MRSL 8, POU Domain; # Q16633

[1-256] m+H = 27647.926
Cleavage at E

Small polar:	D(7)	E(16)	N(2)	Q(14)			
Large polar:	K(5)	R(8)	H(5)				
Small non-polar:	S(21)	T(22)	A(28)	G(11)			
Large non-polar:	L(26)	I(4)	V(20)	M(4)	F(3)	Y(11)	W(4)
Special:	C(4)	P(41)					

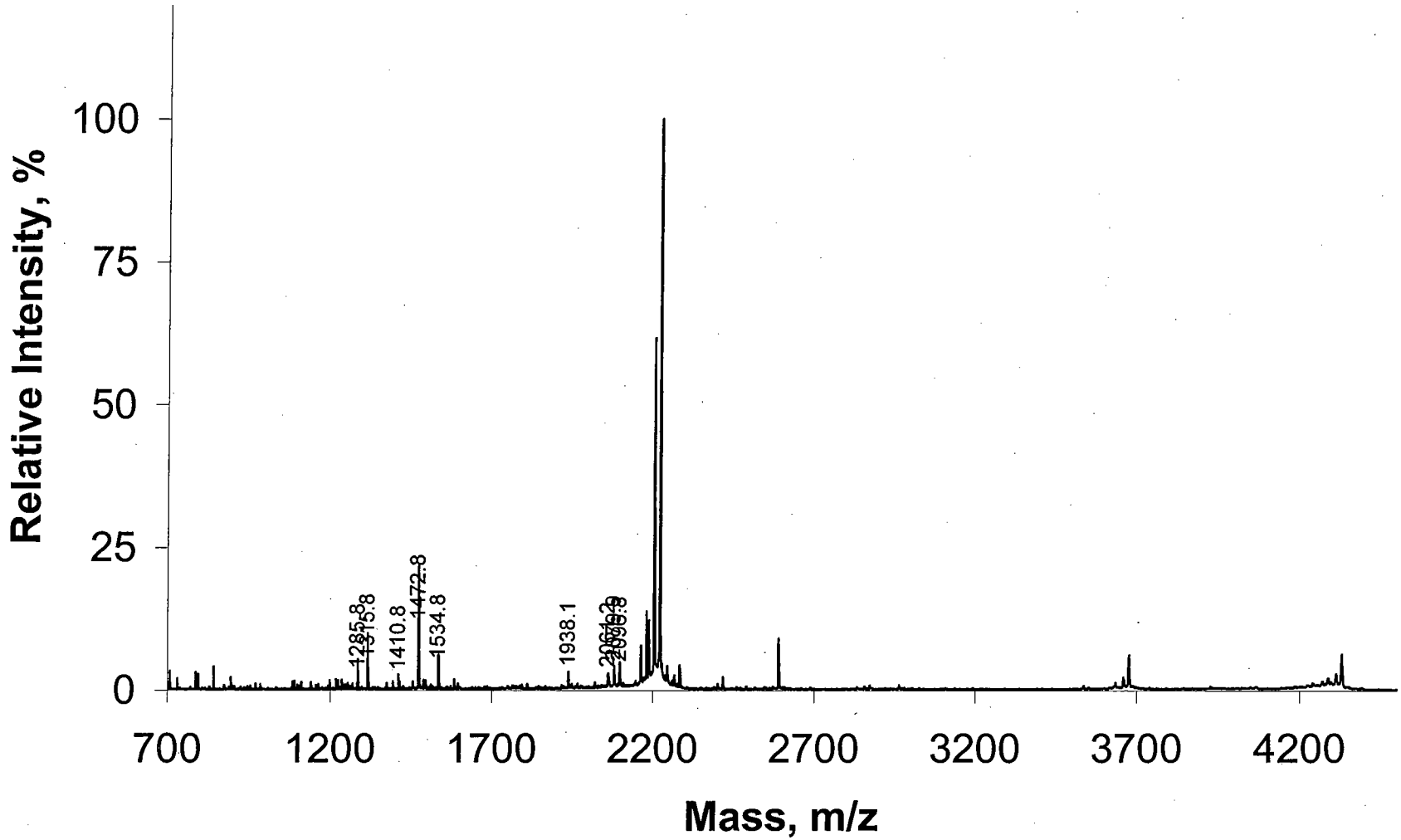
C[67] + 57.05 C[84] + 57.05 C[116] + 57.05 C[128] + 57.05

```
  1 M L W Q K P T A P E q a p a p a r p y q g v r v k e p v k e  30
 31 L L R R K R G H A S S G A A P A P T A V V L P H Q P L A T Y  60
 61 T T V G P S C L D M E g s v s a v t e E a a l c a g w l s q  90
 91 p t p a t l q p l a p w t p y t e Y V P H E a v s c p y s a 120
121 d m y v q p v c p s y t v v g p s s v l t y a s p p l i t n 150
151 v t t r s s a t p a v g p p l e G P E h q a p l t y f p w p 180
181 q p l s t l p t s t l q y q p p a p a l p g p q f v q l p i 210
211 s i p e p v l q d m e D P R R A A S S L T I D K L L L E e E 240
241 d s d a y a l n h t l s v e G F                             256
```

