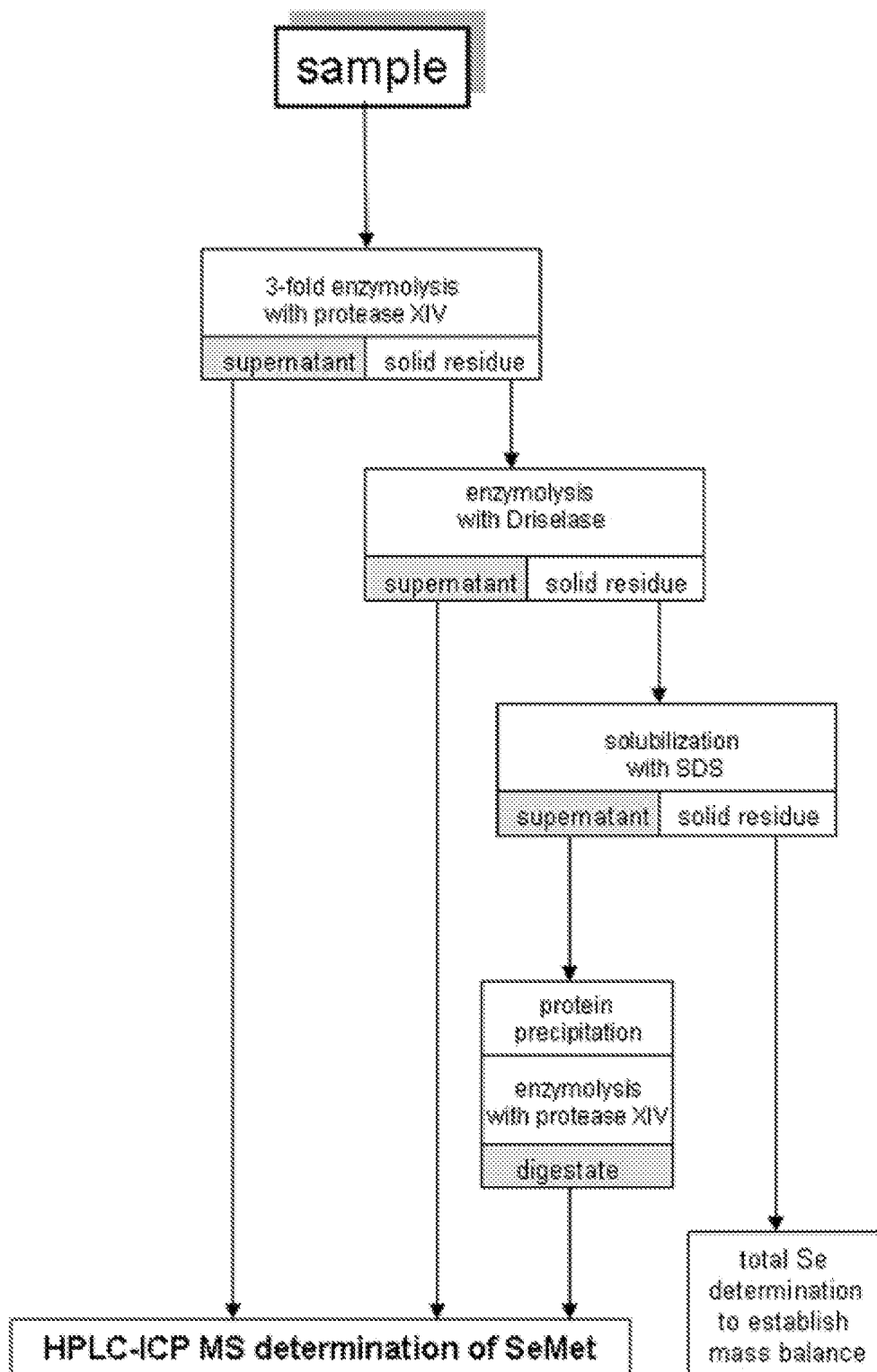


FIGURE 2

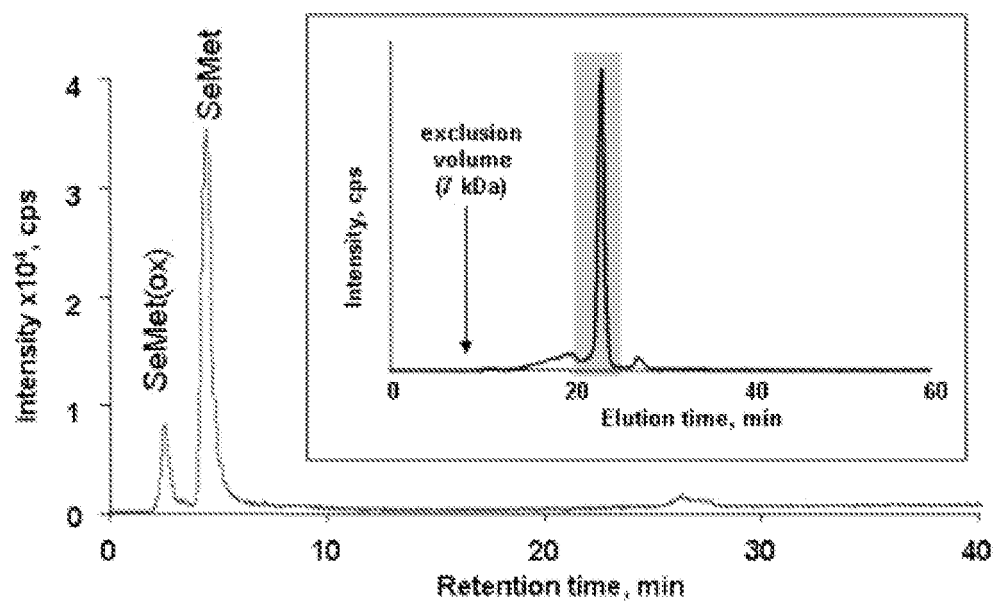


FIGURE 3

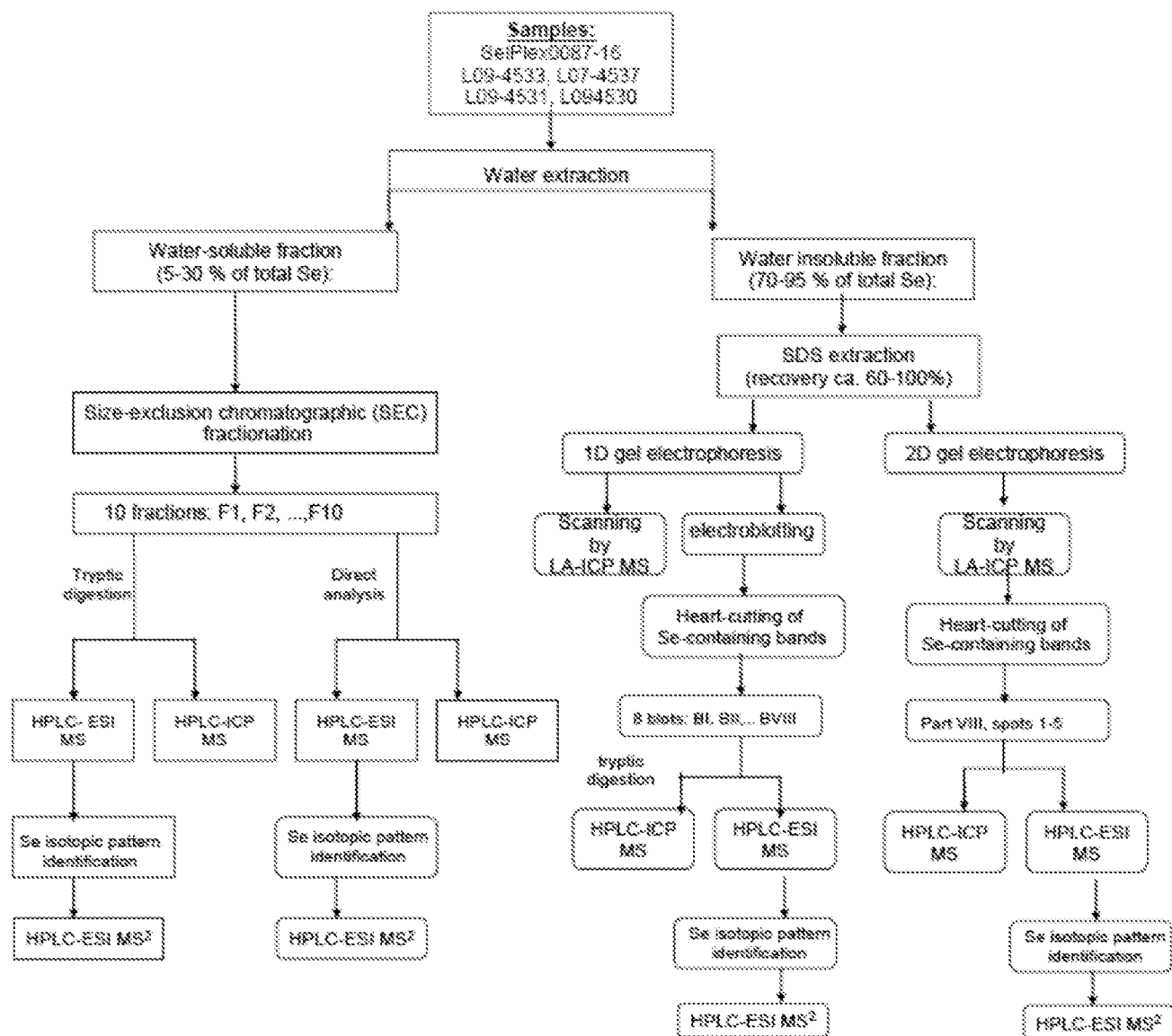


FIGURE 4

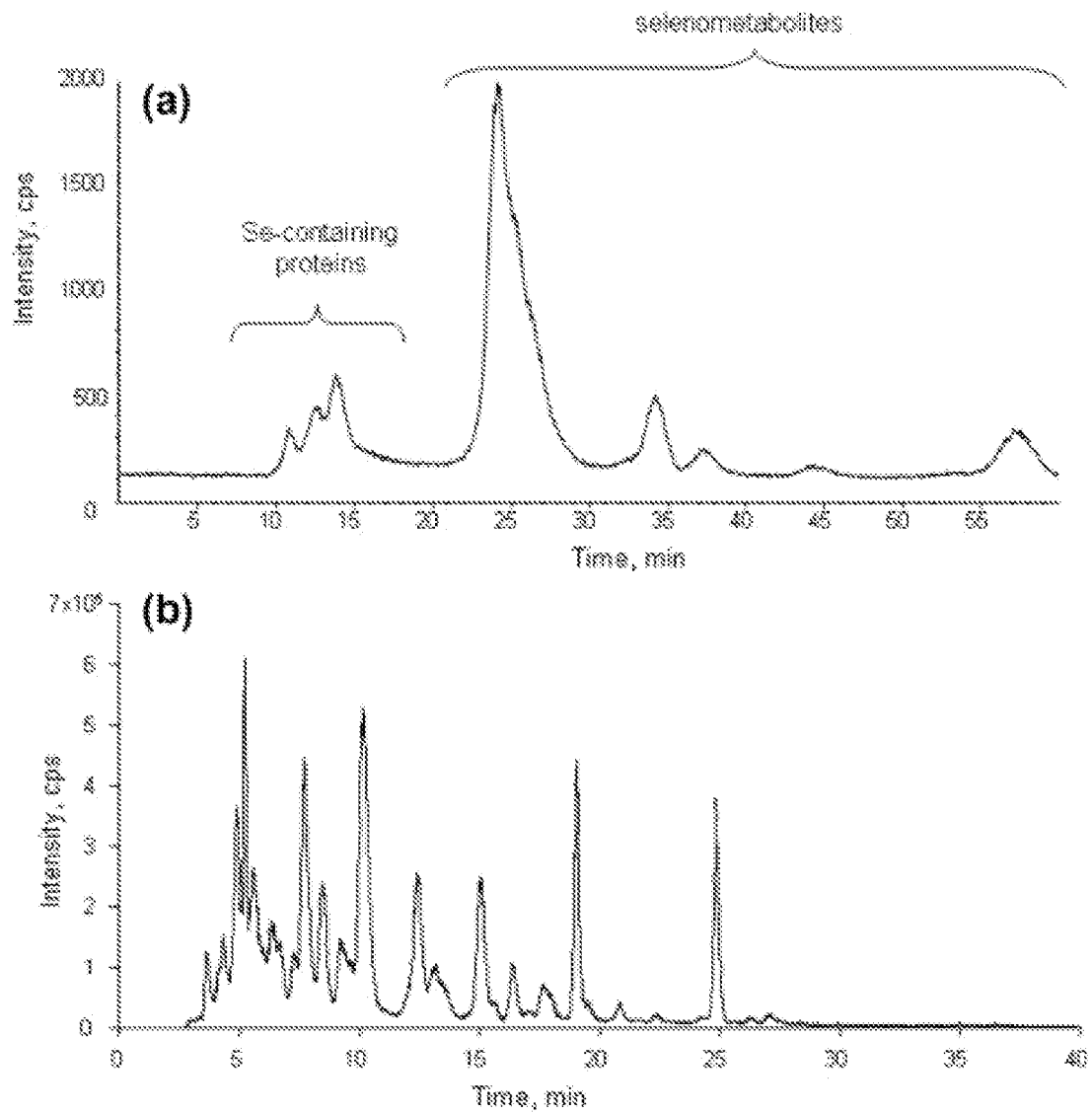


FIGURE 5

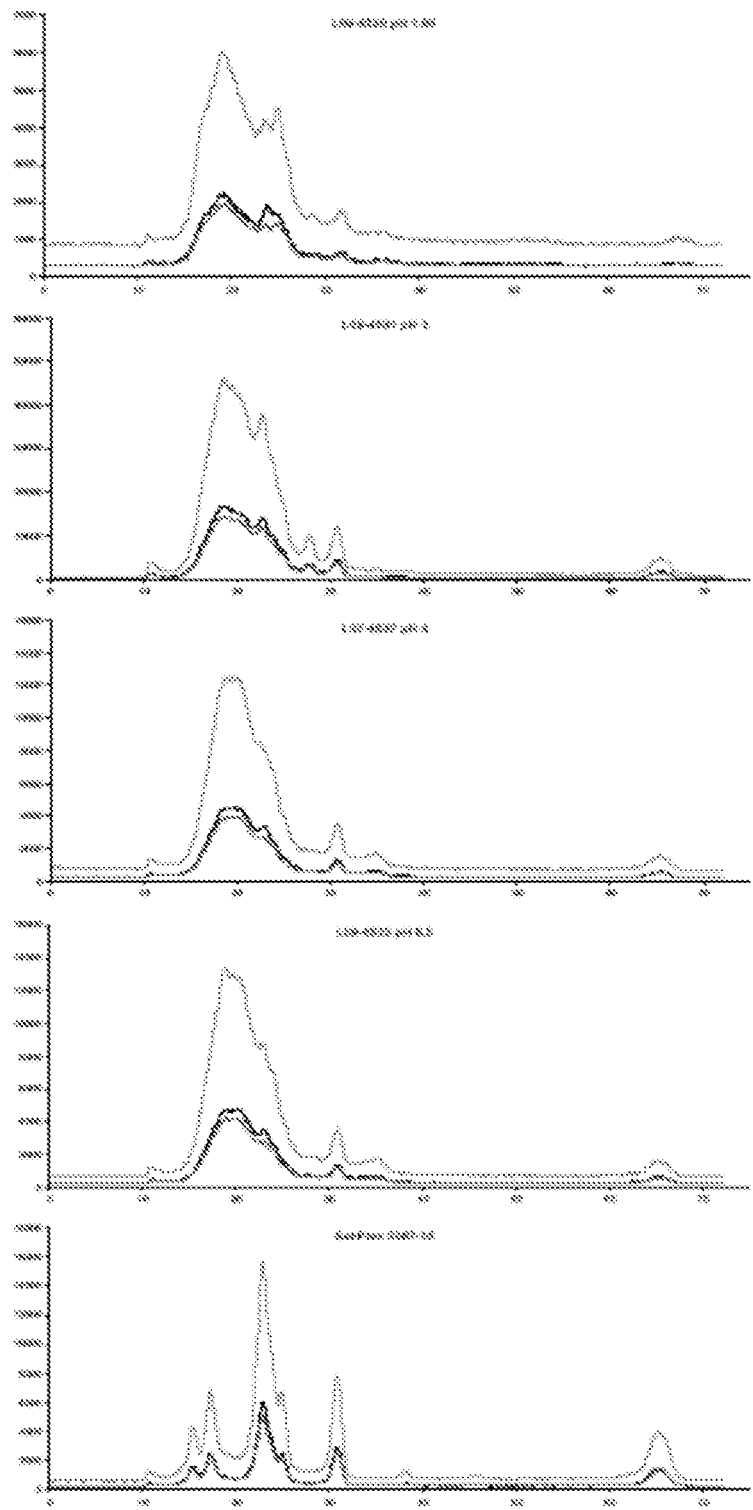
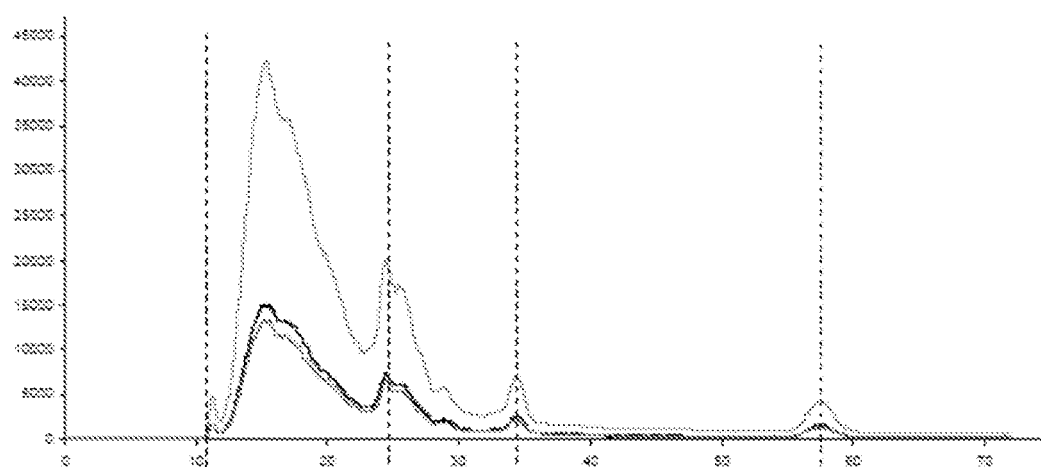


