

**Slide 2. Spectrum from the Kuster dataset validating the *OR6J1* olfactory receptor.**  
Spectrum for peptide MRAVLRSR

**Slide 3. Spectrum from the Kuster dataset validating the *OR6J1* olfactory receptor.**  
Spectrum for peptide MRAVLRSRSR

**Slide 4. Spectrum from the Kuster dataset validating the *OR6J1* olfactory receptor.**  
Spectrum for peptide EYLEINK

**Slide 5. Spectrum from the Kuster dataset validating the *OR6J1* olfactory receptor.**  
Spectrum for peptide YATICPLR

**Slide 6. Spectrum from the Kuster dataset validating the *OR6J1* olfactory receptor.**  
Spectrum for peptide VLANLGSR

**Slide 7. Spectrum from the Kuster dataset validating the *OR6J1* olfactory receptor.**  
Spectrum for peptide RMRAVLR

**Slide 8. Spectrum from the Kuster dataset validating the *OR6J1* olfactory receptor.**  
Spectrum for peptide EYLEINK

**Slide 9. Spectrum from the Kuster dataset validating the *OR6J1* olfactory receptor.**  
Spectrum for peptide NDTVQGVLRDVWVR

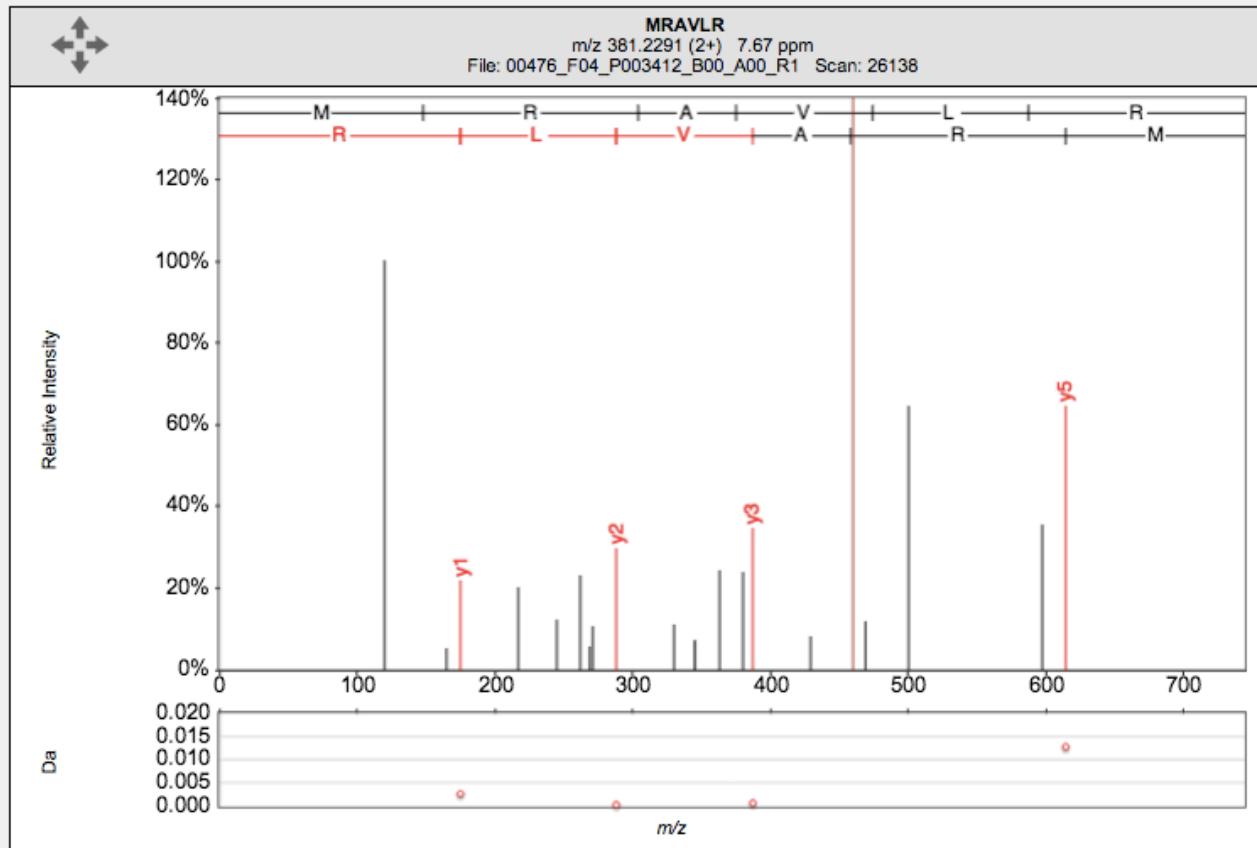
Sequence	-log q...	-log PEP	Search Engl...	Score	Delta Score	z	Theo...	Meas...	Mass...	Fixed...	Varia...	Project	Exper...
MS <sup>2</sup> R.MRAVLR.S	2.2393	0.1	Mascot	24.63	9.46	2	760.4...	760.4...	7.67	Oxidat...	Par1...	batch_1	