(1)	[1-10] = 1200.608	(2)	[11-30] = 2220.225	(3)	[31-71] = 4326.260
(4)	[72-79] = 749.368	(5)	[80-80] = 148.060	(6)	[81-107] = 2940.460
(7)	[108-112] = 644.304	(8)	[113-166] = 5654.774	(9)	[167-169] = 302.135
(10)	[170-221] = 5775.981	(11)	[222-238] = 1898.071	(12)	[239-239] = 148.060
(13)	[240-240] = 148.060	(14)	[241-254] = 1534.702	(15)	[255-256] = 223.108

2nd most abundant peak
could not assign
his tag ?
ptm ?

MALDI mass spectrum of the Glu-C digest of MRSL-8



Centroid Mass	Rel. Intensity	Potential Match	Calc Mass	Mass Error, ppm
1285.769087	1.41			
1315.767641	3.2			
1410.826625	1.12			
1472.799964	10			
1534.769728	3.1	D[241-254]E	1534.702	44
1938.096764	1.87			
2061.167595	1.69			
2079.874096	2.93			
2096.848719	2.68			
2162.682704	4.99			
2179.675791	10.37			
2186.777695	6.72			
2203.331794	55.05			
2220.318168	100	Q[11-30]E	2220.225	42
2242.277816	1.83			
2244.219864	1.28			
2265.186968	1.54			
2282.200005	4.22			
2416.34996	1.74			
2588.438068	8.19			
3674.048973	3.86			
4327.691792	3.64			

MRSL 8, POU Domain; # Q16633

[1-256] m+H = 27647.926
Cleavage at KR trypsin digest

Small polar:	D(7)	E(16)	N(2)	Q(14)			
Large polar:	K(5)	R(8)	H(5)				
Small non-polar:	S(21)	T(22)	A(28)	G(11)			
Large non-polar:	L(26)	I(4)	V(20)	M(4)	F(3)	Y(11)	W(4)
Special:	C(4)	P(41)					