FIGURE 6

A



B

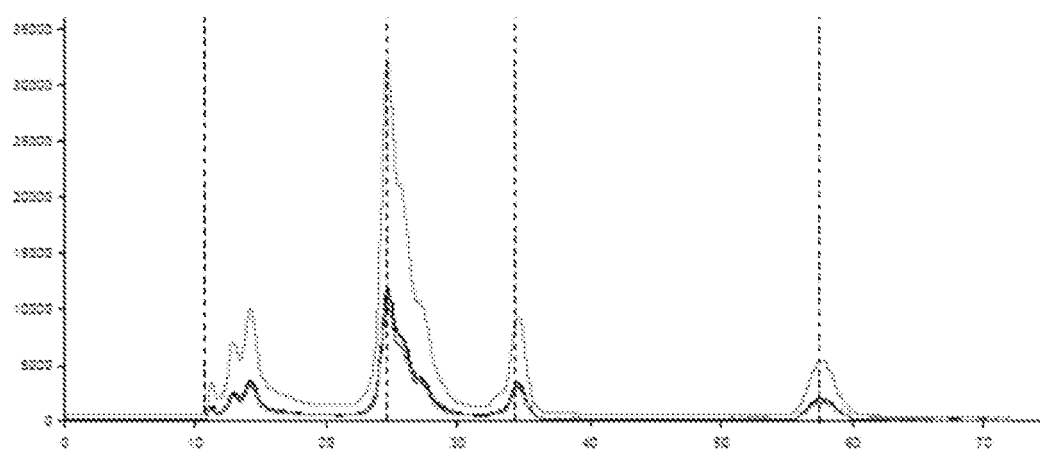


FIGURE 7

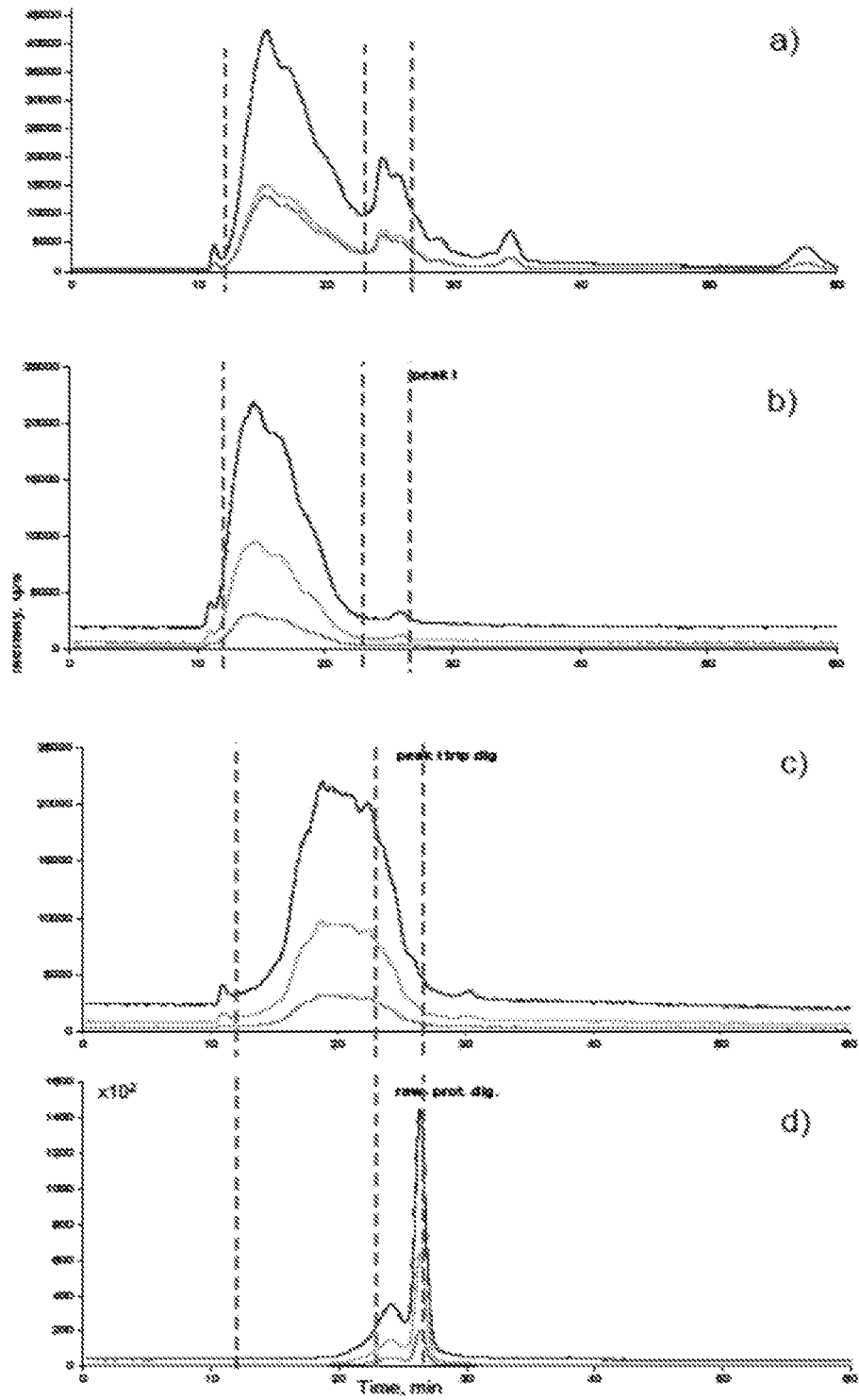


FIGURE 8

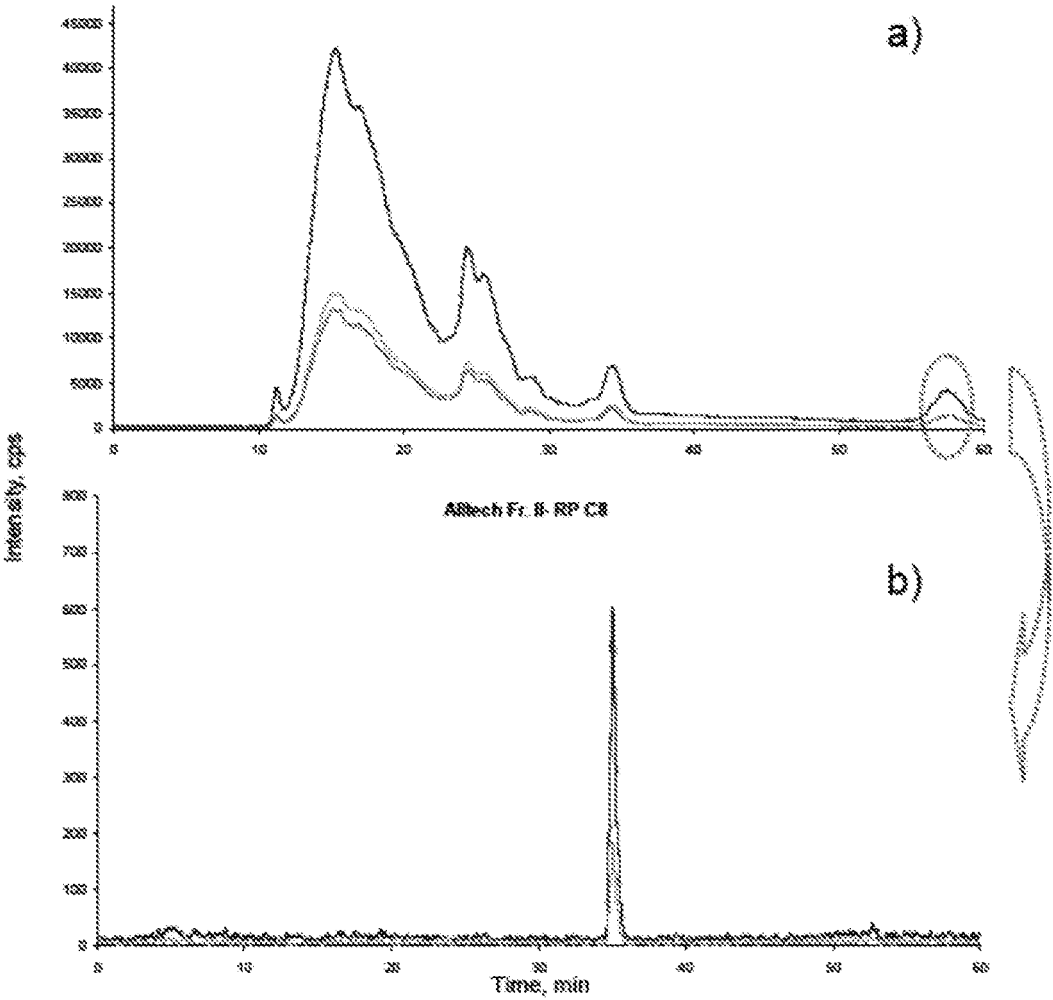


FIGURE 9

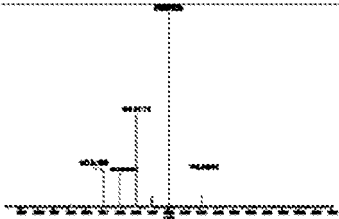
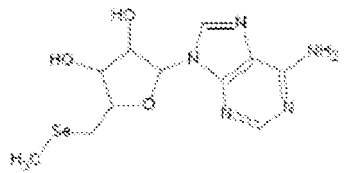
Experimental mass	Theoretical mass	Formula	Name	MS spectrum	Structure
346.04025	346.04129	C ₁₄ H ₁₅ N ₅ O ₇ Se	Se-methyl-Se-adenosine		