> Reference spectrum

< Fragments

Select All Deselect All

a:  1+  2+  3+  
b:  1+  2+  3+  
c:  1+  2+  3+  
x:  1+  2+  3+  
y:  1+  2+  3+  
z:  1+  2+  3+  
yb:   
IM:   
M[H]:   
Neutral loss:  
 NH3  CH2N2  C3H6  
Max neutral loss count: 3  
Mass tolerance:  
0.4 Da  
Expert Mode:  on  off  
> Configuration



#	Seq	#	y1+
1	M	6	
2	R	5	614.4097
3	A	4	458.3085
4	V	3	387.2714
5	L	2	288.203
6	R	1	175.119

Sequence	-log q...	-log PEP	Search Engl...	Score	Delta Score	z	Theo...	Meas...	Mass...	Fixed...	Varia...	Project	Experi...
MS <sup>2</sup> R.MRAVLRSL.R	2.2997	0.21	Andromeda	90.66	34.65	2	1003...	1003...	0.01	Oxidat...	Cutler...	Roch...	

> Reference spectrum

▼ Fragments

Select All Deselect All

a:  1+  2+  3+  
 b: 1+  2+  3+  
 c: 1+  2+  3+  
 x: 1+  2+  3+  
 y: 1+  2+  3+  
 z: 1+  2+  3+  
 yb:  
 IM:  
 M[H]:

Neutral loss:

C3H9N3  H2O  NH3  
 CO  CH4O  CH2N2  
 C4H6N2

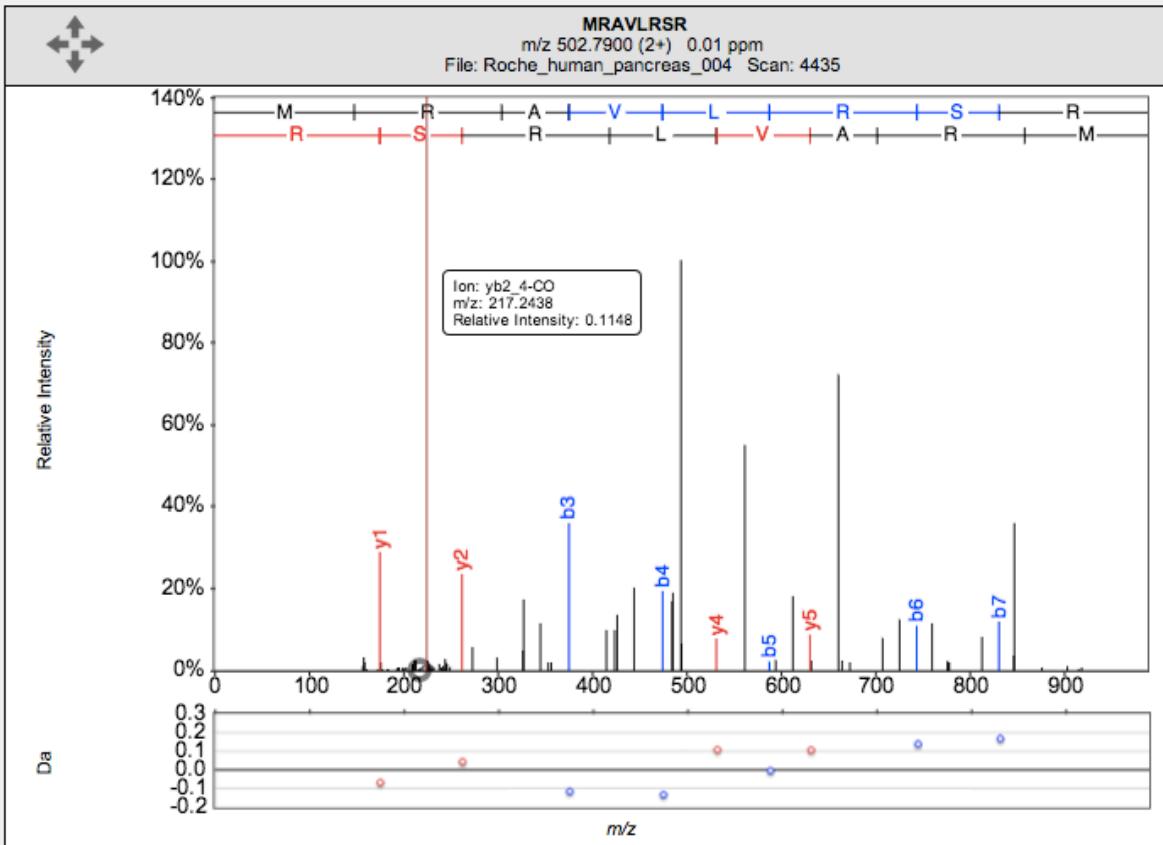
Max neutral loss count: 3

Mass tolerance:

0.4 Da

Expert Mode:  on  off

> Configuration



b1+	#	Seq	#	y1+
148.0427	1	M	8	
304.1438	2	R	7	857.5428
375.1809	3	A	6	701.4417
474.2493	4	V	5	630.4046
587.3334	5	L	4	531.3362
743.4345	6	R	3	418.2521
830.4665	7	S	2	262.151
	8	R	1	175.1119

Sequence		-log q-...	-log PEP	Search Engi...	Score	Delta Score	z	Theo...	Meas...	Mass...	Fixed...	Varia...	Project	Exper...
MS <sup>2</sup>	K.EYLEINK.I	2.9425	1.49	Andromeda	114.19	28.92	2	907.4...	907.4...	0.01			Geige...	MFM
MS <sup>2</sup>	K.EYLEINK.I	2.9425	1.49	Andromeda	114.19	28.92	2	907.4...	907.4...	0.01			Geige...	MFM
MS <sup>2</sup>	K.EYLEINK.I	2.3255	0.93	Andromeda	81.3	12.88	2	907.4...	907.4...	0.01			Geige...	HCC1...
MS <sup>2</sup>	K.EYLEINK.I	2.3255	0.93	Andromeda	81.3	12.88	2	907.4...	907.4...	0.01			Geige...	HCC1...
MS <sup>2</sup>	K.EYLEINK.I	2.2642	0.82	Andromeda	47.92	15.96	2	907.4...	907.4...	0.01			Nagar...	Deep ...