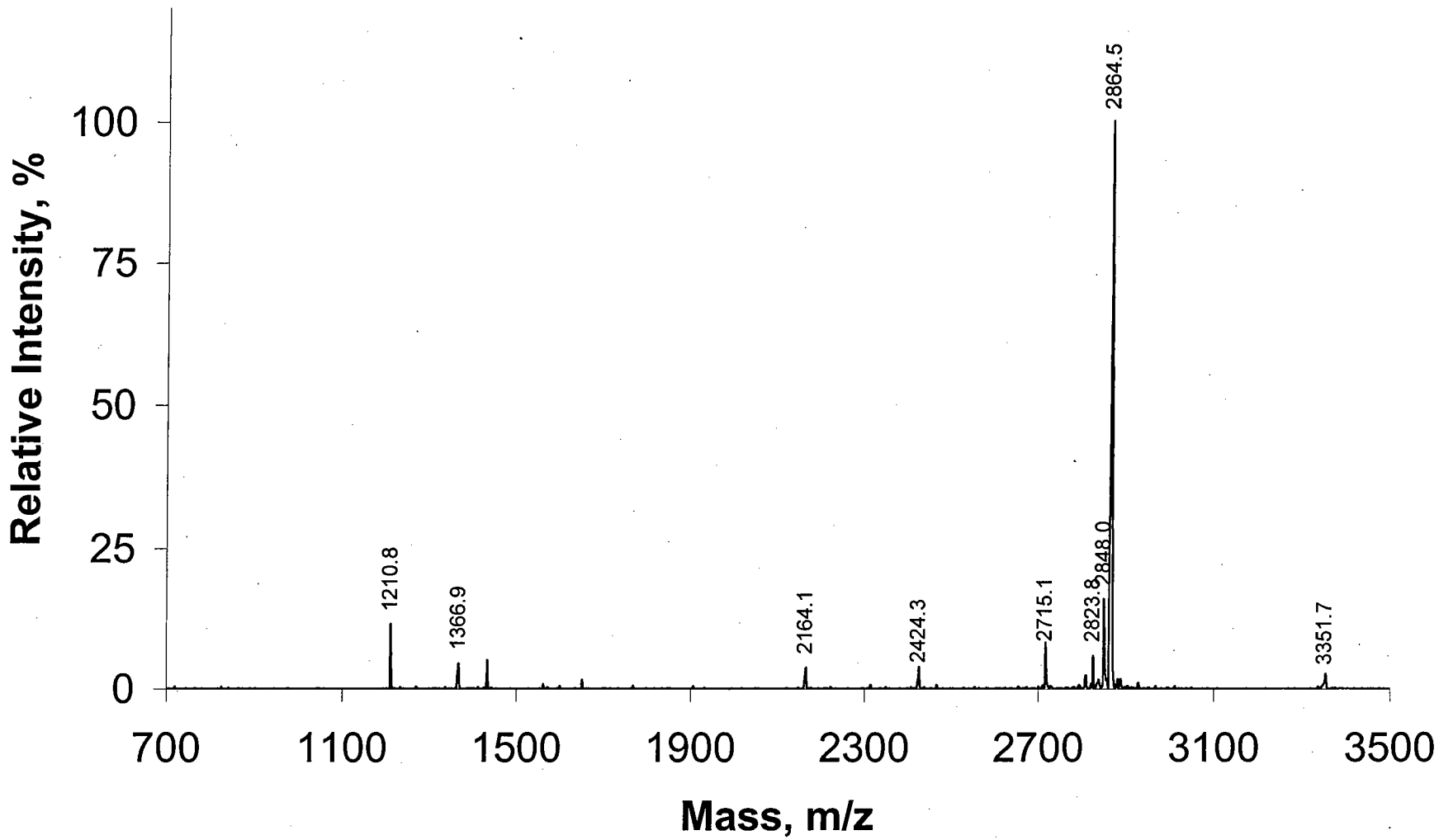
C[67] + 57.05 C[84] + 57.05 C[116] + 57.05 C[128] + 57.05

```
  1 M L W Q K P T A P E Q A P A P A R P Y Q G V R v k E P V K e  30
 31 l l r R k R g h a s s g a a p a p t a v v l p h q p l a t y  60
 61 t t v g p s c l d m e g s v s a v t e e a a l c a g w l s q  90
 91 p t p a t l q p l a p w t p y t e y v p h e a v s c p y s a 120
121 d m y v q p v c p s y t v v g p s s v l t y a s p p l i t n 150
151 v t t r S S A T P A V G P P L E G P E H Q A P L T Y F P W P 180
181 Q P L S T L P T S T L Q Y Q P P A P A L P G P Q F V Q L P l 210
211 S I P E P V L Q D M E D P R r A A S S L T I D K l l l e e e 240
241 d s d a y a l n h t l s v e g f                             256
```