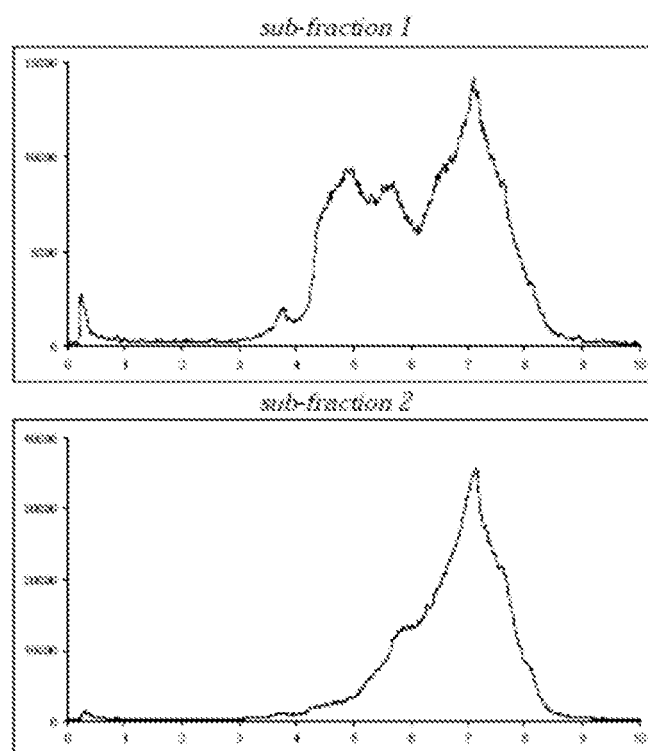
FIGURE 10

Figure 10 continued

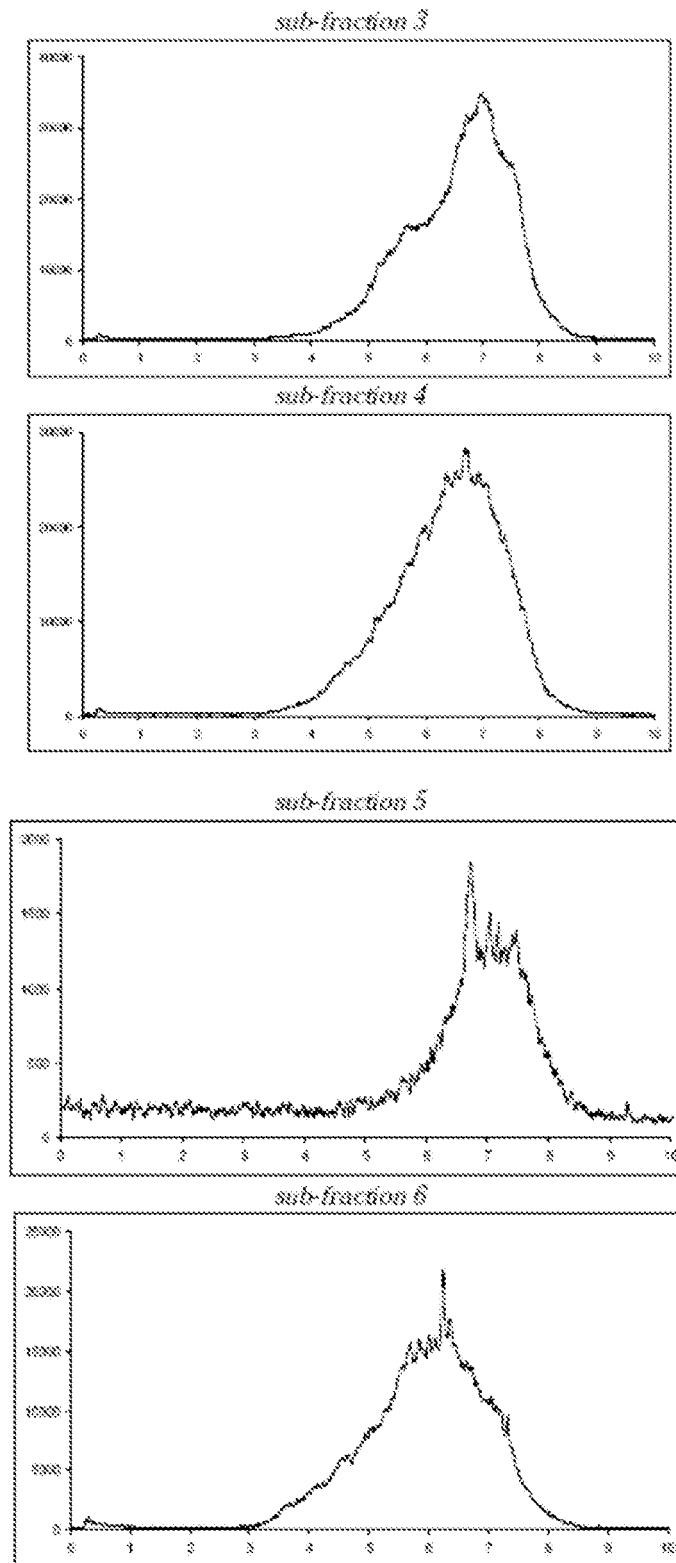


FIGURE 10 CONTINUED

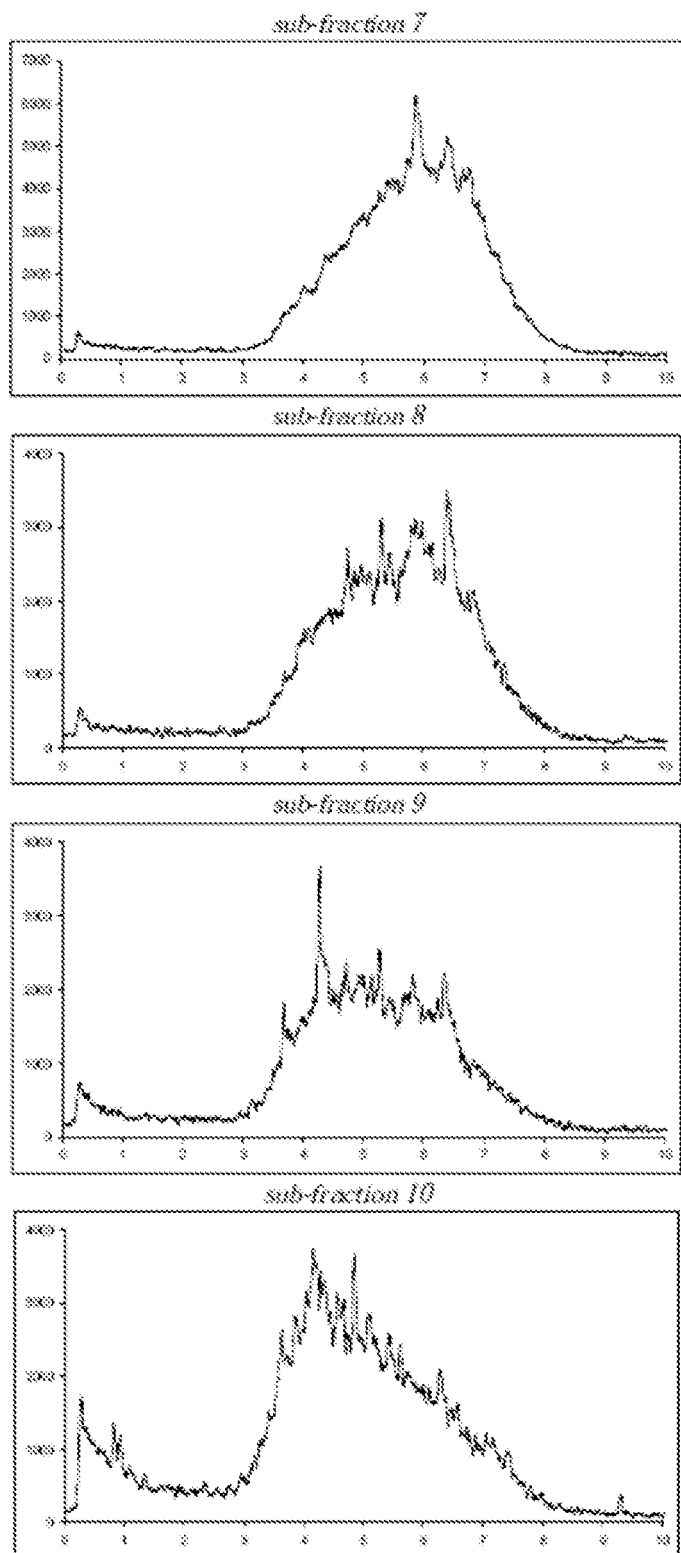


FIGURE 11 CONTINUED

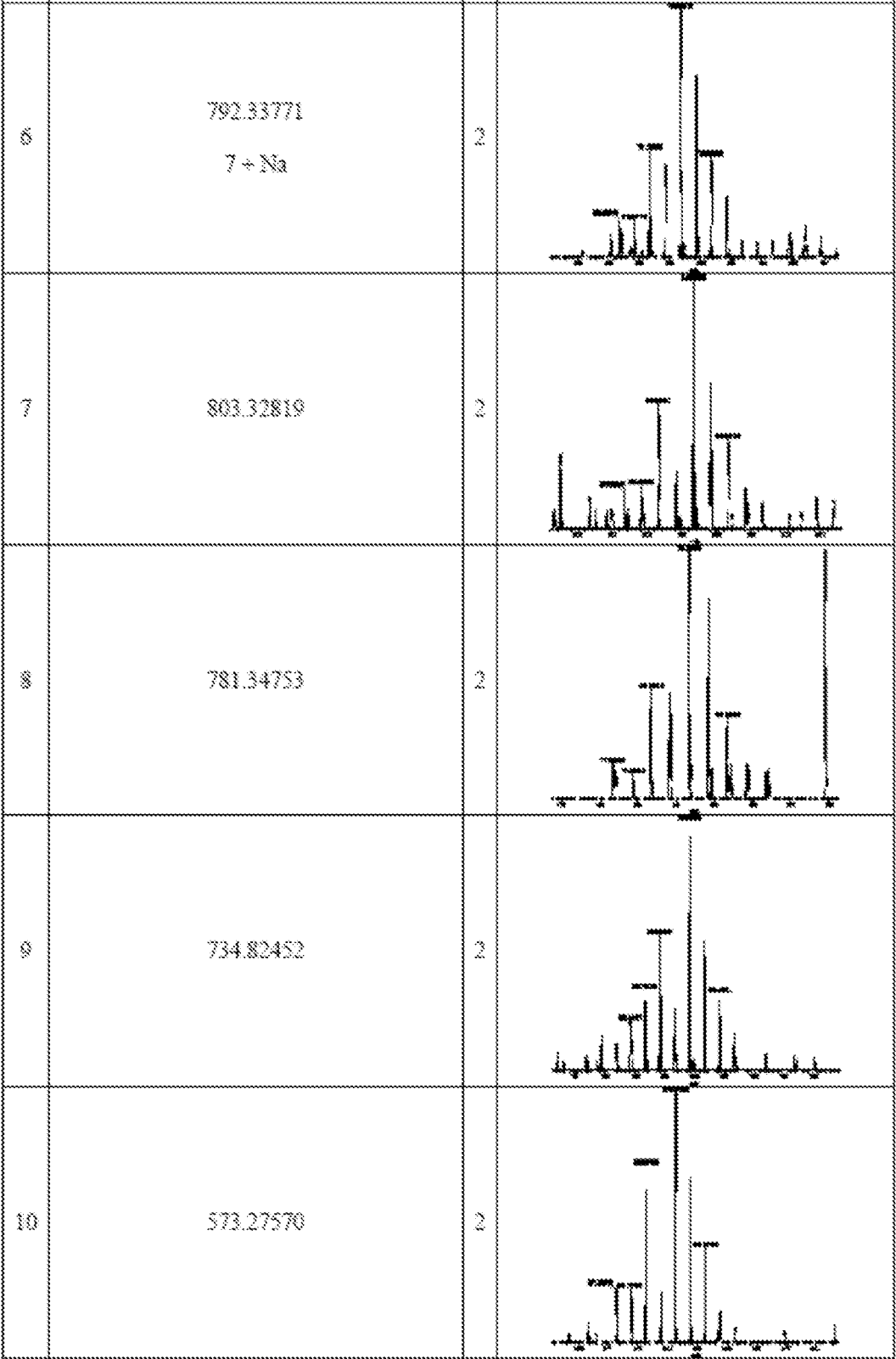


FIGURE 11 CONTINUED

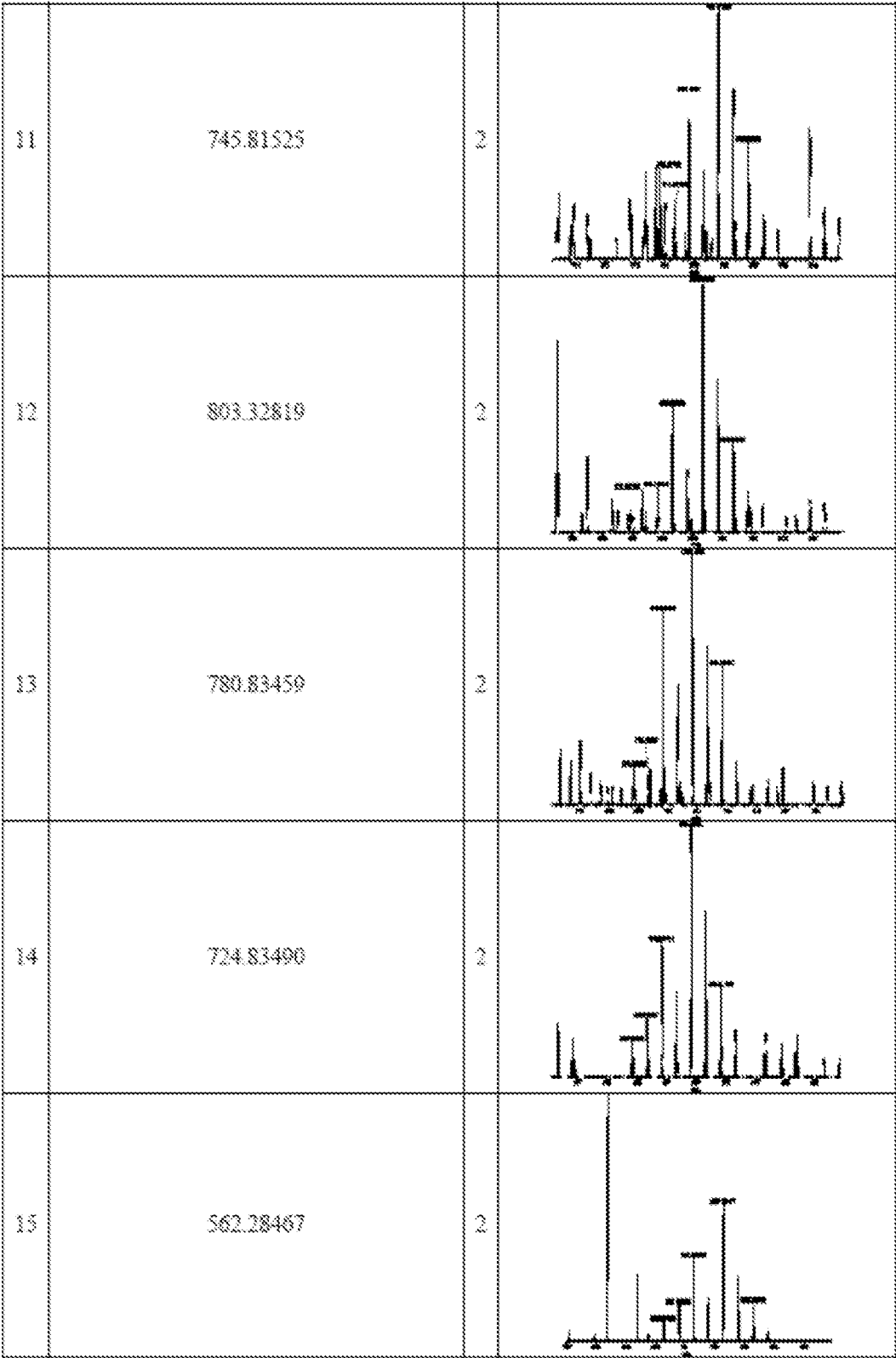


FIGURE 11 CONTINUED

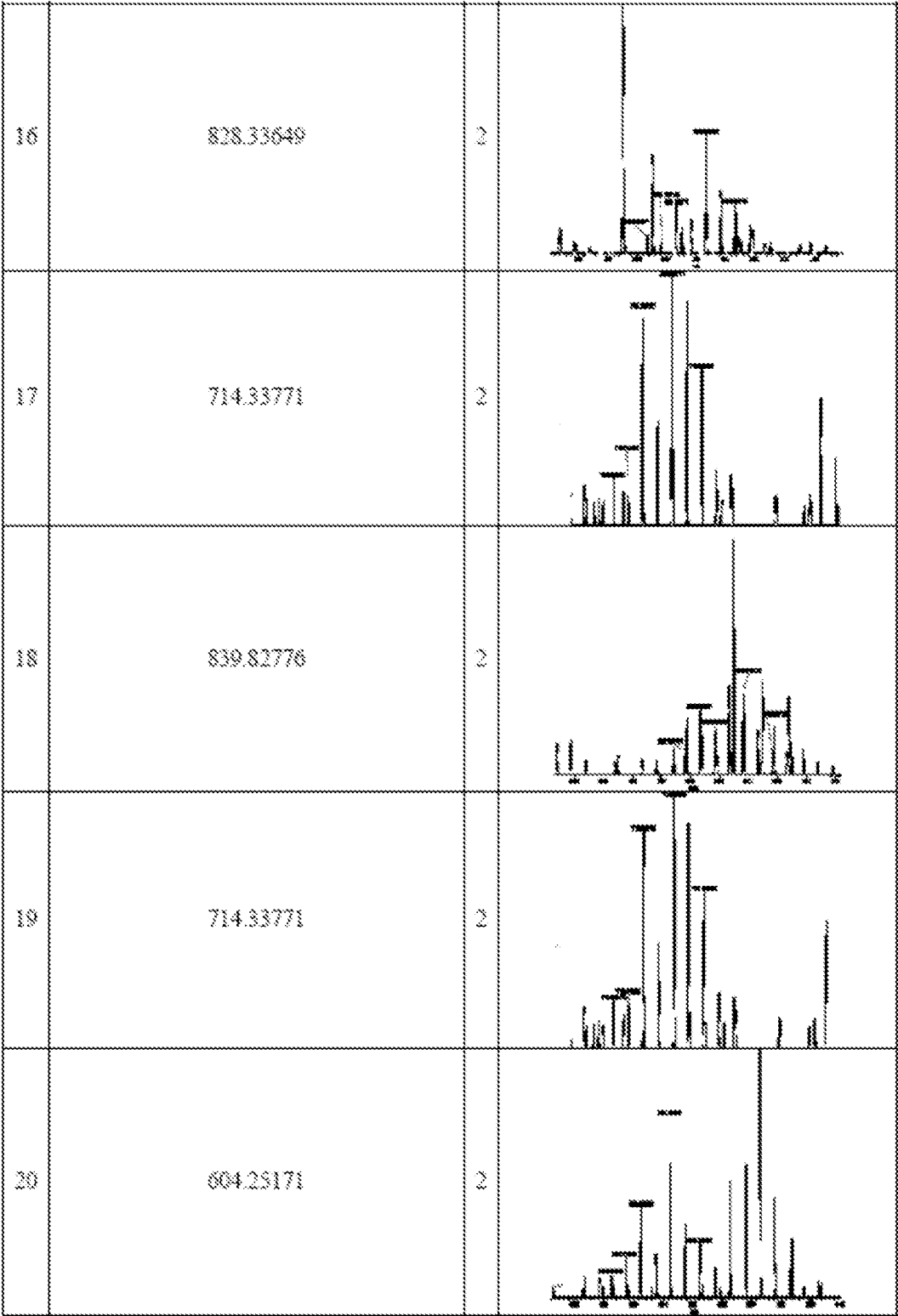


FIGURE 11 CONTINUED

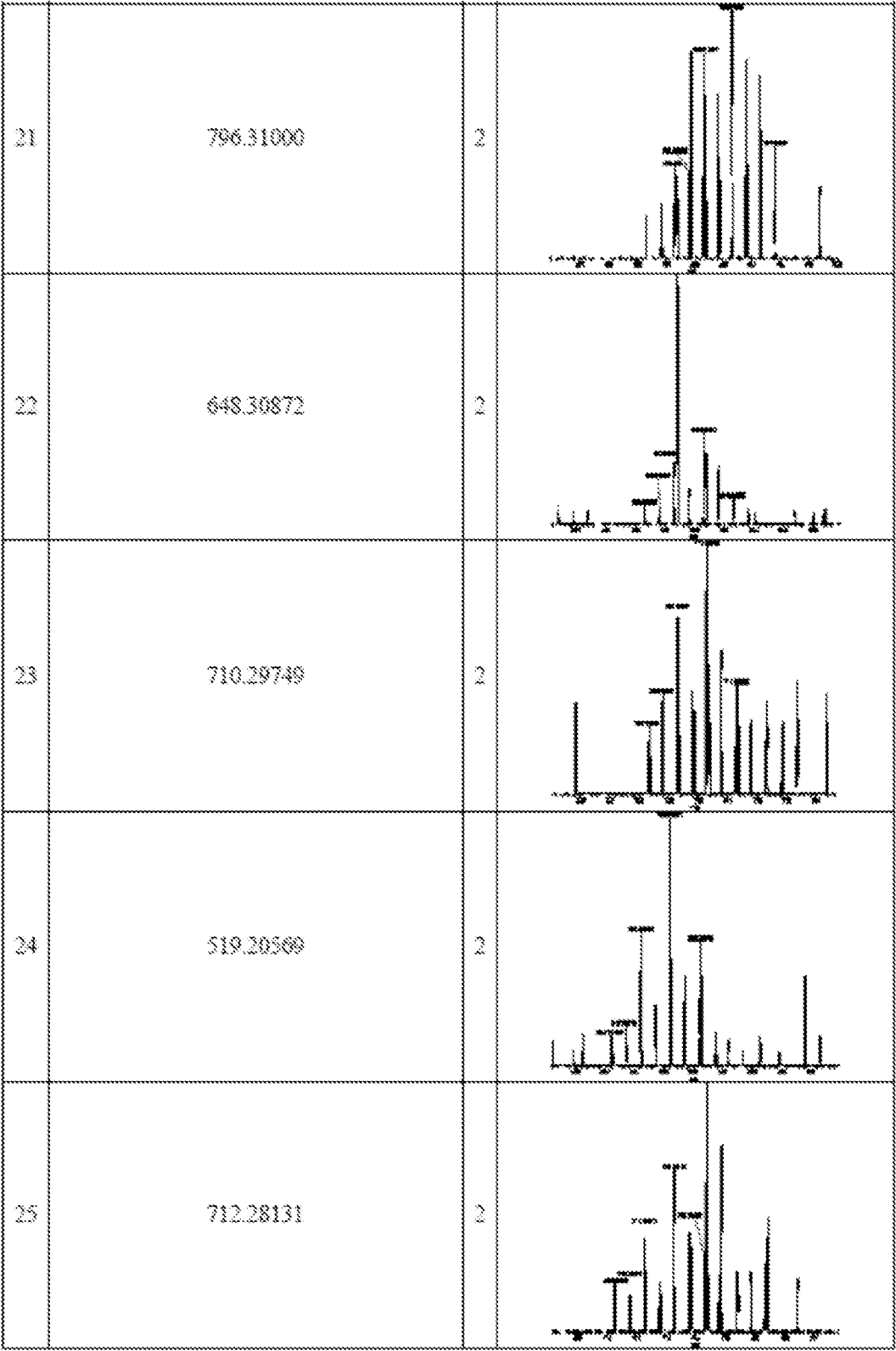


FIGURE 11 CONTINUED

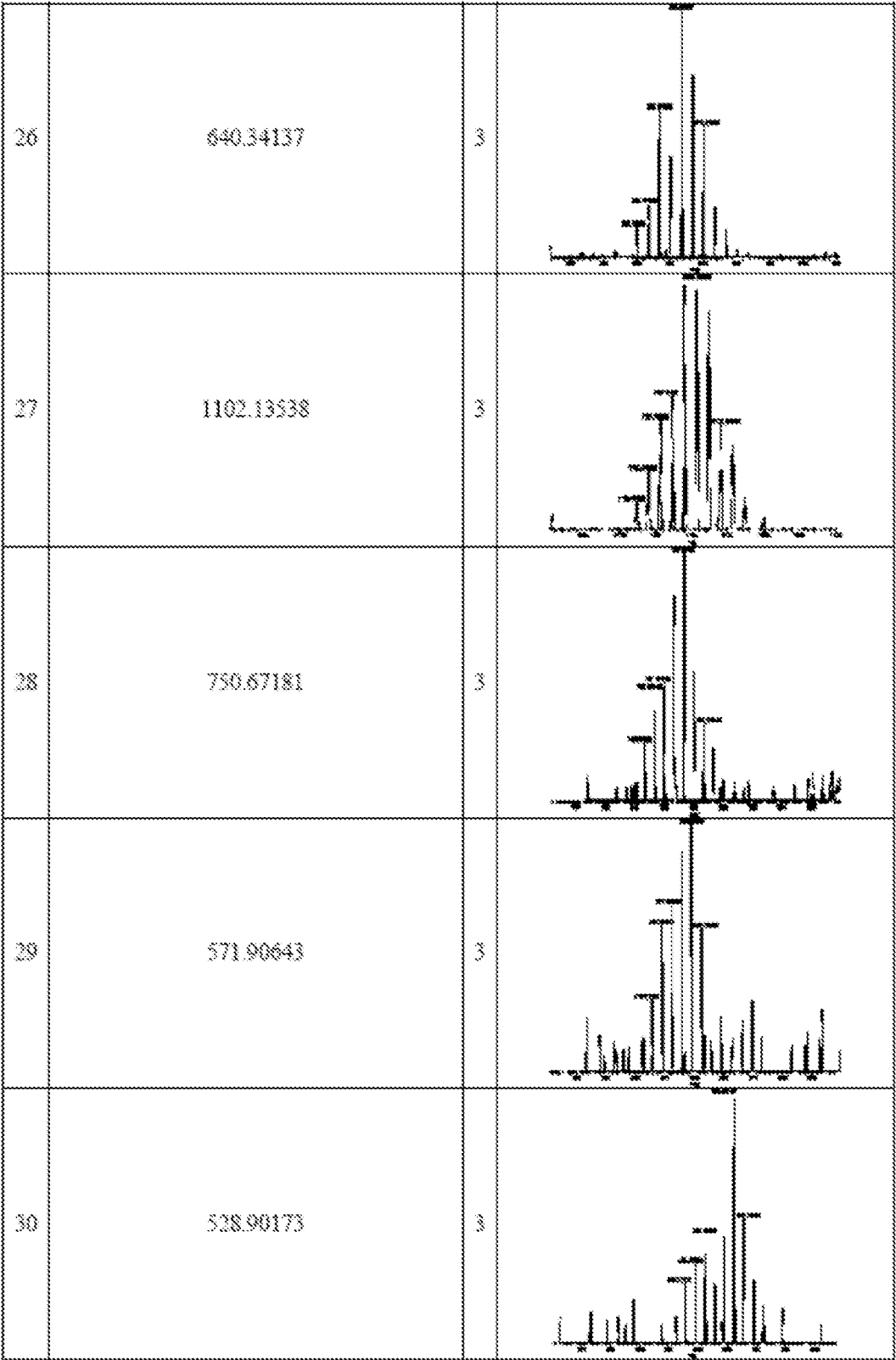


FIGURE 11 CONTINUED

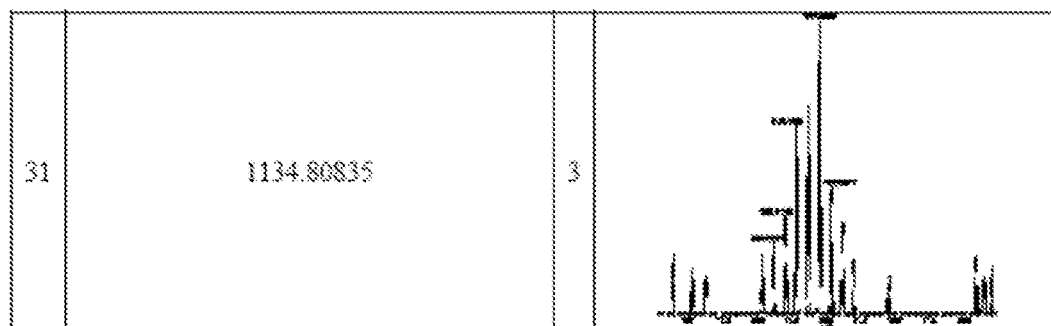


FIGURE 12

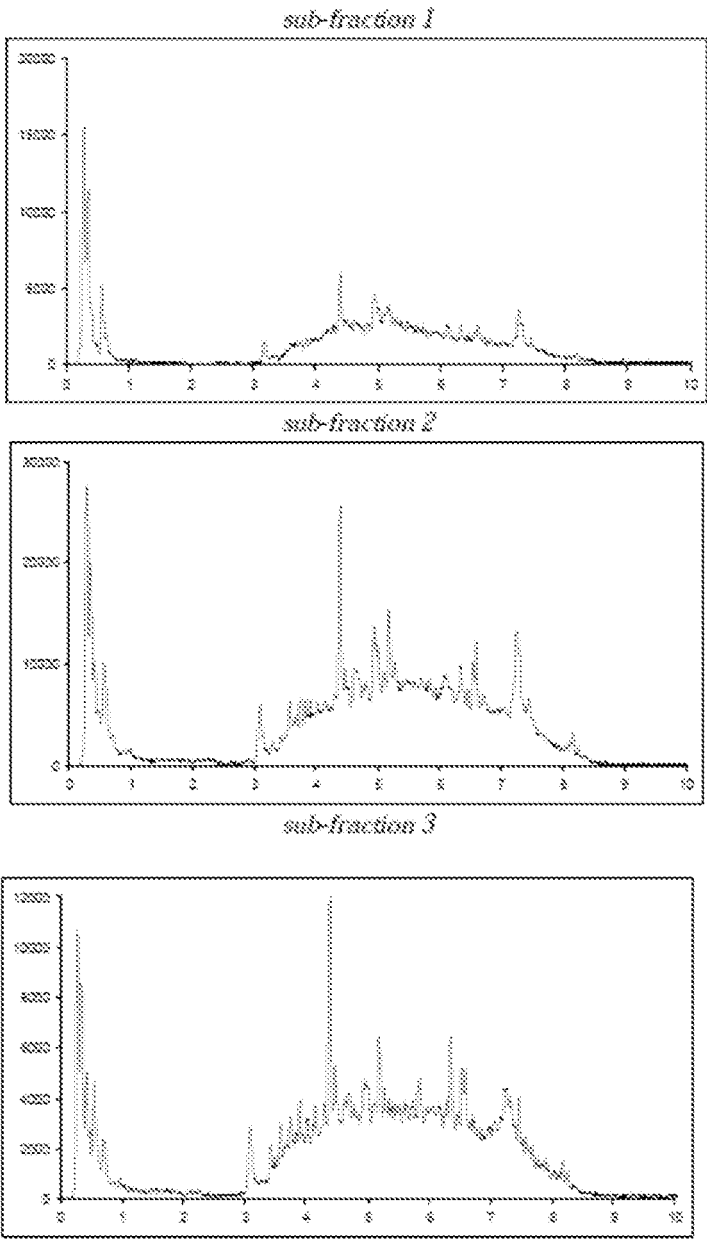


FIGURE 12 CONTINUED

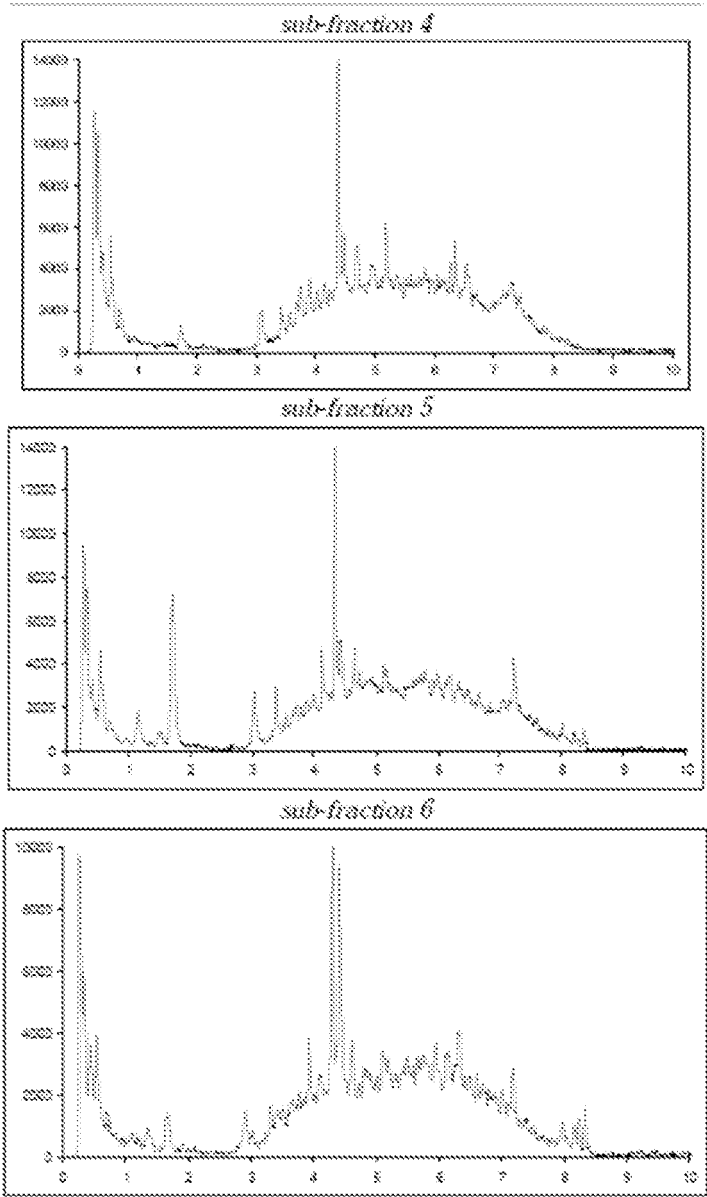


FIGURE 12 CONTINUED

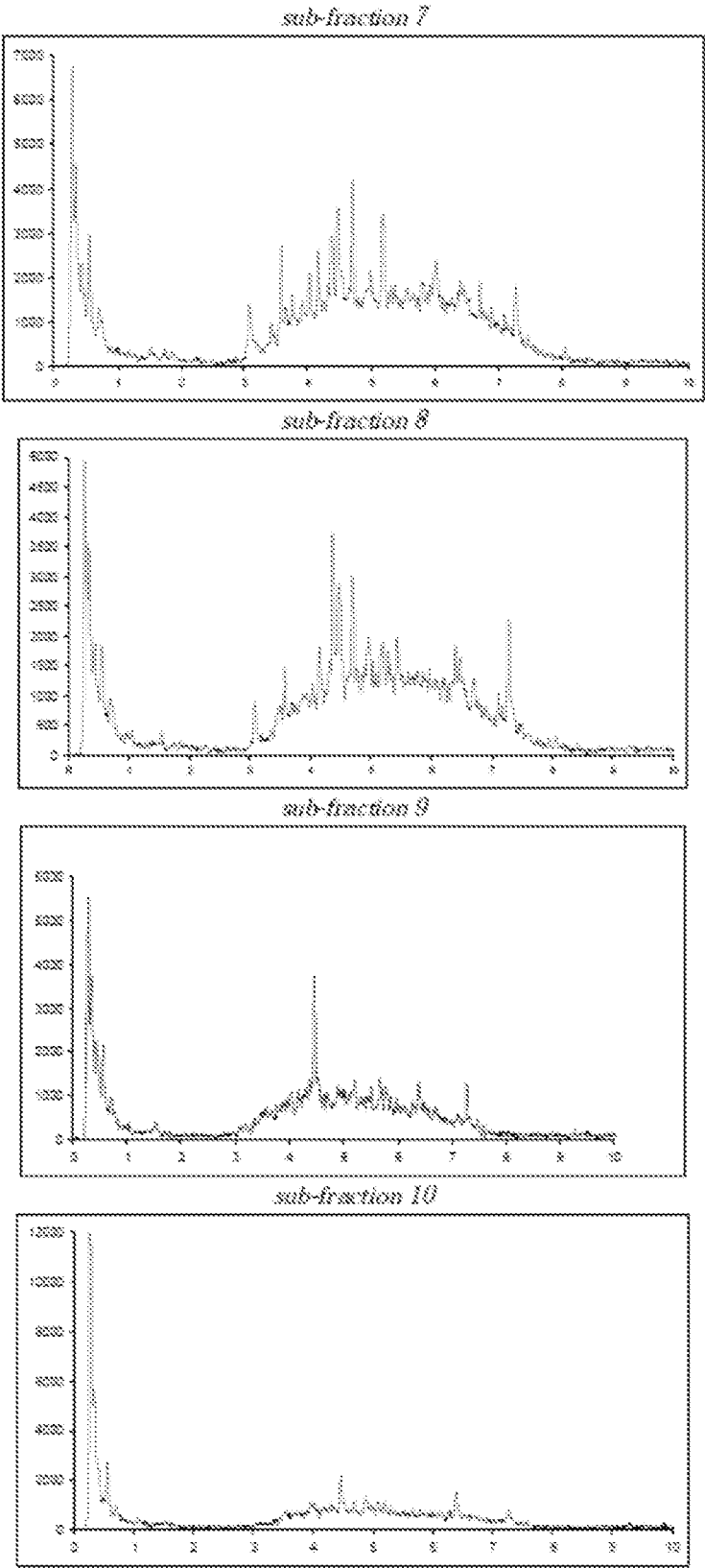


FIGURE 13

	MW (theoretical)	MW (experimental)	Peptide sequence	Z	Protein identification	Compound present in sub fraction:
1	825.32400	825.32611	MVAEAEK	1	HSP70 (heat shock protein 70)	T2, T3, T5, T6
2	803.28210	803.28448	DYMQAAK	1	HSP12 (heat shock protein 12)	T2, T3, T4, T5, T6
3	688.25520	688.25853	YMGAAK	1	HSP12	T5, T6
4	703.82559	703.82629	ELQDIANPMSK	2	HSP70 Scap (Heat shock protein 70)	T2, T5,
5	1655.6931	1655.6972	NQAAMNPSNTVFDK	2	HSP70 Scap (Heat shock protein 70)	T6
6	799.8695	799.87097	NFTPEQISSMVLGK	2	HSP SSA1 (heat shock protein SSA1)	T2, T3,
7	1598.7332	1598.7338	NFTPEQISSMVLGK	2	HSP SSA1 (heat shock protein SSA1)	T2, T3, T4
8	841.31890	841.32074	MVSEAEK	1	HSP SSA2 (heat shock protein SSA2)	T2, T3,
9	951.36690	951.36835	PEVQGDMK	1	SSA1 or SSA2	T2, T3
10	1408.6433	1408.6450	ELQDIANPMSK		Scap	T2, T3
11	599.26350	599.26422	AMSSR	1	Scb2p	T3
12	770.04864	770.04810	VQGSVIGEDLSTINLAVADNEG K	3	Scap	T2
13	822.32430	822.32599	AAAEQPMK	1	TDH1 (glyceraldehyde-3- phosphate dehydrogenase 1)	T2, T3, T4, T5
14	843.36100	843.36316	LTGMAFR	1	TDH (Glyceraldehyde-3- phosphate dehydrogenase)	T2, T3, T4,
15	1552.6590	1552.6580	PFVSNDYAAVMK	2	TDH1 (glyceraldehyde-3- phosphate dehydrogenase 1)	T6

FIGURE 13 CONTINUED

16	1991.51880	1991.52062	AFGIEEGLMITTVHSLTA TQK	2	GPD3 (glyceraldehyde-3-phosphate dehydrogenase)	T5, T6