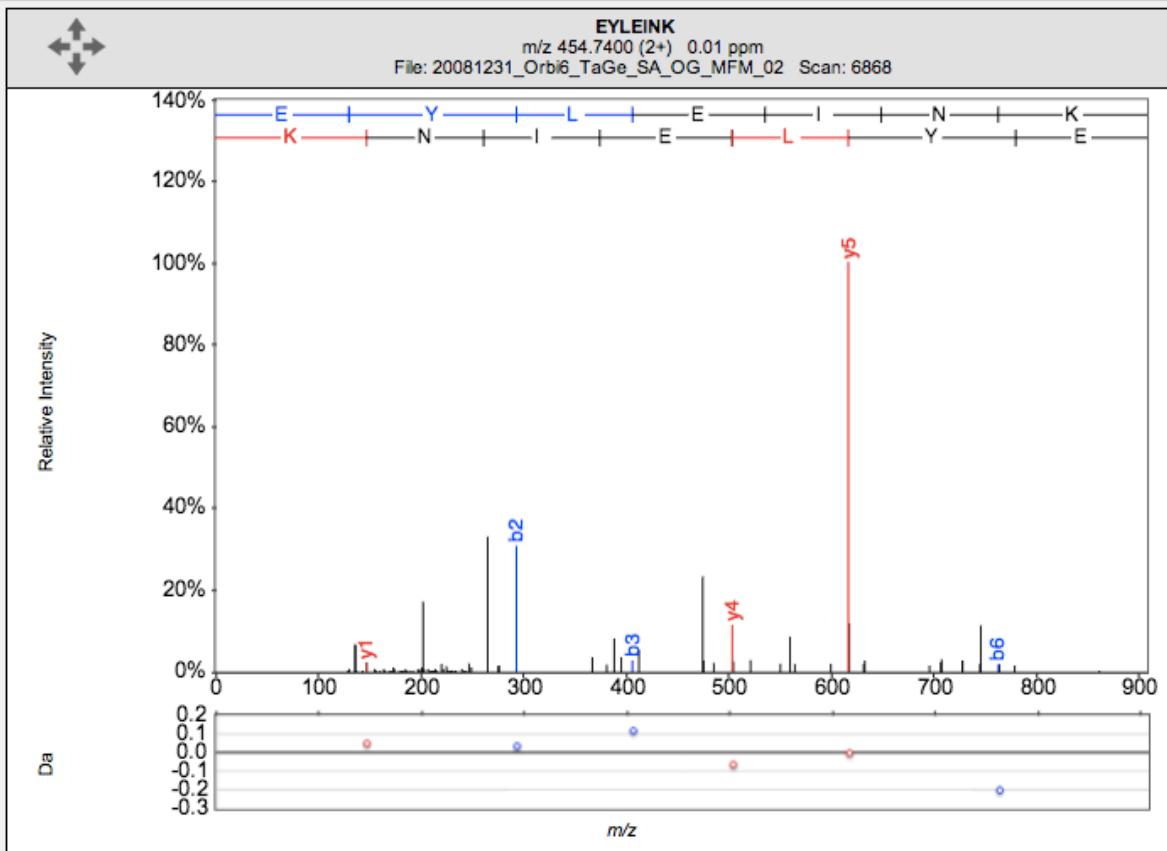
< 1 2 >

> Reference spectrum

▼ Fragments

Select All Deselect All

a:  1+  2+  3+  
b:  1+  2+  3+  
c:  1+  2+  3+  
x:  1+  2+  3+  
y:  1+  2+  3+  
z:  1+  2+  3+  
yb:   
IM:   
M[H]:   
Neutral loss:  
 NH3  H2O  C4H11N  
 CH3NO  C2H4  C4H8  
 C2H4O2  
Max neutral loss count: 3 ▾  
Mass tolerance:  
0.4 Da ▾  
Expert Mode:  on  off  
> Configuration



Sequence	-log q...	-log PEP	Search Engi...	Score	Delta Score	z	Theo...	Meas...	Mass...	Fixed...	Varia...	Project	Exper...
MS <sup>2</sup> R.YATICCPLR.Y	2.2871	1.69	Andromeda	48.28	12.77	2	1152....	1152....	0	Carba...		Pirmor...	Full pr...
MS <sup>2</sup> R.YATICCPLR.Y	2.0744	0.91	Andromeda	43.08	11.59	2	1152....	1152....	0	Carba...		Pirmor...	Full pr...

> Reference spectrum

< Fragments

Select All Deselect All

a:  1+  2+  3+  
 1+  2+  3+  
 1+  2+  3+  
 1+  2+  3+  
 1+  2+  3+  
 1+  2+  3+  
yb:   
IM:   
M[H]:

Neutral loss:

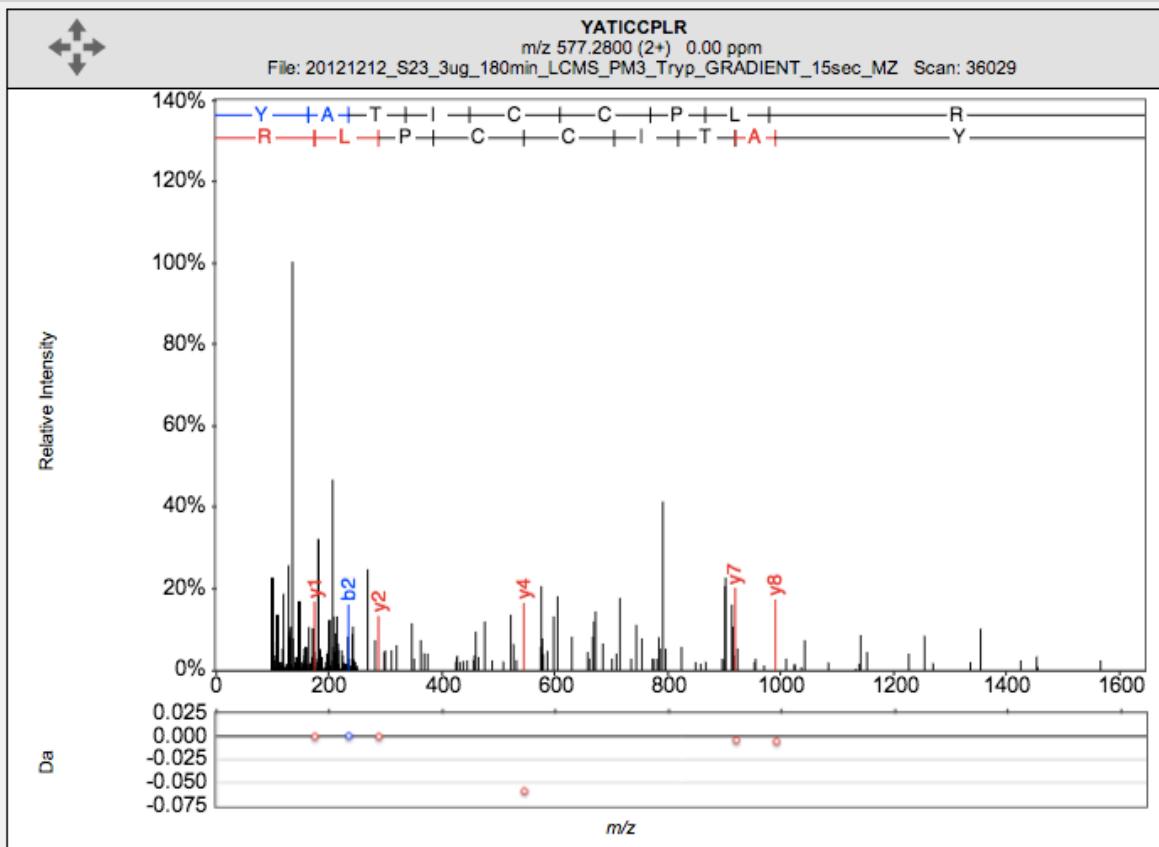
H2O  NH3  C4H6N2  
 C3H9N3  C4H8  CH2N2  
 C3H6  CO  C2H4O