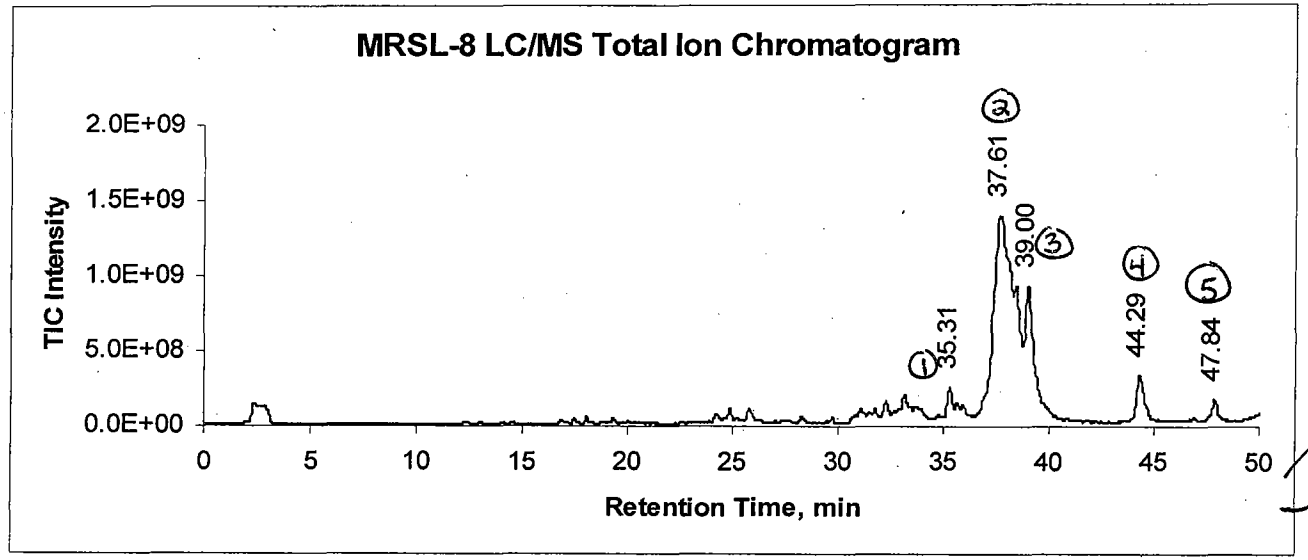
(1)	[1-23] = 2592.350	(2)	[24-25] = 246.181	(3)	[26-29] = 472.277
(4)	[30-33] = 530.330	(5)	[34-34] = 175.119	(6)	[35-35] = 147.113
(7)	[36-36] = 175.119	(8)	[37-154] = 12439.010	(9)	[155-224] = 7533.839
(10)	[225-225] = 175.119	(11)	[226-234] = 905.494	(12)	[235-256] = 2465.172

most abundant
peak could not
assign

MALDI mass spectrum of the trypsin digest of MRSL-8



Centroid Mass	Rel. Intensity	Potential Match	Calc Mass	Mass Error, ppm
1210.774287	2.85	V[24-33]R	1210.752	18
1366.885042	1.13	V[24-34]R	1366.853	23
2164.127847	1.99			
2424.255086	2.31			
2715.061579	6.2			
2807.439559	1.1			
2823.841801	5.46			
2847.991578	13.12			
2864.529627	100			
2880.478915	1.35			
2886.469874	1.1			
3351.690891	1.9	A[226-256]F	3351.648	13