17	1628.6903	1628.6921	PFITNDYAAAYMEK	2	GPD3 (glyceraldehyde-3-phosphate dehydrogenase)	T6
18	1239.64200	1239.64514	PGMVVTFAPAGVTTEV K	2	EF1a (translation elongation factor 1-alpha)	T2
19	2478.2761	2478.2824	VETGVIRQGVVTFAPAGVTTE VK	2	EF1a (translation elongation factor 1-alpha)	T2, T3
20	883.37710	883.37915	AAATAAMTK	1	elongation factor 3A	T5
21	944.93745	944.93878	SIVPSGASTGVHEALEM R	2	Enolp (enolase 1)	T2, T3
22	569.1990	569.1997	WMGK	1	Enolp (enolase 1)	T3, T6
23	1888.8670	1888.8690	SIVPSGASTGVHEALEM R	2	Enolp (enolase 1)	T2, T3, T4, T6
24	622.24460	622.24628	AMPQK	1	Yislp	T2
25	539.20730	539.20911	AAMAK	1	Yislp	T2
26	502.70729	502.70691	HVGDMEIR*	2	Nop4p*	T2
27	748.34379	748.34375	VIEPTTSETAMK	2	60S RPL25 (ribosomal protein)	T2
28	956.43449	956.43091	VLQALEEIGIVEISPK- iodine	2	Rps19ap	T2
29	776.37185	776.37103	LPAASLGDMVMATVK	2	Rpl23ap	T2
30	896.41077	896.40948	AGMTTIVR	1	RPL3 (Ribosomal protein L3)	T5
31	896.4107	896.4087	AGMTTIVR	1	RPL3 (Ribosomal protein L3)	T2, T4
32	667.27390	667.27521	MLMPK	1	40S ribosomal protein S10-A	T5
33	555.20447	555.20270	TMGAK	1	Fba1p	T2, T3, T4, T5, T6
34	596.20380	596.20404	MNAGR	1	SIP18	T2, T4, T6
35	833.29270	833.29449	TYENMK	1	SIP18	T3
36	504.68551	504.68597	MGHDSQGTK	2	SIP18	T3
37	864.37357	864.37231	GEAIMAPK	1	Hrd3p	T2, T5
38	783.30790	783.30902	Ac-MNVFGK	1	Cnlp	T5
39	1039.4326	1039.43225	AMEVVASER	1	Lsp1p	T3
40		955.92926		2	to be identified	
41	566.25480	566.25519	IVMR	1	to be identified	
42	538.22390	538.22510	MA(TL)R	1	to be identified	T2, T3, T4
43	581.2564	581.2565	AMXAK	1	Bio2p	T3
44	1236.5378	1236.5374	DLETITMHTK	2	Rpl32p	T3

FIGURE 14

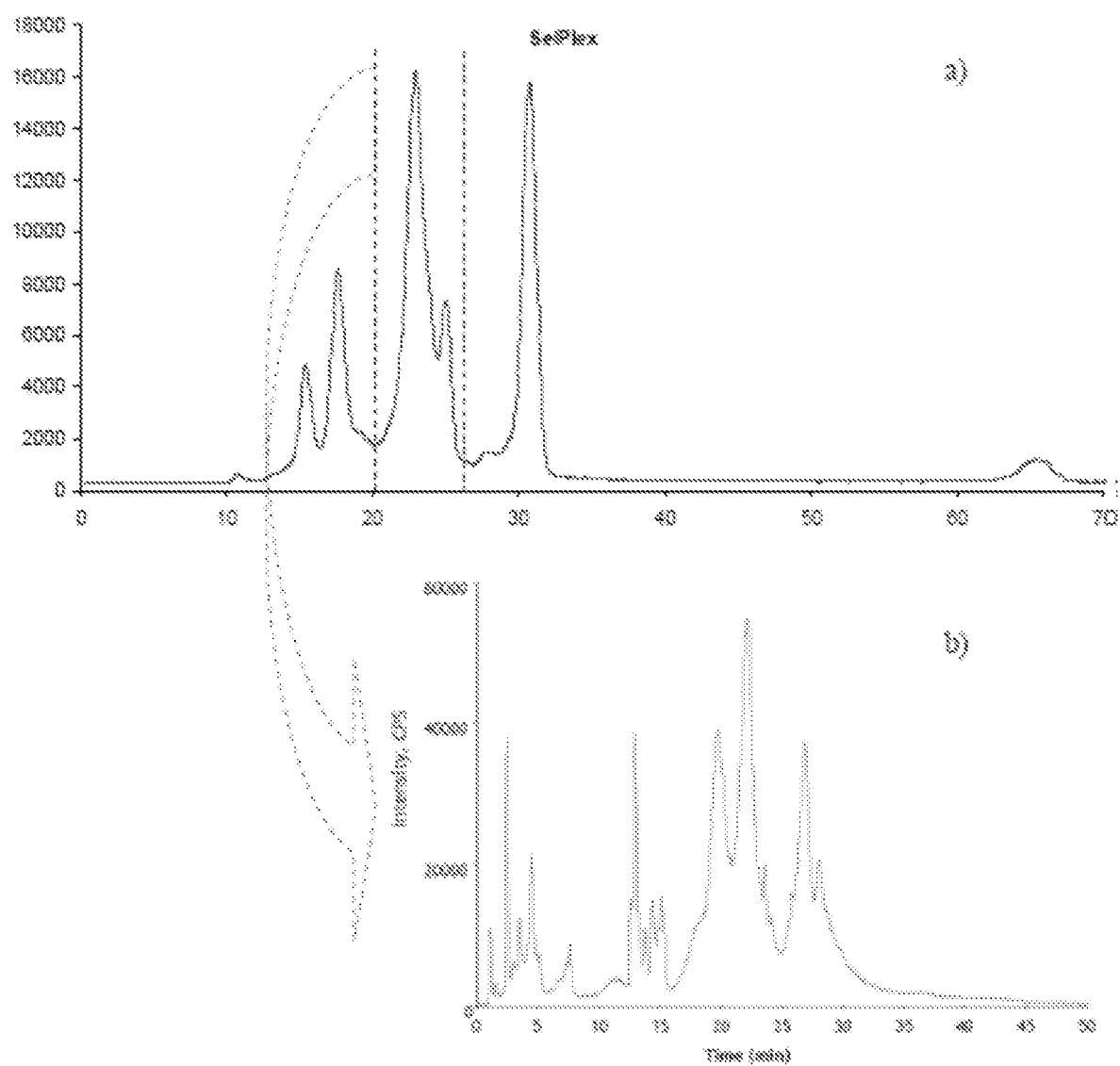


FIGURE 15

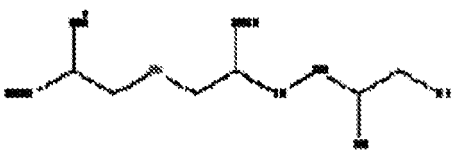
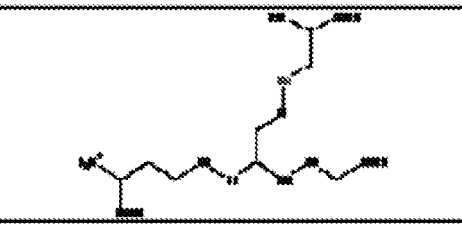
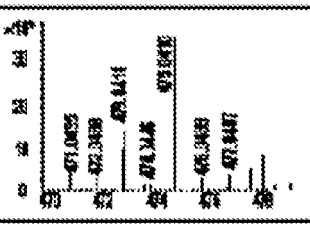
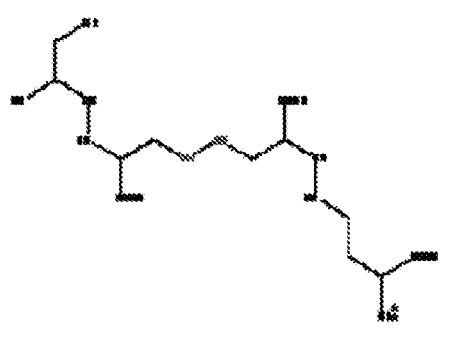
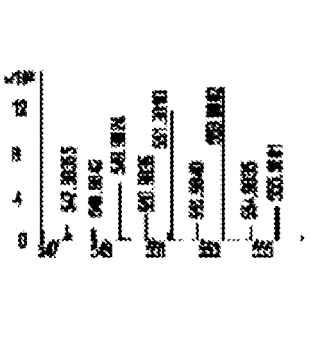
	Formula	Theoretical mass: [M+H] ⁺	Experimental mass: [M+H] ⁺	Structures	Isotopic pattern
	$C_{14}H_{27}N_3O_9S_2^{+}$	345.0196	345.0204		
	$C_{12}H_{23}N_4O_9SS_2^{+}$	475.0396	475.0410		
	$C_{14}H_{27}N_3O_{10}SS_2^{+}$	553.9787	553.9802		