Max neutral loss count: 3

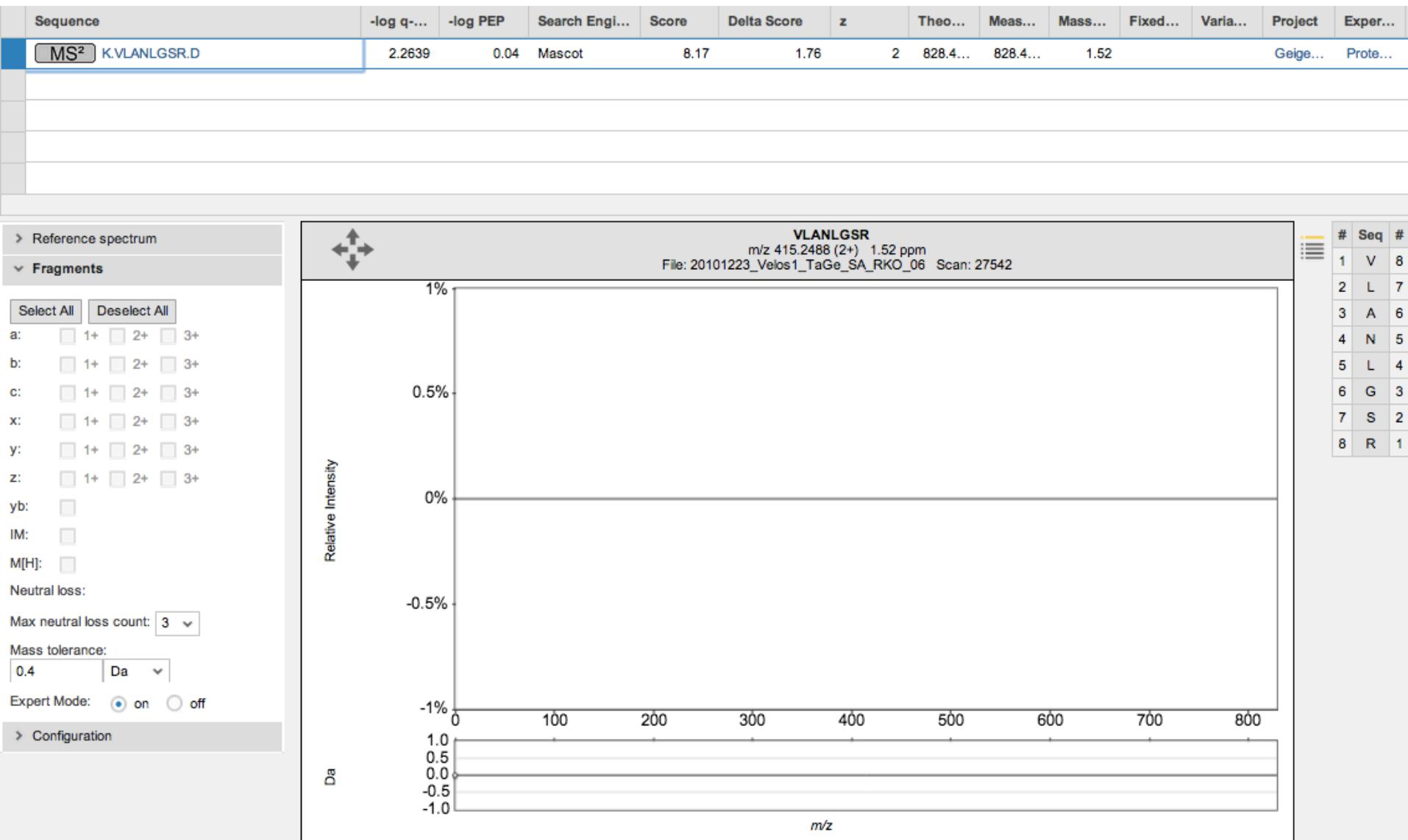
Mass tolerance:  
0.4 Da

Expert Mode:  on  off

> Configuration



b1+	#	Seq	#	y1+
164.0706	1	Y	9	
235.1077	2	A	8	990.4859
336.1554	3	T	7	919.4488
449.2395	4	I	6	818.4011
609.2701	5	C	5	705.3171
769.3008	6	C	4	545.2864
866.3535	7	P	3	385.2558
979.4376	8	L	2	288.203
	9	R	1	175.119



Sequence	-log q...	-log PEP	Search Engi...	Score	Delta Score	z	Theo...	Meas...	Mass...	Fixed...	Varia...	Project	Exper...
MS <sup>2</sup> K.RMRAVL.R.S	2.4405	1.03	Mascot	22.78	1.77	2	900.5...	900.5...	6.99			Geige...	MCF10a
MS <sup>2</sup> K.RMRAVL.R.S	2.4405	1.03	Mascot	22.78	1.77	2	900.5...	900.5...	6.99			Geige...	MCF10a
MS <sup>2</sup> K.RMRAVL.R.S	2.0027	0.02	Mascot	23.97	n/a	2	900.5...	900.5...	4.92			CPTA...	Clinic...