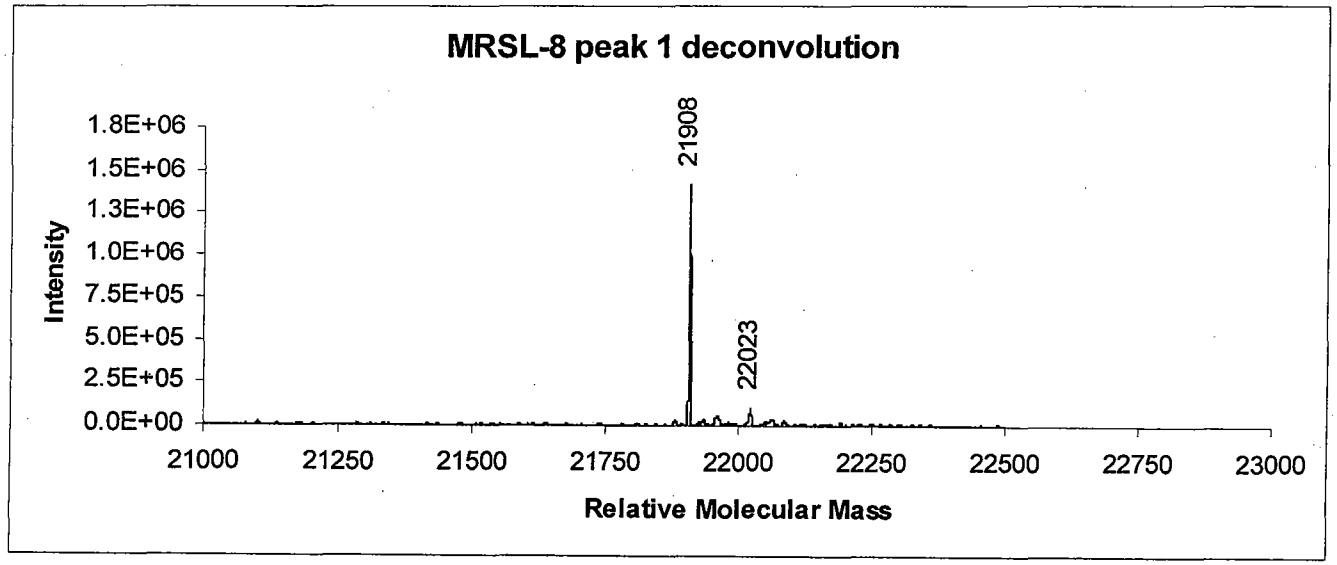


different chromatography from MRSL-7

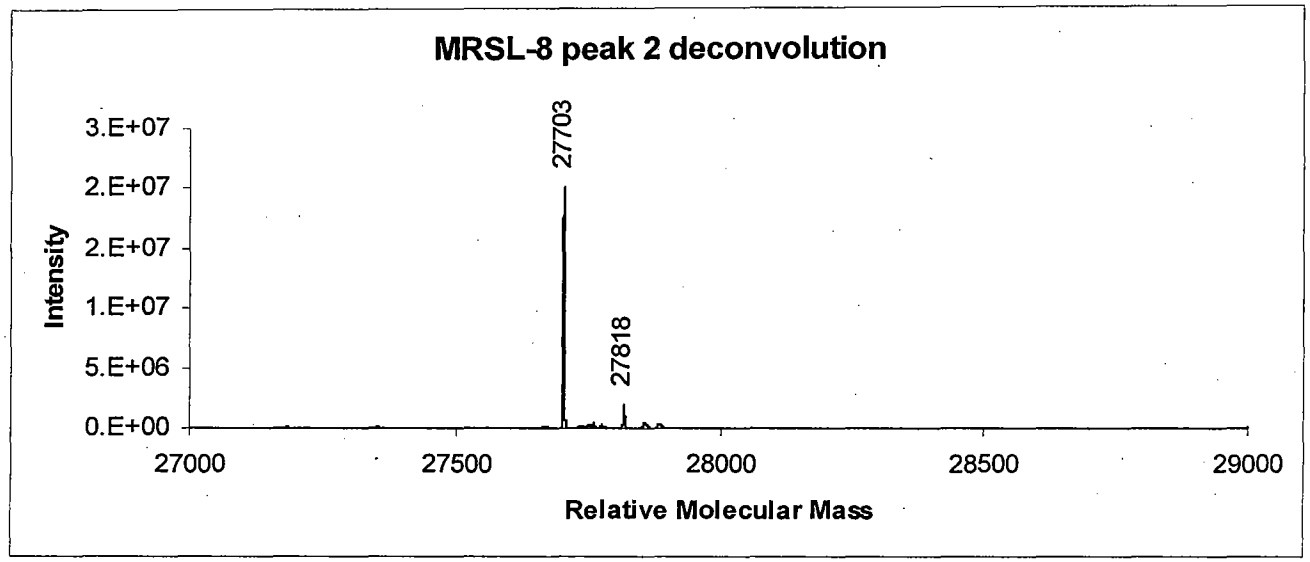
not an absolute measure

Column = Supelco Discovery BIO Wide Pore C5, 10 cm x 0.32 mm, 3 µm; #44493-01
Mobile Phase A = 0.05 % (v/v) trifluoroacetic acid in water