FIGURE 15 CONTINUED

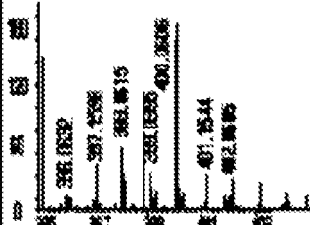
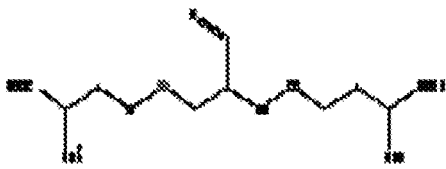
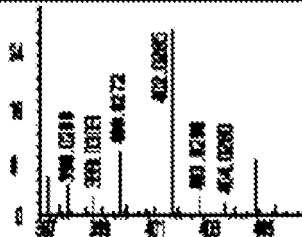
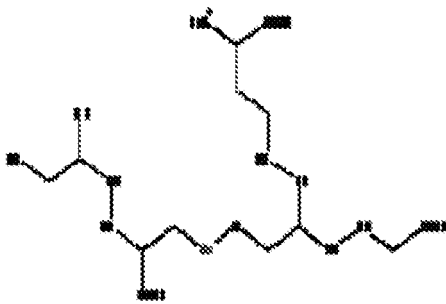
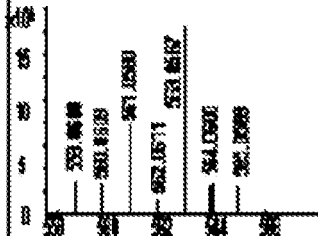
Formula	Theoretical mass: [M+H] ⁺	Experimental mass: [M+H] ⁺	Structures	Isotopic pattern
$C_{12}H_{22}N_6O_7S^{+}$	400.0618	400.0606		
$C_{11}H_{21}N_6O_5S^{+}$	402.0233	402.0255		
$C_{16}H_{27}N_6O_{11}SS^{+}$	563.0557	563.0567		

FIGURE 15 CONTINUED

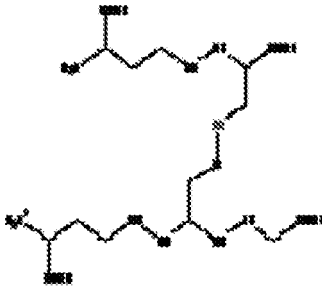
Formula	Theoretical mass: [M+H] ⁺	Experimental mass: [M+H] ⁺	Structures	Isotopic pattern
$C_{18}H_{30}N_6O_5S_2^{2+}$	604.0823	604.0842		

FIGURE 15 CONTINUED

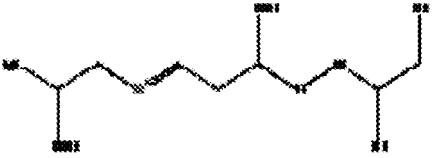
	Formula	Theoretical mass: [M+H] ⁺	Experimental mass: [M+H] ⁺	Structures	Isotopic pattern
	$C_{18}H_{17}N_2O_7S_2^{2-}$	357.0196	357.0218 (359-2H ⁺)		

FIGURE 15 CONTINUED

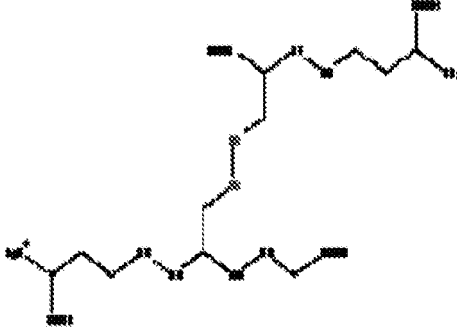
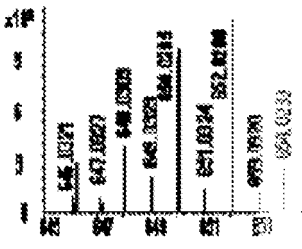
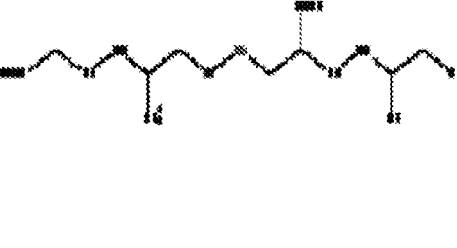
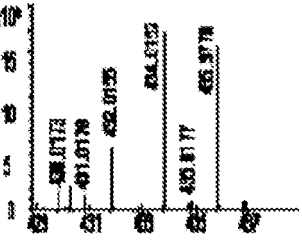
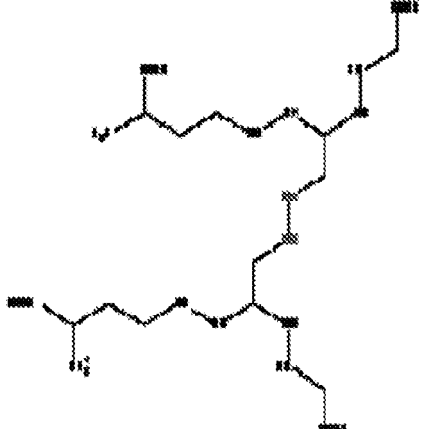
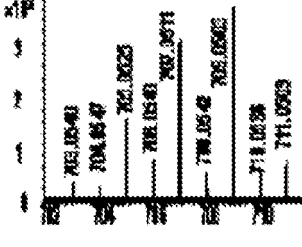
Formula	Theoretical mass: [M+H] ⁺	Experimental mass: [M+H] ⁺	Structures	Isotopic pattern
$C_{18}H_{30}N_4O_4S_2^{+}$	652.0271	652.0258		
$C_{11}H_{20}N_4O_5S_2^{+}$	434.0131	434.0152		
$C_{20}H_{30}N_4O_5S_2^{+}$	709.0486	709.0503		

FIGURE 15 CONTINUED

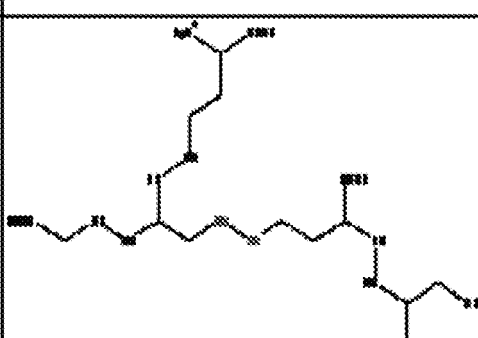
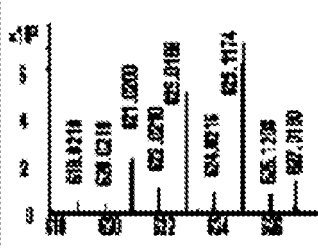
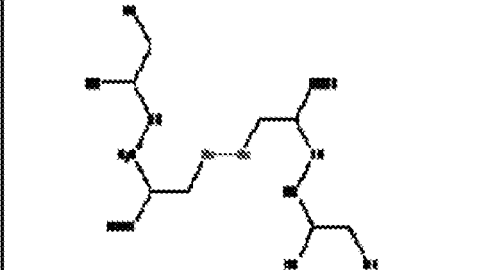
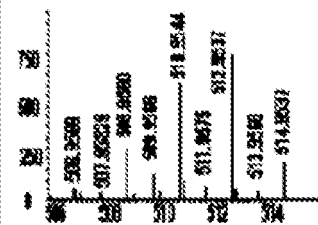
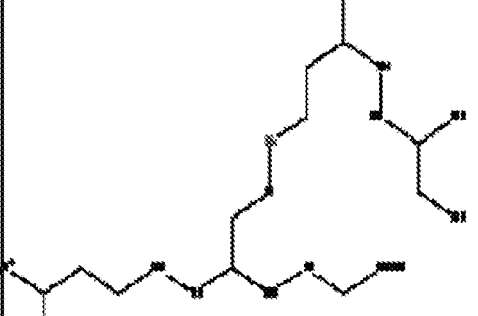
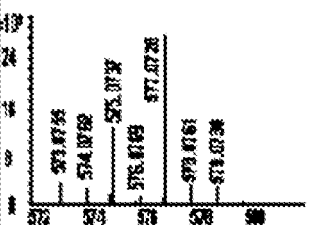
Formula	Theoretical mass: [M+H] ⁺	Experimental mass: [M+H] ⁺	Structures	Isotopic pattern
$C_{17}H_{29}N_4O_{11}Se_2^+$	625.0162	625.1174		
$C_{12}H_{21}N_4O_8Se_2^+$	512.9521	512.9537		
$C_{17}H_{29}N_4O_{11}Se^+$	577.0714	577.0728		

FIGURE 16

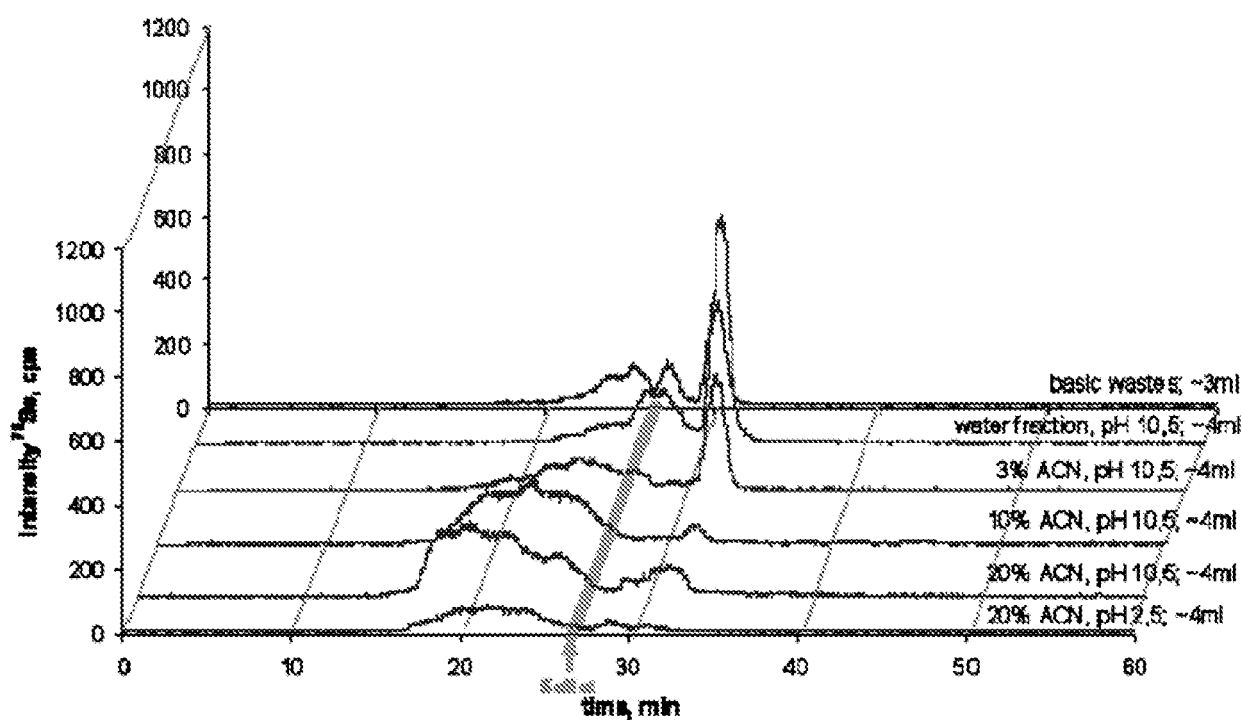
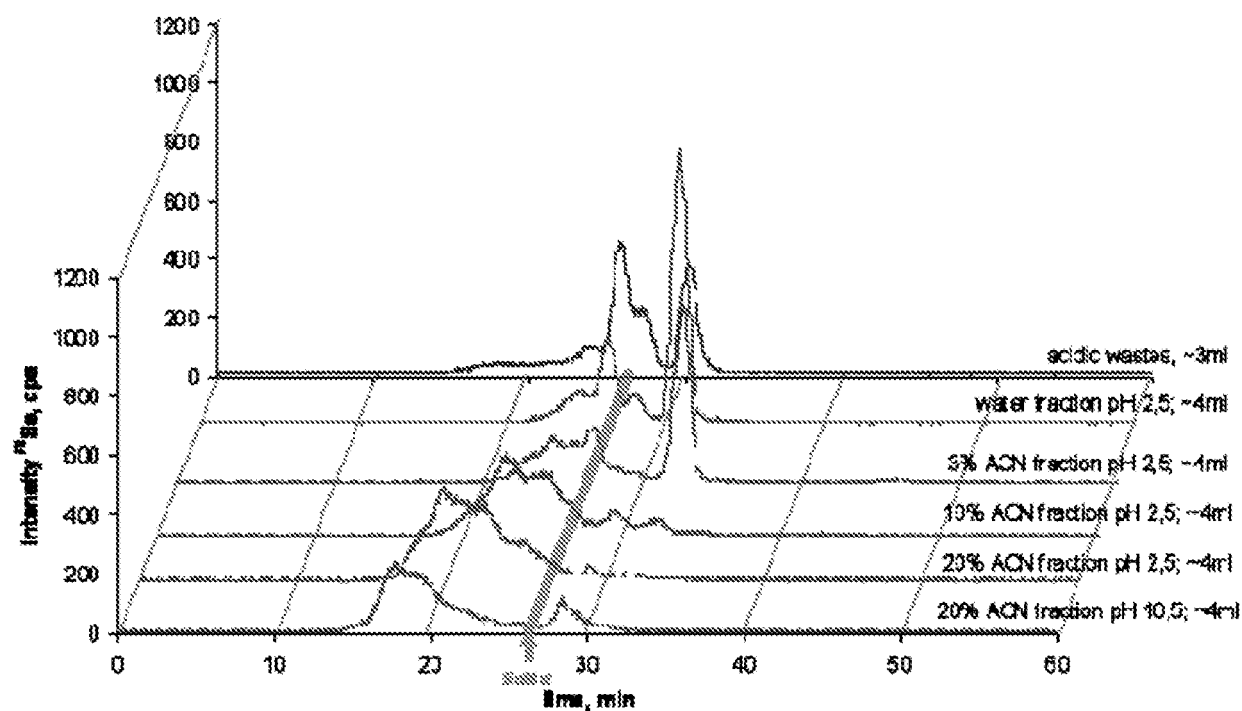


FIGURE 17

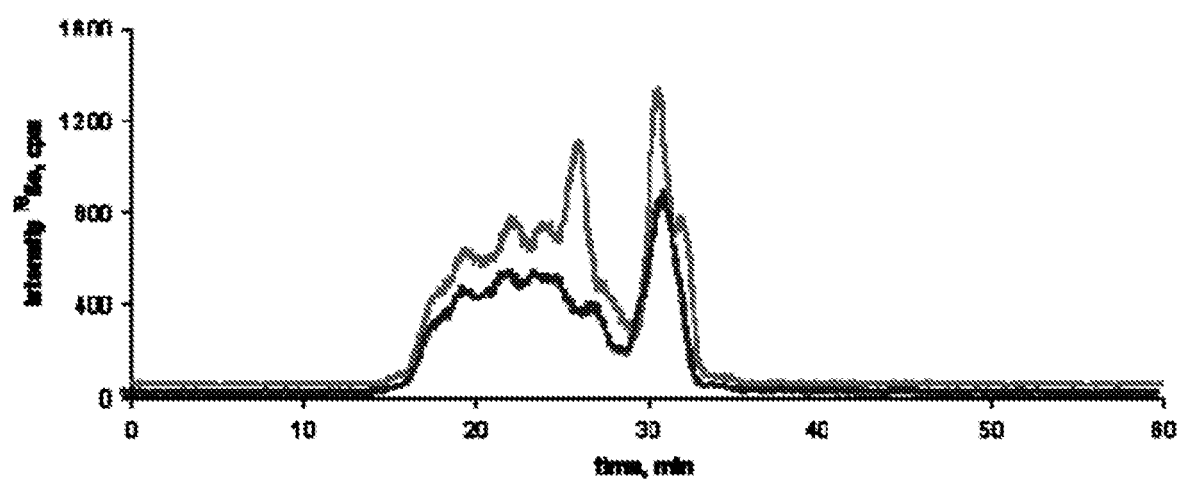
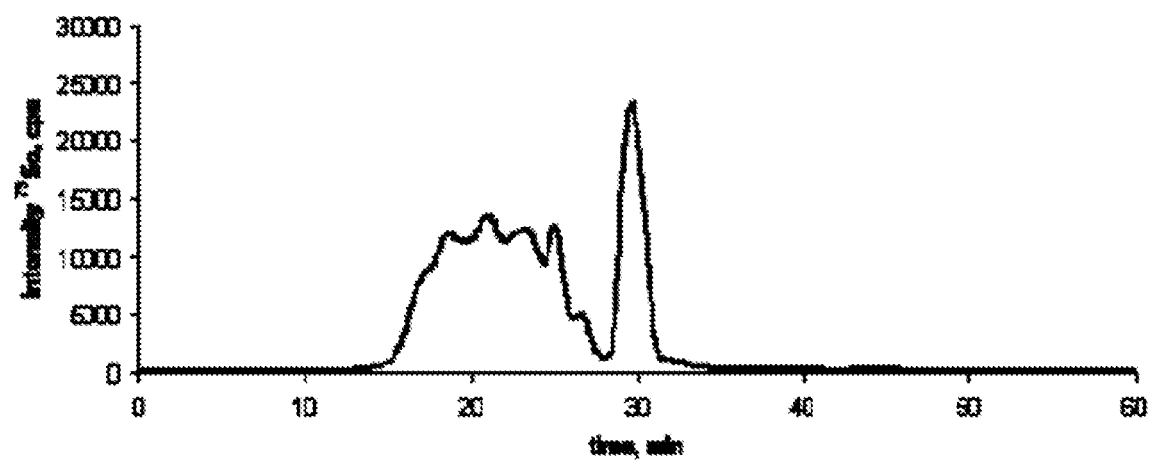