> Reference spectrum

< Fragments

Select All Deselect All

a:  1+  2+  3+

b:  1+  2+  3+

c:  1+  2+  3+

x:  1+  2+  3+

y:  1+  2+  3+

z:  1+  2+  3+

yb:

IM:

M[H]:

Neutral loss:

C4H6N2  C3H6S  C3H9N3

H2O  C3H6  CH2N2

C4H8  NH3  C2H4S

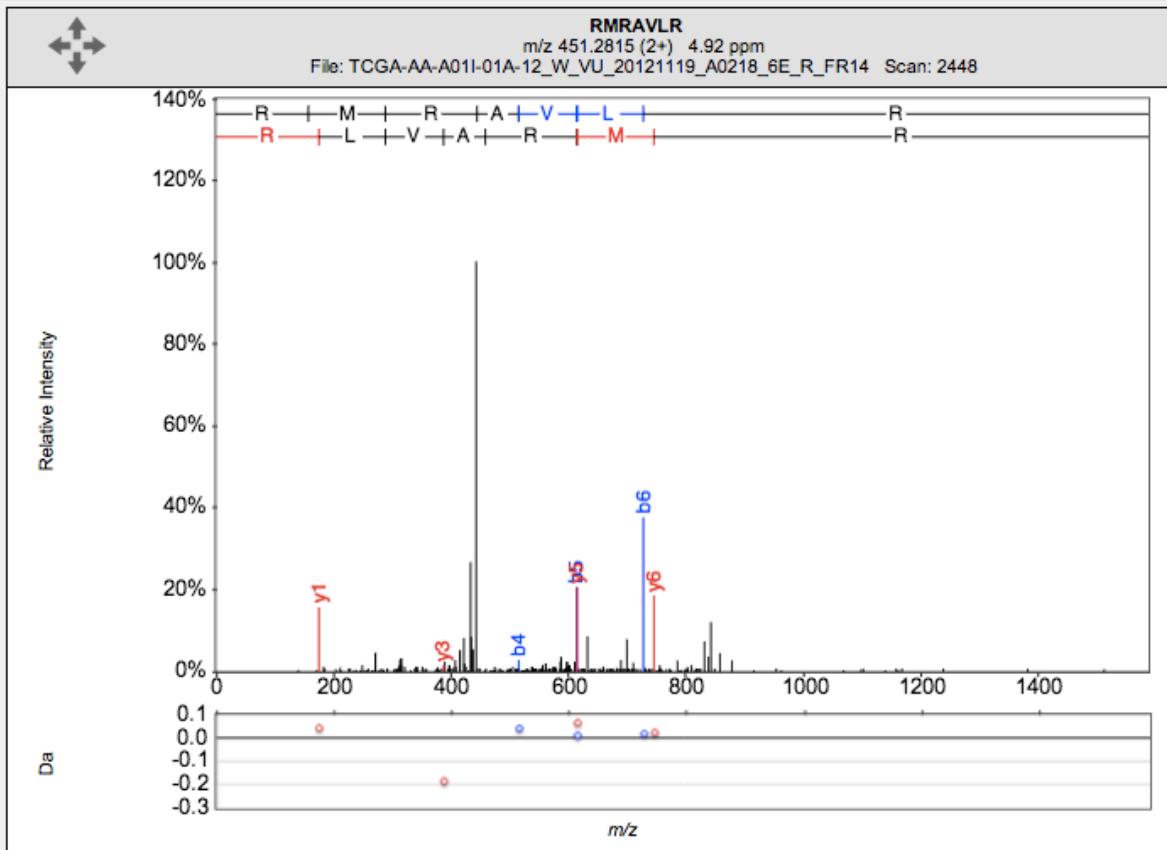
Max neutral loss count: 3

Mass tolerance:

0.4 Da

Expert Mode:  on  off

> Configuration



b1+	#	Seq	#	y1+
157.1084	1	R	7	
288.1489	2	M	6	745.4501
444.25	3	R	5	614.4097
515.2871	4	A	4	458.3085
614.3555	5	V	3	387.2714
727.4396	6	L	2	288.203
	7	R	1	175.119