Mobile Phase B = 0.05 % (v/v) trifluoroacetic acid in acetonitrile
Method File = NCI Proteins-Polar
Column Temp = 50 °C
Injection Volume = 5 µL (full loop injection)

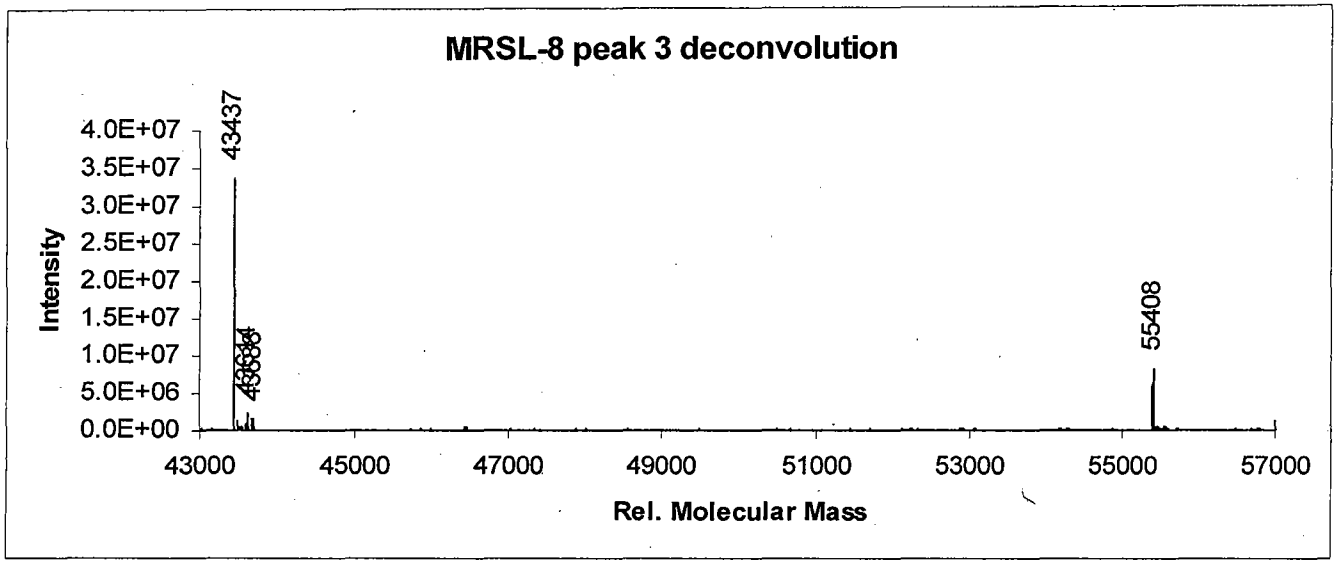
Time, min	% B	Flow, µL/min
0	15	6
5	15	6
45	60	6
50	95	6
55	95	6
56	15	6
80	15	6