FIGURE 18

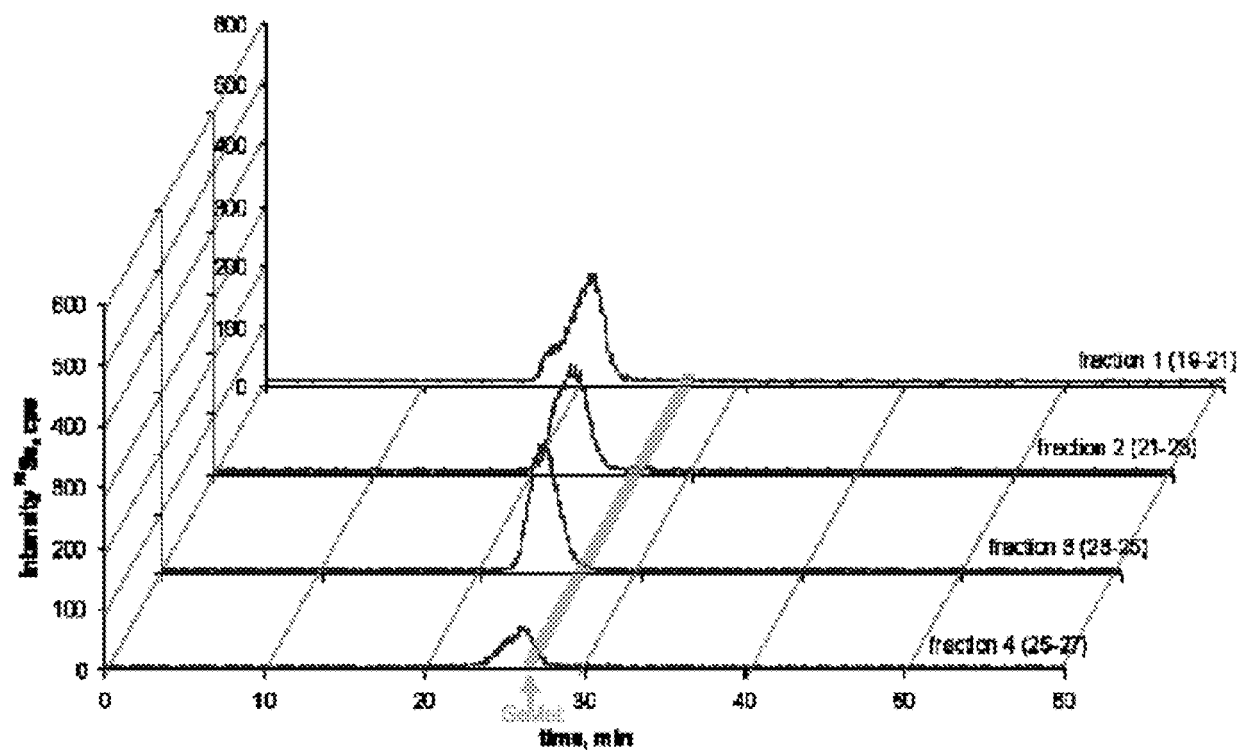


FIGURE 19

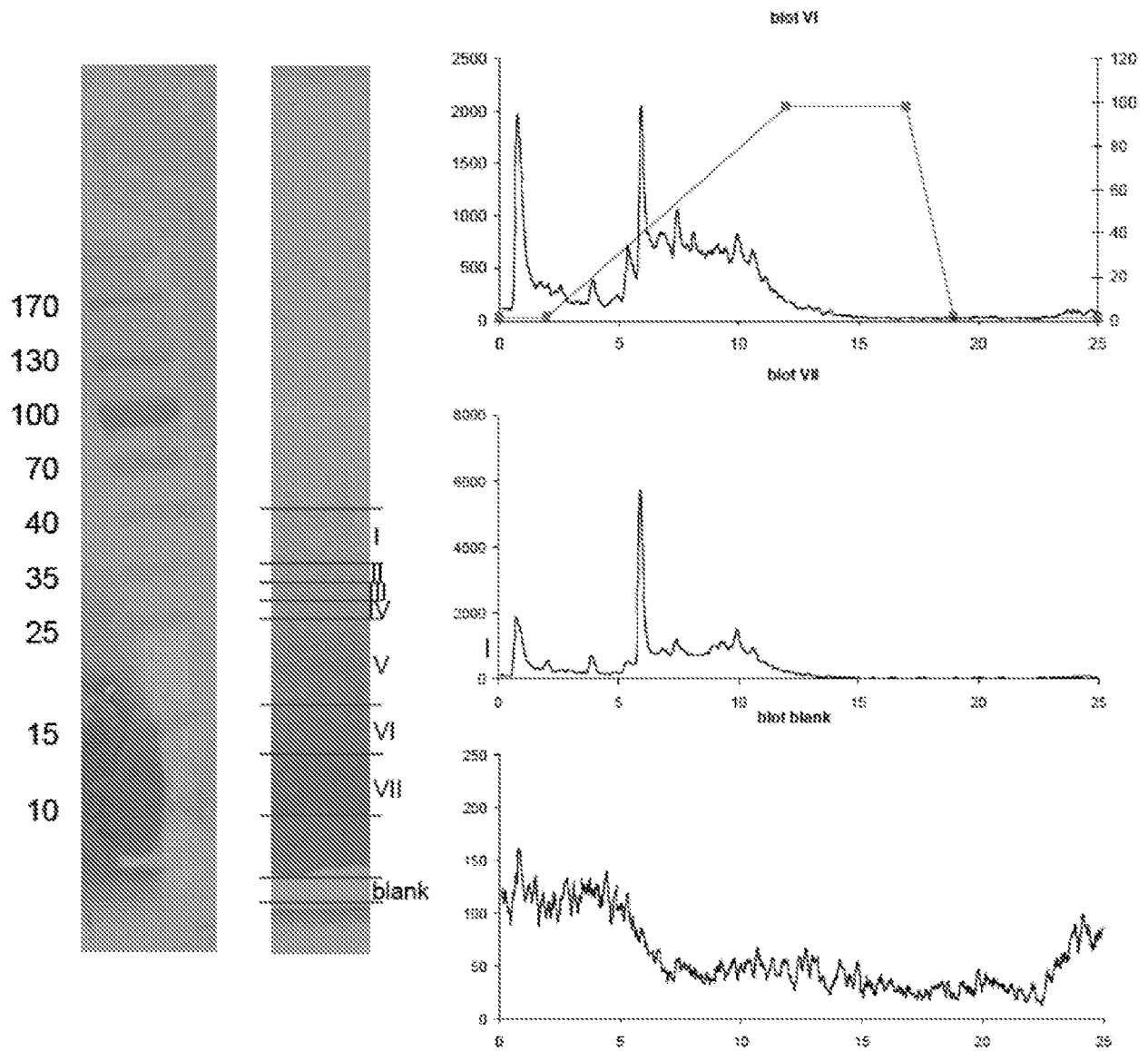


FIGURE 20

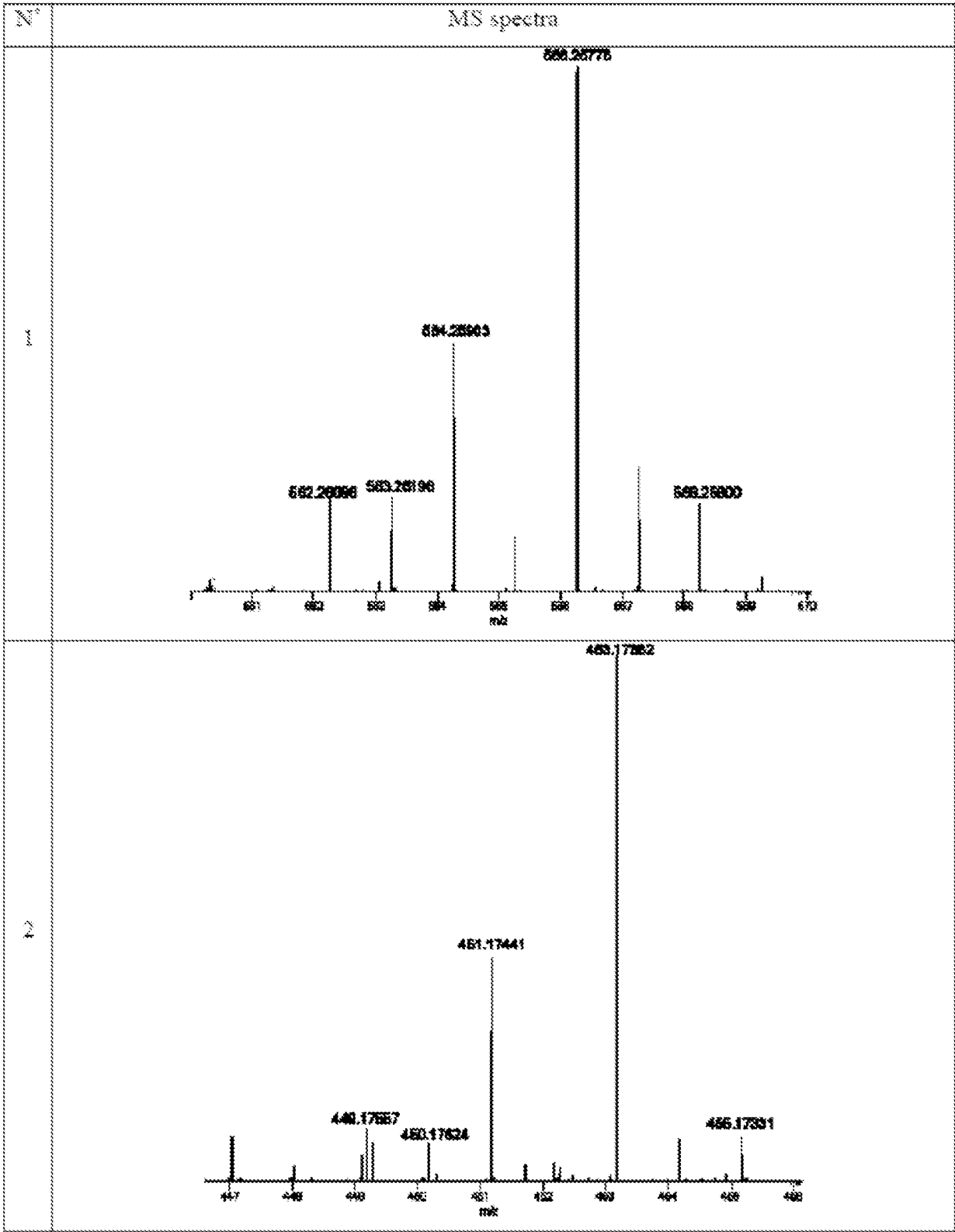


FIGURE 20 CONTINUED

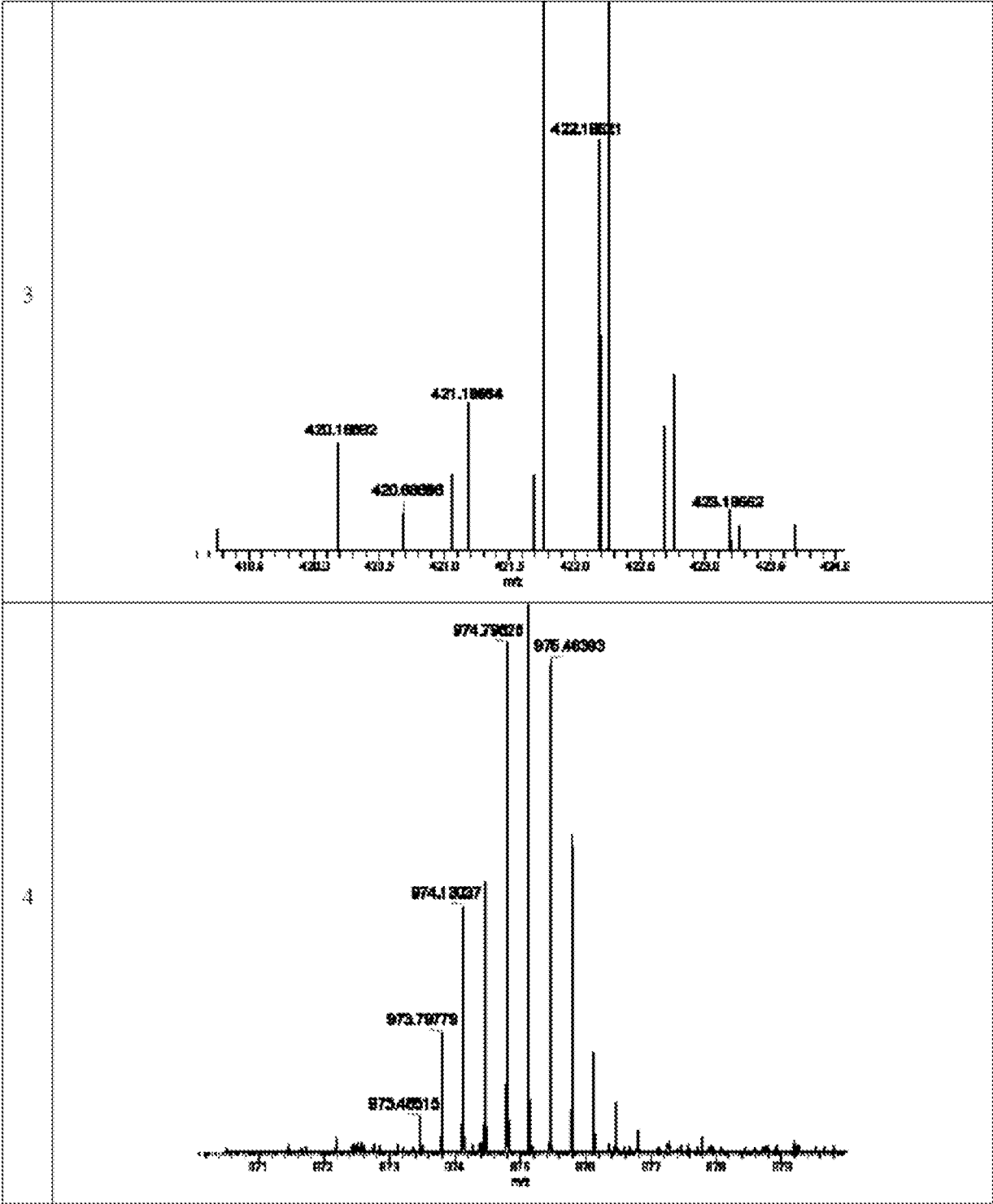


FIGURE 20 CONTINUED

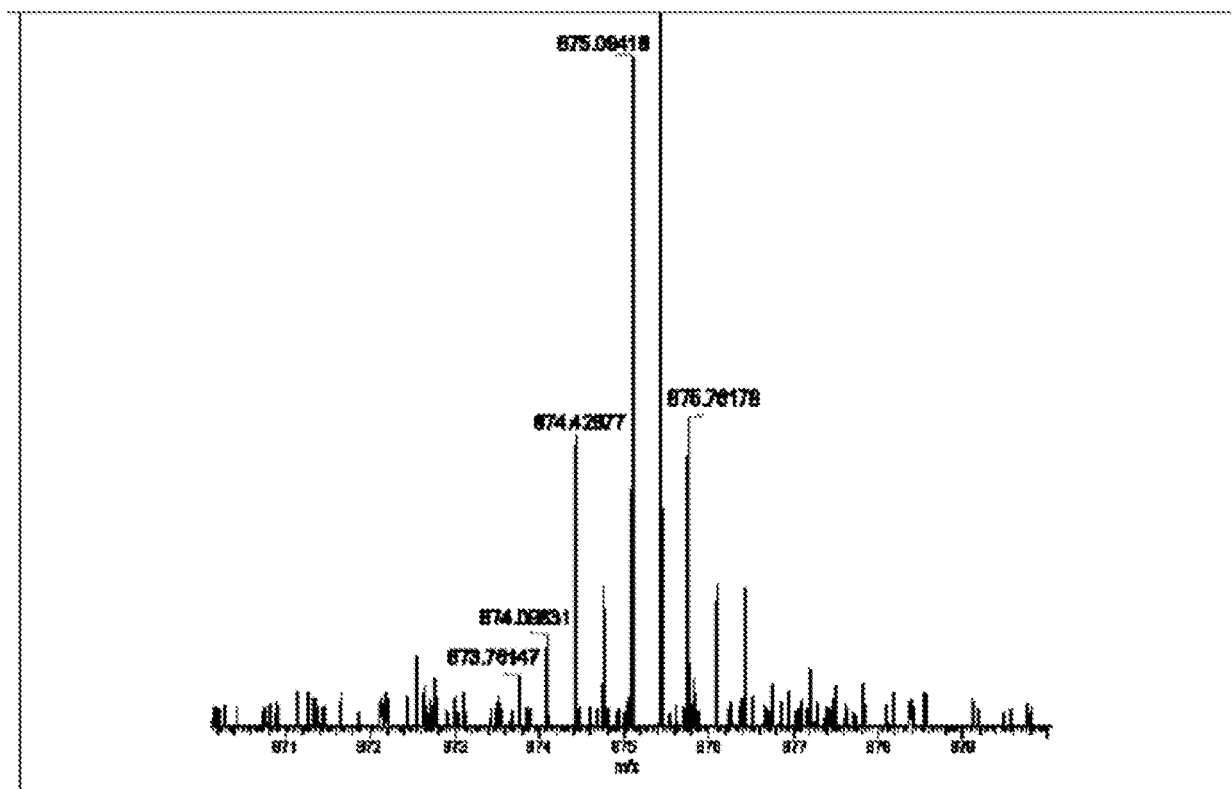


FIGURE 21

	Sequence	Charge	Exp. mass	Theor. mass	Protein
1	LVMR	1	566.25800	566.2568	Glyceraldehyde-3-phosphate dehydrogenase 3; (GAPDH3)
2	VMR	1	453.17352	453.1727	
3	LTGMAFR	2	422.18521	422.18545	
4	SRPNVEVVVALNDPFIT NDYAAAYMFK	3	974.79626	974.7912	
5	VINDAFGIEEGLMTT VHSLTATQK	3	875.09418	875.08923	