Sequence	-log q...	-log PEP	Search Engi...	Score	Delta Score	z	Theo...	Meas...	Mass...	Fixed...	Varia...	Project	Exper...
MS <sup>2</sup> K.EYLEINK.I	2.9425	1.49	Andromeda	114.19	28.92	2	907.4...	907.4...	0.01			Geige...	MFM
MS <sup>2</sup> K.EYLEINK.I	2.9425	1.49	Andromeda	114.19	28.92	2	907.4...	907.4...	0.01			Geige...	MFM
MS <sup>2</sup> K.EYLEINK.I	2.3255	0.93	Andromeda	81.3	12.88	2	907.4...	907.4...	0.01			Geige...	HCC1...
MS <sup>2</sup> K.EYLEINK.I	2.3255	0.93	Andromeda	81.3	12.88	2	907.4...	907.4...	0.01			Geige...	HCC1...
MS <sup>2</sup> K.EYLEINK.I	2.2642	0.82	Andromeda	47.92	15.96	2	907.4...	907.4...	0.01			Nagar...	Deep ...

< 1 2 >

> Reference spectrum

< Fragments

Select All Deselect All

a:  1+  2+  3+  
b:  1+  2+  3+  
c:  1+  2+  3+  
x:  1+  2+  3+  
y:  1+  2+  3+  
z:  1+  2+  3+  
yb:  
IM:  
M[H]:

Neutral loss:

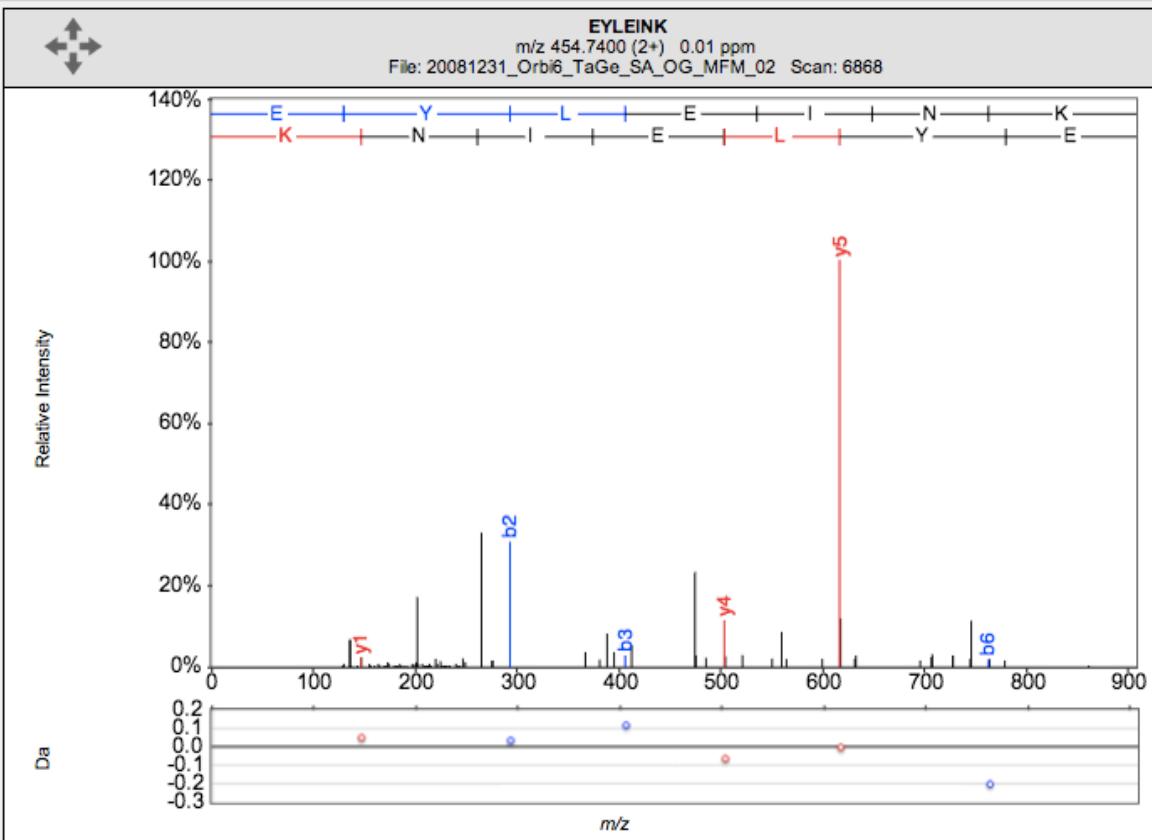
NH3  H2O  C4H11N  
 CH3NO  C2H4  C4H8  
 C2H4O2

Max neutral loss count: 3

Mass tolerance:  
0.4 Da

Expert Mode:  on  off

> Configuration



Sequence	-log q...	-log PEP	Search Engi...	Score	Delta Score	z	Theo...	Meas...	Mass...	Fixed...	Varia...	Project	Exper...
MS <sup>2</sup> R.NDTVQGVLRDVWVR.V	2.3816	2.45	Andromeda	98.9	38.35	2	1655....	1655....	0			CPTA...	Clinic...