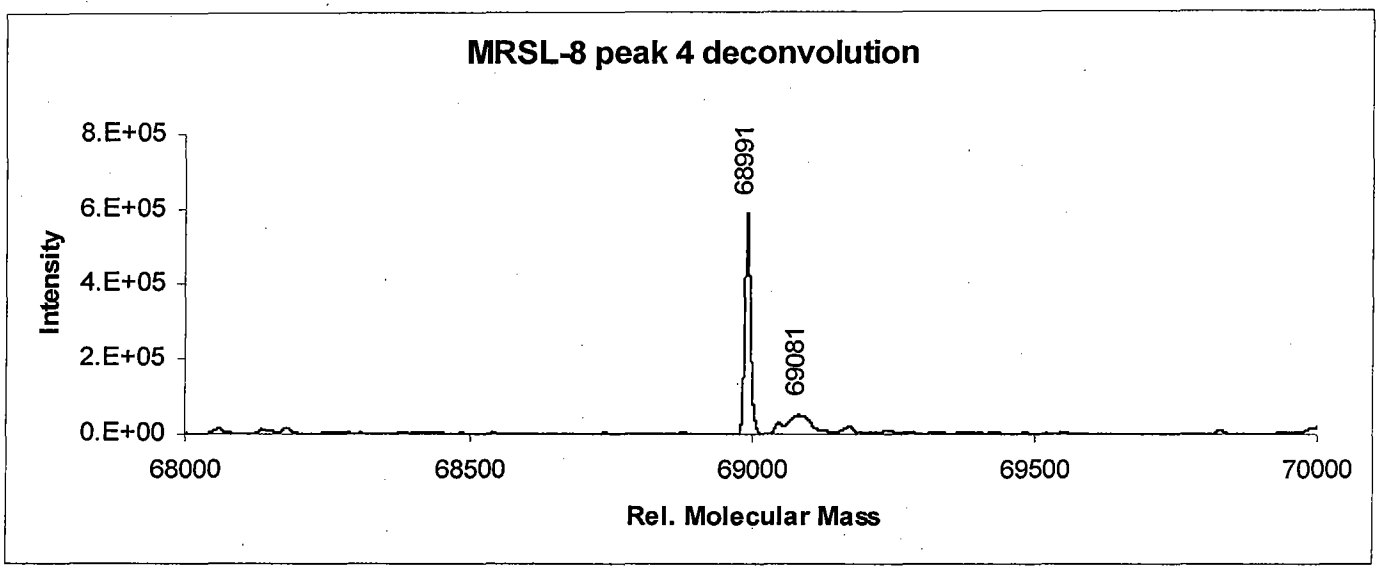
Rel Molecular Mass	Intensity	Potential ID
21908	1.42E+06	
22023	9.82E+04	



Rel. Molecular Mass	Intensity	Potential ID		
27703	2.01E+07	MRSL-8 Calculated Mr =	27436.2	(without disulfides)
27818	1.99E+06		27432.1	(with 2 disulfides)



Rel. Molecular Mass	Intensity	Potential ID
43437	3.36E+07	same species observed at Mr 43441 in peak 1 in MRSL-7 LC/MS results
43614	2.37E+06	same species observed as Mr 43616 in peak 1 in MRSL-7 LC/MS results
43688	1.50E+06	same species observed at Mr 43697 in peak 1 in MRSL-7 LC/MS results
55408	8.10E+06	covalent dimer of Mr 27703 (MRSL-8 peak 2) species



Rel. Molecular Mass	Intensity	Potential ID
68991	5.89E+05	same species observed at Mr 68998 in peak 2 in MRSL-7 LC/MS results
69081	5.04E+04	same species observed at Mr 69104 in peak 2 in MRSL-7 LC/MS results