FIGURE 22

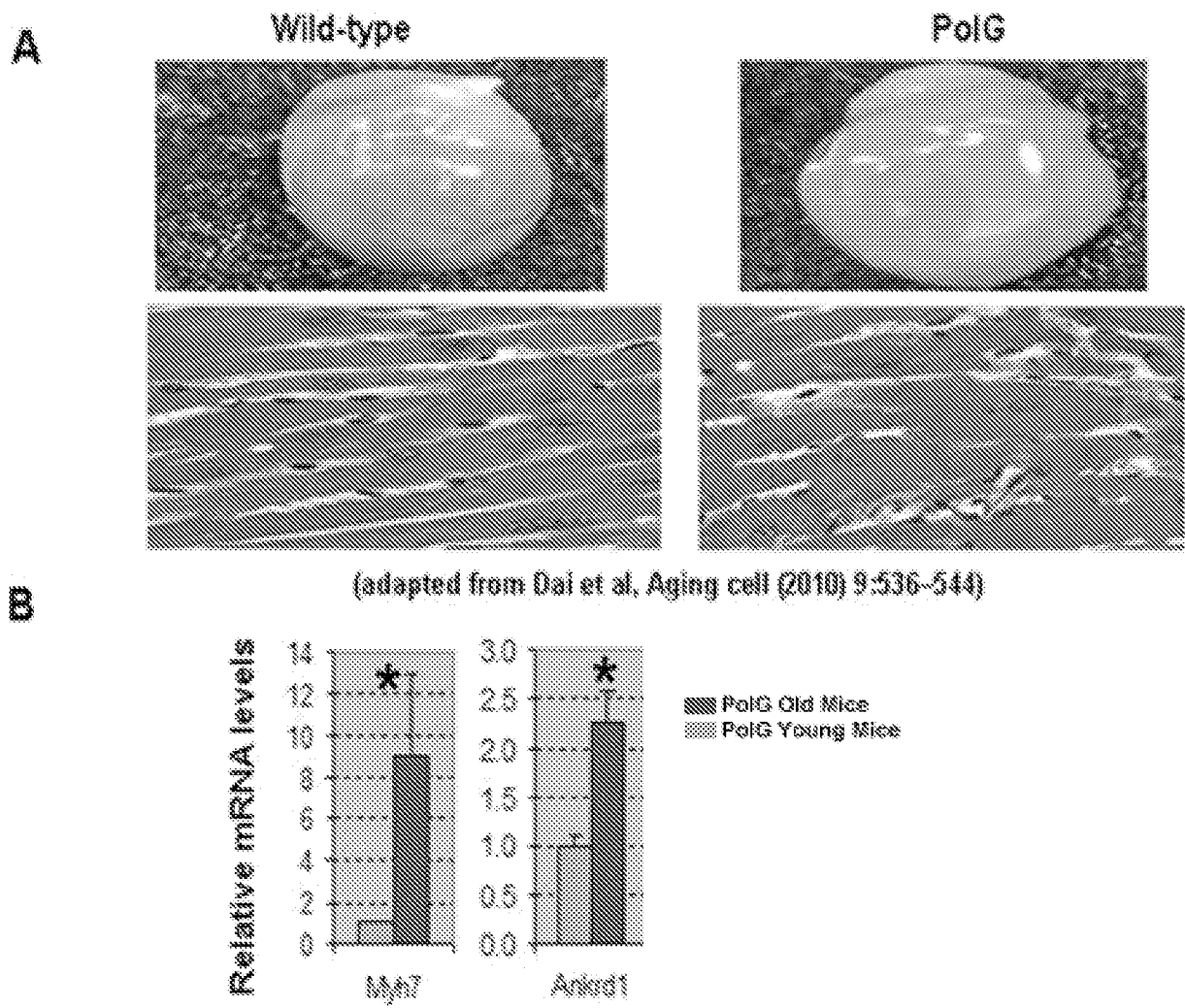


FIGURE 23

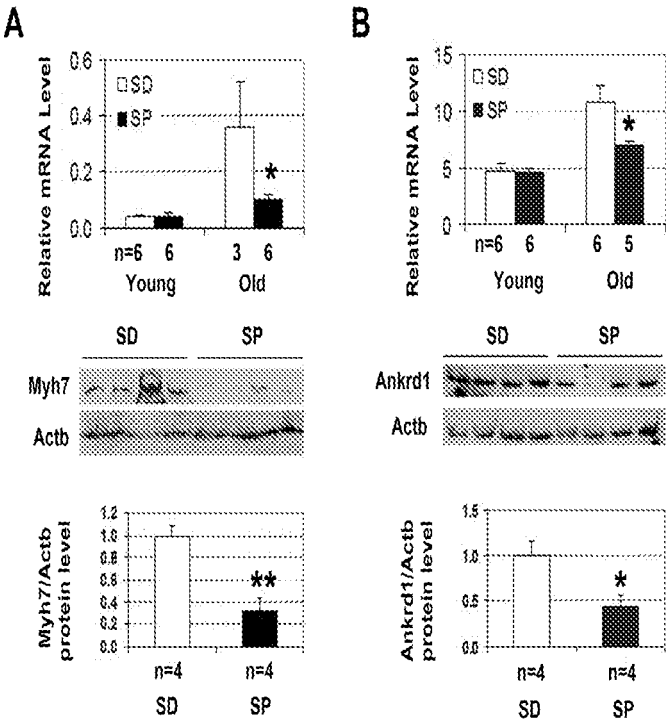


FIGURE 24

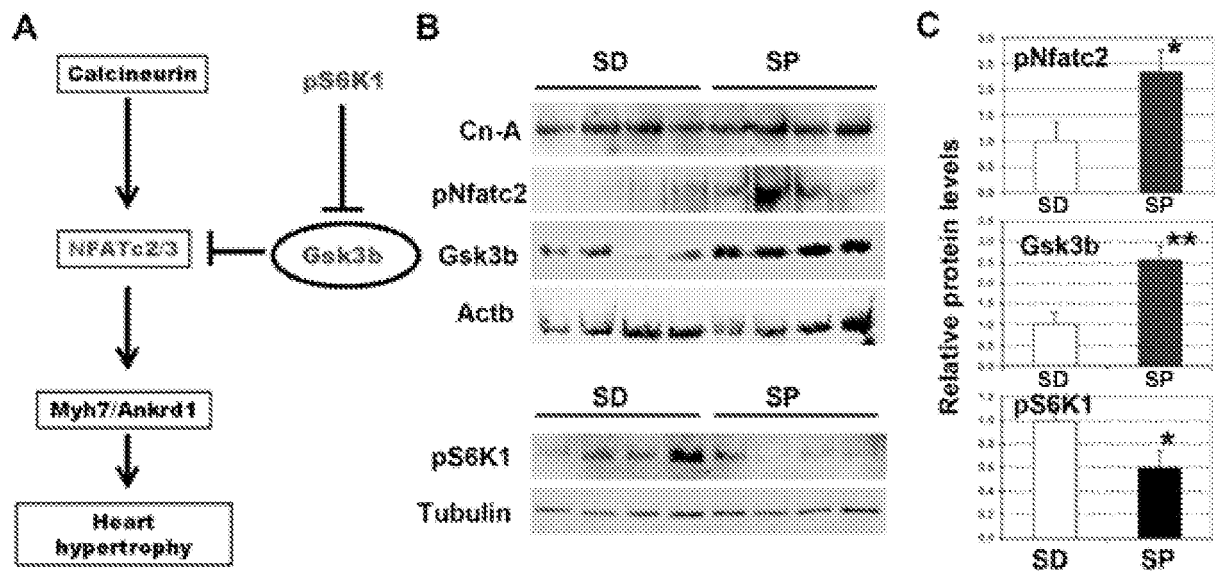


FIGURE 25

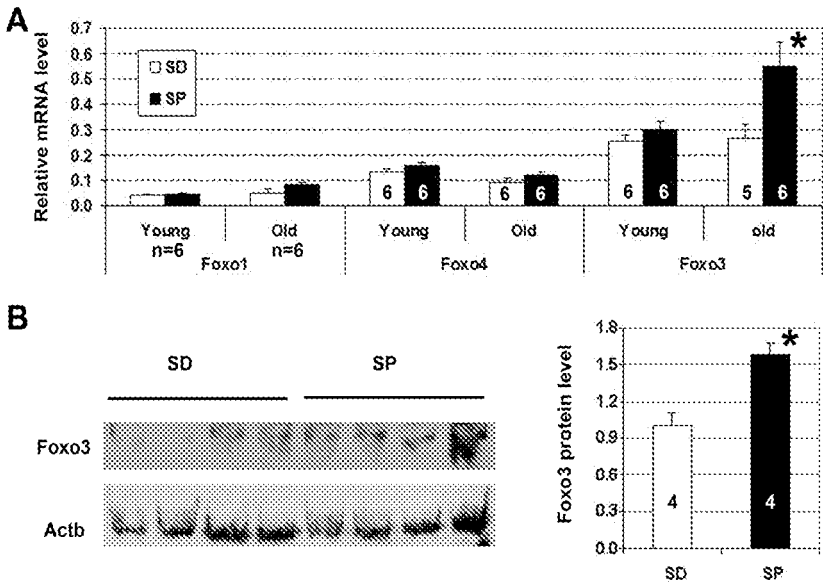


Figure 26

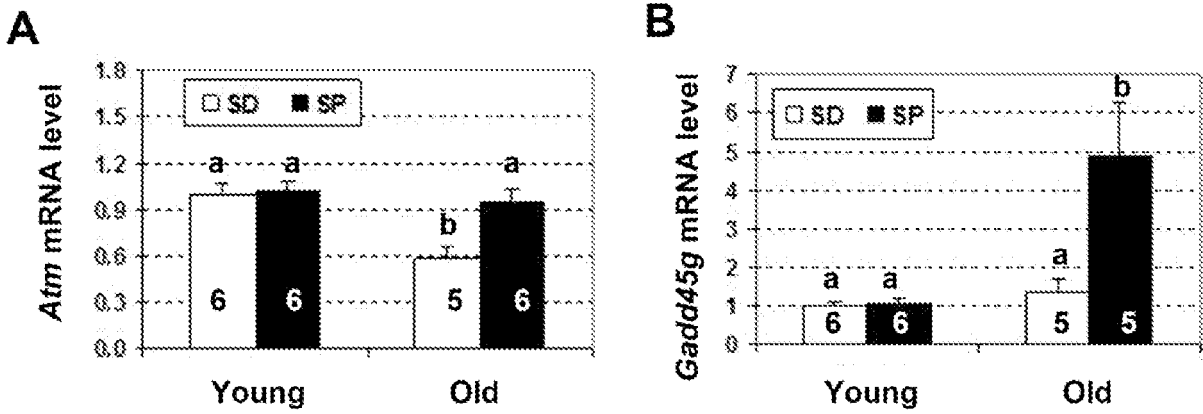


Figure 27

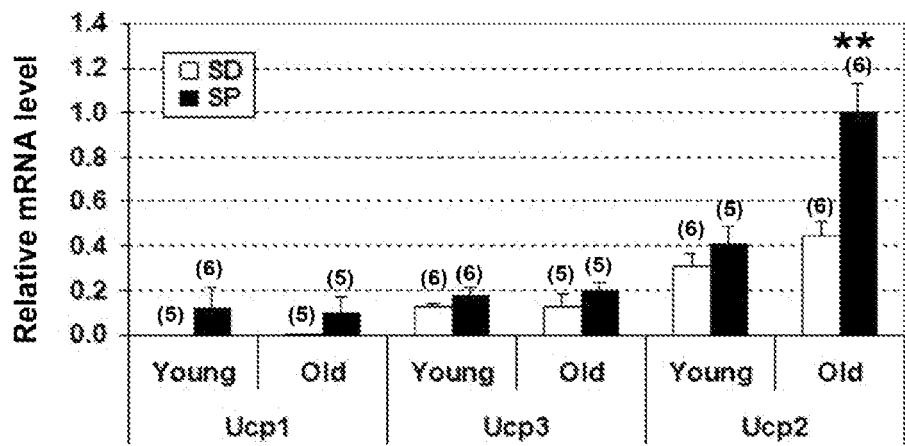


FIGURE 28

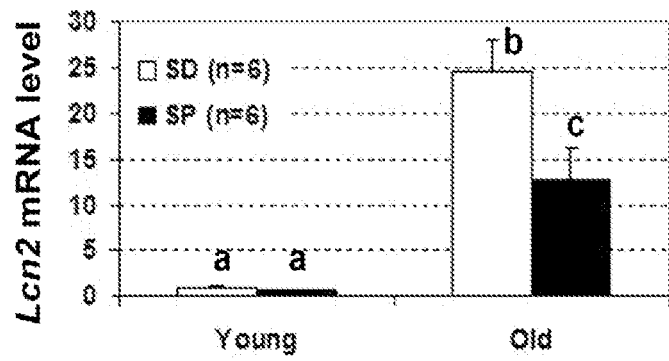


Figure 29

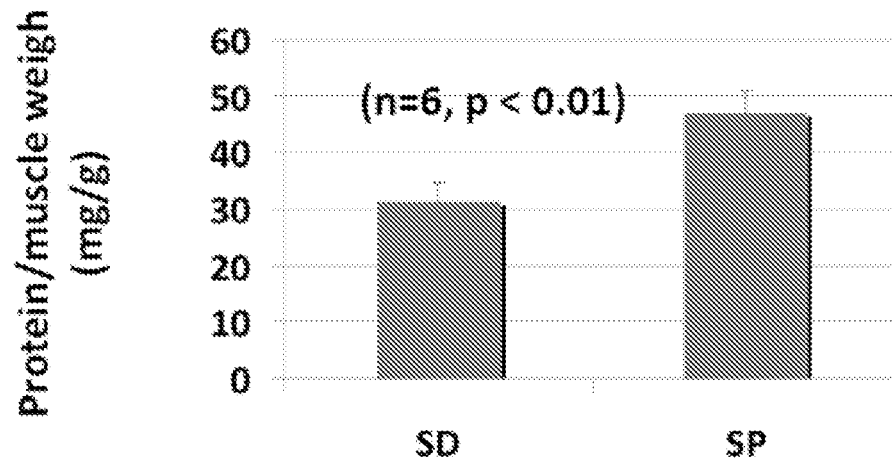


FIGURE 30

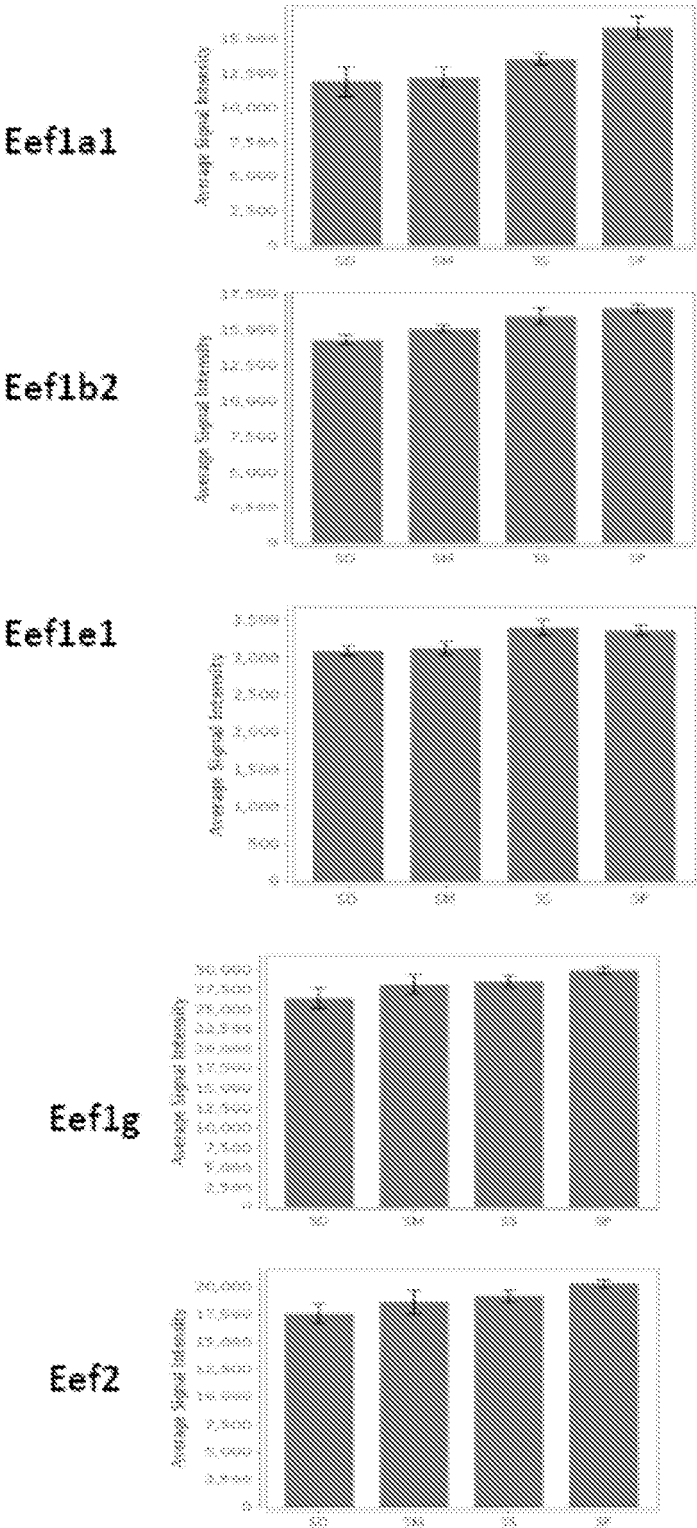


FIGURE 31

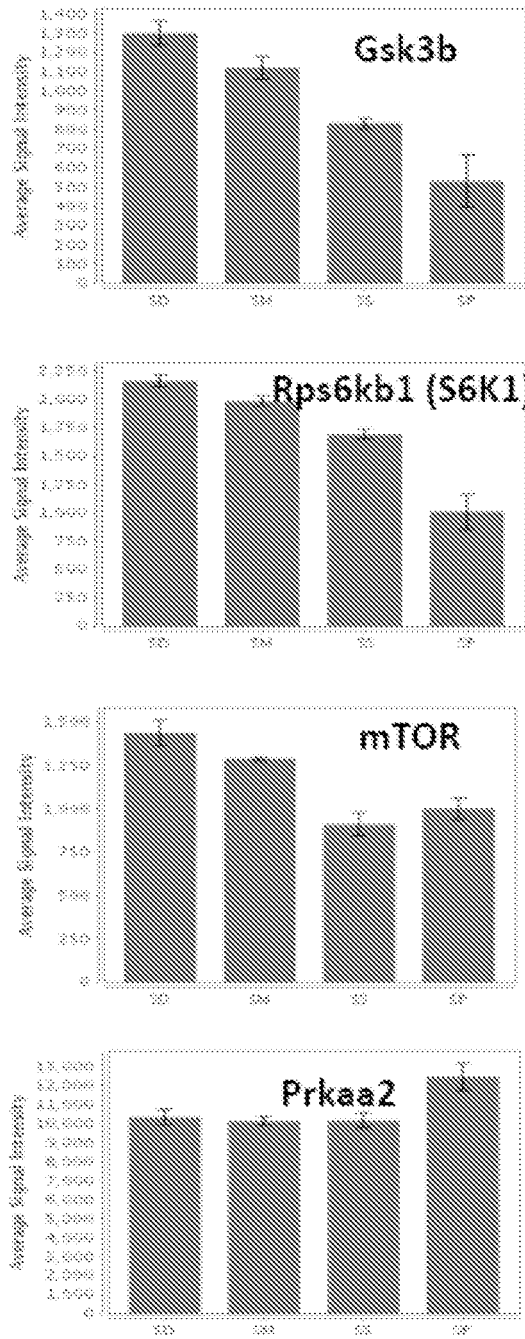


FIGURE 32