> Reference spectrum

< Fragments

Select All   Deselect All

a:  1+  2+  3+  
 1+  2+  3+

b:  1+  2+  3+

c:  1+  2+  3+

x:  1+  2+  3+

y:  1+  2+  3+

z:  1+  2+  3+

yb:

IM:

M[H]:

Neutral loss:

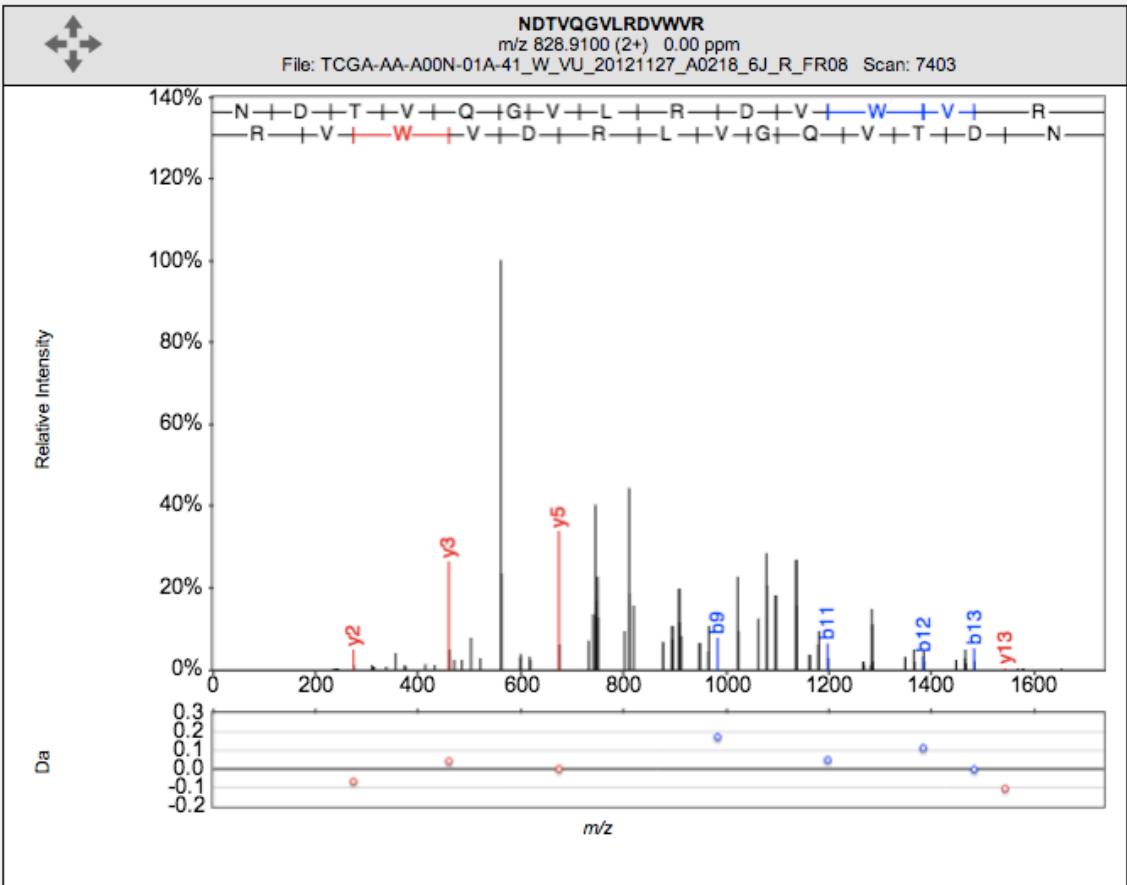
C2H5NO  CO2  C2H4O  
 C4H8  C2O  C2H4O2  
 C4H6N2  NH3  C3H5NO  
 H2O

Max neutral loss count: 3

Mass tolerance:  
0.4 Da

Expert Mode:  on  off

> Configuration



b1+	#	Seq	#	y1+
115.0502	1	N	14	
230.0771	2	D	13	1542.8387
331.1248	3	T	12	1427.8118
430.1932	4	V	11	1326.7641
558.2518	5	Q	10	1227.6957
615.2733	6	G	9	1099.6371
714.3417	7	V	8	1042.6156
827.4258	8	L	7	943.5472
983.5269	9	R	6	830.4631
1098.5538	10	D	5	674.362
1197.6222	11	V	4	559.3351
1383.7015	12	W	3	460.2667
1482.77	13	V	2	274.1874
	14	R	1	175.119