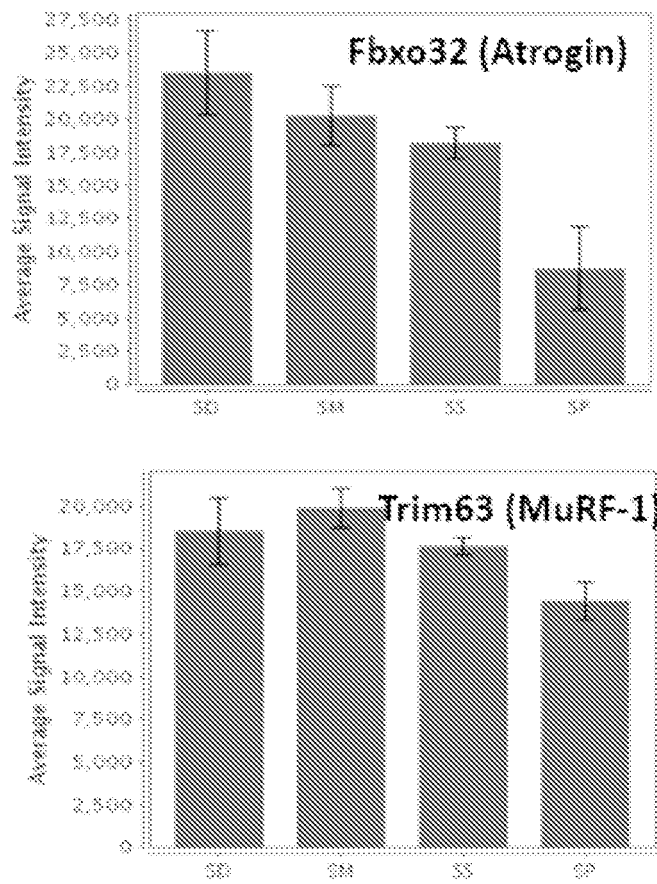


FIGURE 33

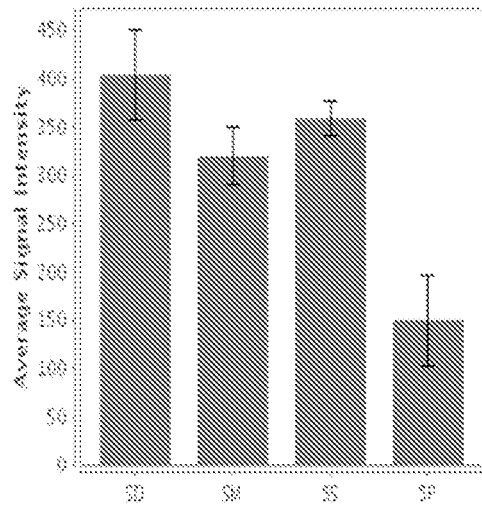


FIGURE 34

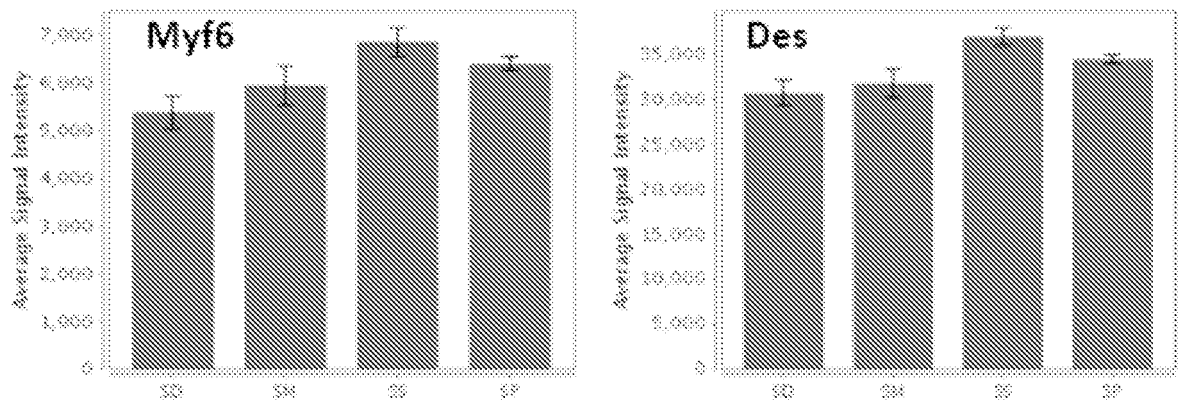


FIGURE 35

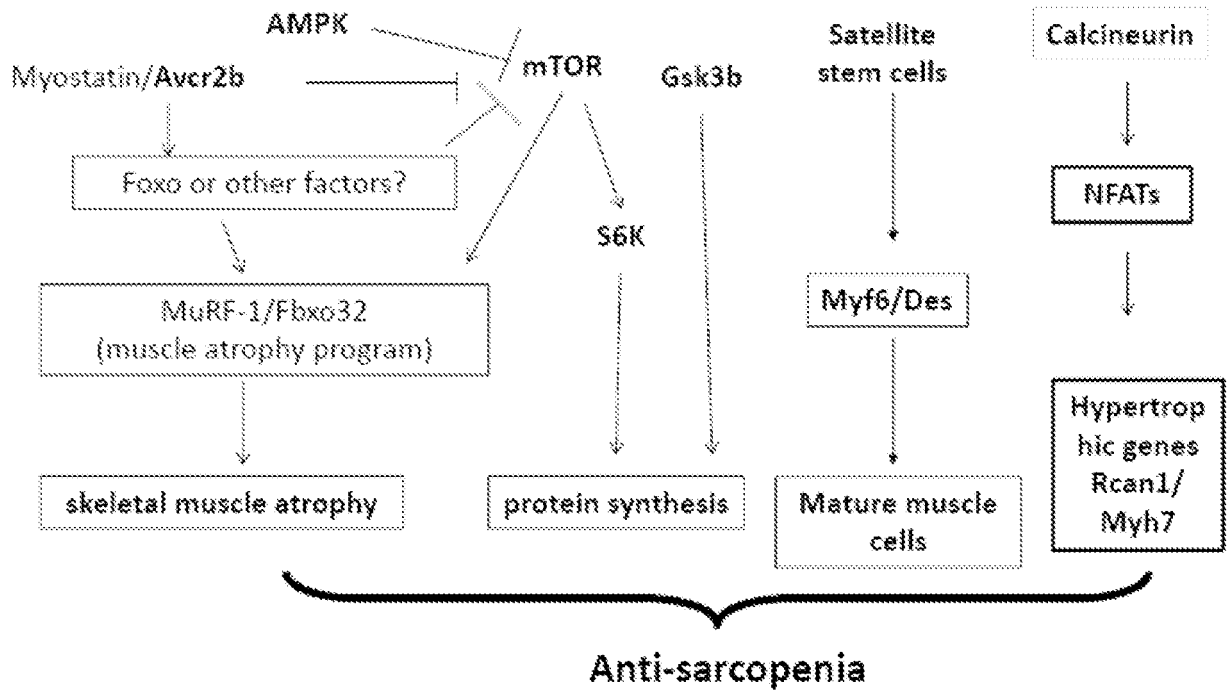


FIGURE 36

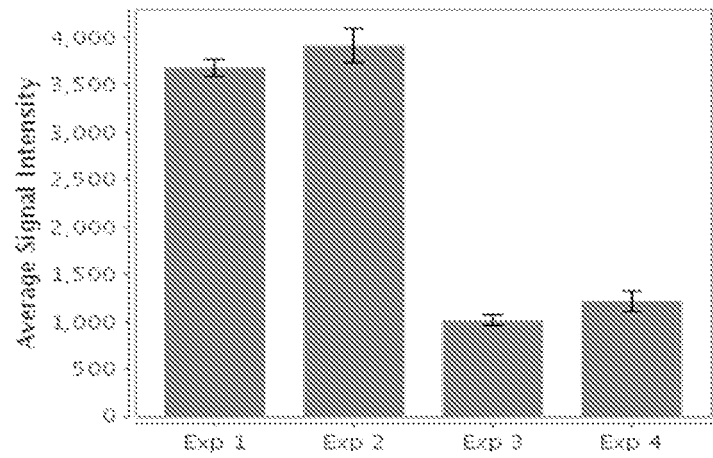


FIGURE 37

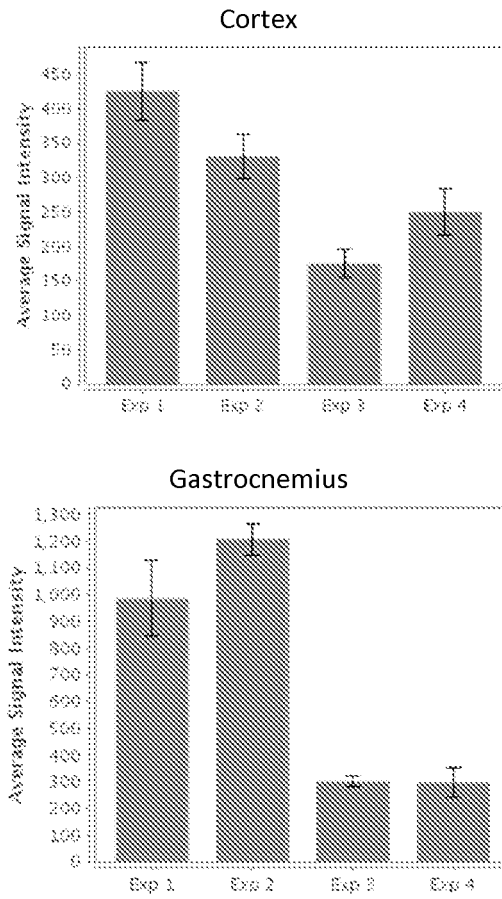
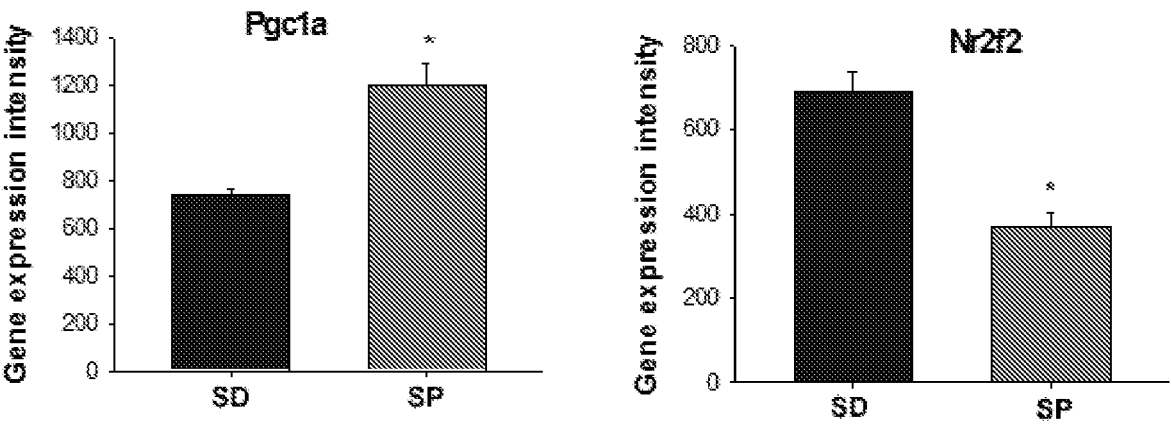


FIGURE 38

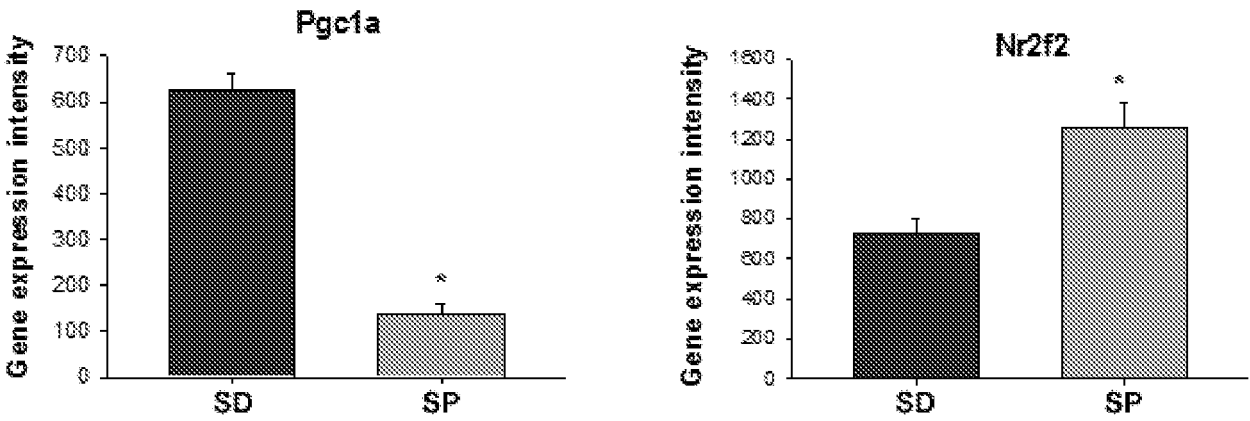
Skeletal muscle



* $p < 0.05$

FIGURE 39

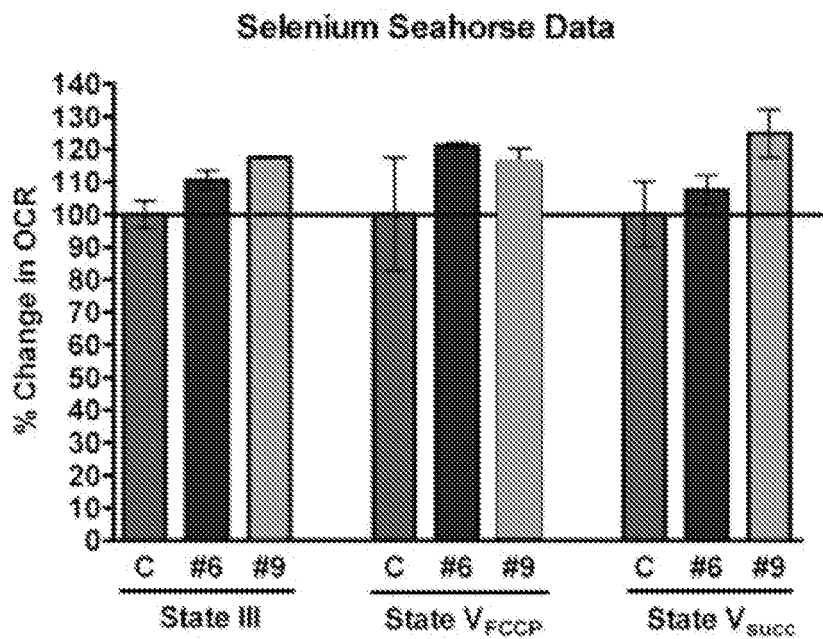
Liver



* $p < 0.05$

FIGURE 40

A



B

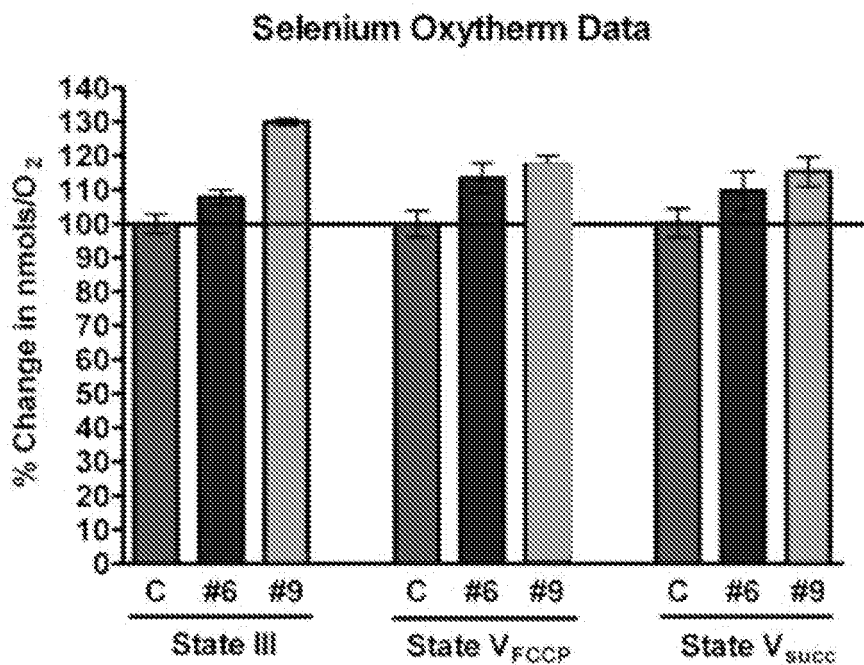


FIGURE 41

